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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 28, 2005, 09:42:27; Search time 26.0601 Seconds (without alignments) 1631.912 Million cell updates/sec

US-10-622-237-2 Title:

2283 1 MASVVLPSGSQCAAAAAAA.....AIINAEGGQNNSEEKKEYFI 442 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	hypothetical prote		hemicentin precurs	poliovirus recepto	poliovirus recepto	poliovirus recepto	poliovirus recepto	Ч	PRR2 delta - human	poliovirus recepto	poliovirus recepto		neural cell adhesi	connectin/titin -	neurotrimin - rat	cell adhesion mole		elastic titin - hu	sculin	neural cell adhesi	neural cell adhesi	PRR2 alpha - human	opioid-binding pro	surface glycoprote	adhesion molecule	opioid-binding cel	cell adhesion mole	perlecan precursor	opioid-binding pro
ID	T08732	T20992	T43290	JC4024	A53437	A44194	HLMSP3	JE0099	168093	B44194	RWHUPD	RWHUPA	IJXLNL	T42633	156551	B42632	A42632	I38346	T13669	JE0100	JN0635	153960	. S03199	A45254	JH0506	JC4025	C42632	9	JC1239
03	7	8	۲N 	~	7	8	-	8	~	~	-	-	-	~	~	~	~	7	~	7	-	~	, ,	~	~	7	7	7	~
Length	407	5175	5198	518	530	417	467	725	538	392	392	417	1088	4162	344	812	932	1962	101	725	1092	478	345	288	588	345	765	4391	345
% Query Match Length	11.7	11.5	11.5	10.9	10.8	10.7	10.7	10.6	10.6	10.6	10.5	10.5	10.5	10.1	10.1	9.9	6.6	o. 0.	9.8	9.8	9.8	7.6	9.6	9.6	9.5	9.5	9.5	9.4	9.5
Score	268	263.5	263.5	248	247.5	244	244	243	242.5	241.5	240	240	239	230.5	230	226	226	225	223.5	223	223	222	218.5	218.5	217	216.5	216	214	210.5
esult No.		7	٣	4	ហ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

s-gicerin precurso	50K glycoprotein p	carcinoembryonic a	limbic-system-asso	cell surface glyco	opioid-binding pro	heparan sulfate pr	connectin 3B - chi	. differentiation an	CD22 homolog/B lym	B-cell adhesion pr	neogenin - chicken	nephrin - human	alcam - human	neural cell adhesi	duttl protein - mo
150419	JC5519	A36319	JC4776	I38049	JC1238	S18252	PN0568	I49583	A46512	JH0371	150600	T37190	139428	IJCHNL	T30805
7	~	~	~	~	~	~	~	N	~	~	N	~	~	٦	~
584	338	702	338	646	338	3707	1323	862	898	847	1443	1241	583	1091	1612
9.5	9.5	9.0	9.0	9.0	9.0	8.9	8.9	8.9	8.9	8.8	8.8	8.7	9.8	8.6	9.8
S	209	206	205.5	205.5	204.5	204	203	202.5	202.5	202	202	199.5	197	196	195.5
209			• •												

ALIGNMENTS

11-Ju	RESULT 1 Typothetical protein DKF2p566B0846.1 - human (fragment) Typothetical protein DKF2p566B0846.1 - human (fragment) Typothetical protein Baguence_revision 11-Jun-1999 #text_change 09-Jul-2004 C;Dacession: 108732 The protein Sequence Database, May 1999 The protein Database Database, May 1999 The protein Sequence Database, May 1999 The protein Sequence Database, May 1999 The protein Database Database Database, May 1999 The protein Sequence Database Database, May 1999 The protein Sequence Database Data	<pre>(fragment) m-1999 #text_change 09-Jul-2004 W.; Gassenhuber, J.; Wiemann, S. May 1999 nS0071</pre>	; Score 268; DB 2; Length 407; ; Pred. No. 1.5e-11; 60; Mismatches 123; Indels 48; Gaps 13;	120 GRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDJAVEGEEIEVNCTAMASKPAT 175	176 TIRWEKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGN 230	231 LQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTMVRVDDEMPQH 290 ::	AVLSGPNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLXVXDPPTTIPPPTT 342	TTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVVRAMLCLLI- 393 ADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFC 285
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| |||:: 286 YRRRTFRGDYFAKN 300

g

-----ILGRYFARH 402

394

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RESULT 2
T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T20992; T24733

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C;Accession: JC4024
R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubre Gene 155, 261-265, 1995
A;Title: Complementary DNA characterization and chromosomal localization of a human gene A;Reference number: JC4024; MUID:95237621; PMID:1721102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: GDB:583951
A,Map position: 11023-11624
A,Map position: 11023-11624
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Superfamily: poliovirus receptor: immunoglobulin homology
C;Keywords: glycoprotein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;1-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F;356-379/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JC4024
poliovirus receptor related protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-518 <LOP>
A;Cross_references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
                                                                                                                   A; Experimental source: clone F15G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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hemicentin precursor - Caenorhabditis elegans
C.Specias: Caenorhabditis elegans
C.Specias: Caenorhabditis elegans
C.Specias: Caenorhabditis elegans
C.Specias: Caenorhabditis elegans
C.Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 09-Jul-2004
C.Accession: T43290; T20993; T24734
R;VOGEI, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A;Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ-A;Reference number: Z22396
A;Recession: T43290
A;Retus: preliminary, translated from GB/EMBL/DDBJ
A;Ross-references: UNIPROT:076518; EMBL:AF074901; PIDN:AAC26792.1
R;Sulston, J.
Submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
A;Accession: T20993
Risulston, J.
submitted to the EMBL Data Library, December 1994
A; Reference number: Z1935
A; Accession: T20992
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-5175
A; Cross-references: UNIPROT: Q810L3; EMBL: Z47068; PIDN: CAA87335.1; GSPDB: GN00028; CESP: F1
A; Experimental source: clone F15G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Firsthaw, J.
Submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Reference number: Z19929
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rosidues: 1-5175 «WIZ>
A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A;Genetics:
A;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 KVSLTNVSISDEGRYFCQLYTDPPQESYT-TITVLVPPRNLMIDIOKD-TAVEGEEIEVN 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%; Score 263.5; DB 2; Length 5175; 24.6%; Pred. No. 8.2e-10; tive 66; Mismatches 129; Indels 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTAMASKPATTIRWFKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 24.6
Matches 87; Conservative
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A;Inčróns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1 1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-5198 <WIL>
A;Cross-references: EMBb:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
                                                                                                                                                                 Rikershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Accession: T24734
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5198 «WI2>
A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
A;Experimental source: clone T09B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 KVSLTNVSISDEGRYFCQLYTDPPQESYT-TITVLVPPRNLMIDIQKD-TAVEGEEIEVN 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 CTAMASKPATTIRWFKG------NTELKGKSEVEEWSDMYTVTSQLMLKVHK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 AIGKPQPVMVTWVRVDDEMPQHAVL----SGPNLFINNLNKTDNGTYRCEASNIVGKAHS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 VTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPL----KDSRFQLLNFSSSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2468 DFKVSMLVAPSFDEPNIVRRITVNSGNPSTLHCPAKGSPSPTITWLKDGNAIE 2520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 11.5%; Score 263.5; DB 2; Similarity 24.6%; Pred. No. 8.3e-10; 87; Conservative 66; Mismatches 129;
preliminary; translated from GB/EMBL/DDBJ
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F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted Query Match Query Match Best Local Similarity 25.4%; Pred. No. 5.38-10; Matches 105; Conservative 60; Mismatches 154; Indels 94; Gaps 20;	Db 164 IGPQSVAVARCVSTGGRPPARITWISSLGGEAKDTQEPGIQAGTVTIISRYSLVPVGRAD 223 Qy 215 GVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQWTYPLQGLTREGDALELTCEAIGKPQ 274
Qy 74 IQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPF 131 : : : :	QY 275 PVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPP 334
QY 132 QESYTIIVLVPPRNLMIDIQKD-TAVEGEEIEVNCTAMASKPATTIRWFKGNTELK 187	 Qy 335 TIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
QY 188 GKSEVEEWSDMYTVTSQLMLKVHKEDDGVPUICQVEHPAVTGNLQTQRYLE 238	RESULT 6 A44194
Qy 239 VQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSG 295	poliovirus receptor (clone AGM-alpha-1) - green monkey C;Species: Cercopithecus aethiops (green monkey, grivet) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 C;Accession: A44194
QY 296 PNLFINN-LNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTT 354	R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A. J. Virol. 66, 7059-7066, 1992 A;Title: A second gene for the African green monkey poliovirus receptor that has no puta A;Reference number: A44194; MUID:93059651; PMID:1331508
Qy 355 LTIITDSRAGEEGSIRAVDHAVIGGVVAVVPPAMLCLLIILGRYPARHKGTYFT 408 Db 346HGRRAGPVPPATIGGVAGSIIJVI-IVVGGTVVALRBRRHFFGDVST 392	A;Accession: A44194 A;Status: preliminary A;Molecule type: DNA A:Residines: 1-417 < KOI.
409HEAKGADDAADADTAIINAEGGONNSEEKKE 439 393 KKHYYGNGYSKAGIPOHHPPNAONLOYPDDSODEKKAGPLGGSSYEEEEE	A;Cross-references: UNIPROT:P32506; GB:S48777 C;Superfamily: poliovirus receptor; immunoglobulin homology C;Keywords: transmembrane protein F:559-314/Domain: immunoglobulin homology <imm></imm>
	Query Match Best Local Similarity 23.5%; Pred. No. 7.86-10; Matches 108; Conservative 70; Mismatches 192; Indels 90; Gaps 18;
poliovirus receptor mPVR - mouse C;Species: Mus musculus (house mouse) C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C;Accession: A53437	LFSAAALIPTGDGQN : TLLELSWPPPGTGDI
R;Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A. J. Biol. Chem. 269, 8431-8438, 1994 A;Title: Amino acid residues on human poliovirus receptor involved in interaction with P A;Reference number: A53437; MUID:94179228; PMID:8132569	QY 69 SDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVS1 116 56 MEETHVSQLTWSRHGESGSMAVFHQTQGPNYSEPKRLEFVAARLGTBLRDASLRMFGLRV 115
A;Accession: A54437 A;Status: preliminary A;Molecule type: mRNA	OY 117 SDEGRYPCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEV-NCTAWASK 172
A;Cross-references: UNIPROT: P32507; GB:D26107; NID:g475017; PIDN:BAA05103.1; PID:g825507 A;Experimental source: C57/BL6, brain A;Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIP:146667) C;Superfamily: poliovirus receptor; immunoglobulin homology	173 PAHITWHSDLGGMPNTSQAFGTVTSLMLKVHKEDDGVPVICQVEHESFE 173 PAHITWHSDLGGMPNTSQAFGFLSGTVTVTSLMLLVPSSQVDGKSVTCKVEHESFE
F;47-133/Domain: immunoglobulin nomology <pre>crystolery Match Query Match Best Local Similarity</pre>	QY 229 GNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMYTWVRVDDEMP 288 230 KPQLLTVNLTVYYPPEVSIS-GYDNNWYLSQNEA-TLTCDARSNPEPTGYNWSTTMGPLP 287
15 AAAAAAPPGLRIKELLILEFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQV 6	Qy 289 QHAVLSGPNLFINNLMKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPFTTTTTT 348 Db 288 PFAVAQGAQLLIRPVDKPINTTFICAVTNALGARQAELTVQVKGGPPSEPSGMSSN 343
	Qy 349 TTTILIIIDSRAGEEGSIRAVDHAVIGGVVAVVVPAMLCLLIILGRYFARHK 403
ELKVSLTNVSISDEGRYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIE : :: :	Qy 404 GTYFTHEAKGADDAADADININAEGGQNNSEEKKE 439 ' : : : :: : :: :
164 VNCTAMASKPATTIRWFKG-NTELKGKSEVEEWSDMYTVTSQLMLKVHKEDD	RESULT 7 HLMSP3

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A; Molecule type: mRNA
A; Residues: 1-725 < KUD>
A; Residues: 1-725 < KUD>
A; Cross-references: UNIPROT:073633; DDBJ:AB008162; NID:g3116226; PIDN:BAA25931.1; PID:g33
A; Experimental source: heart
C; Comment: This protein mediates and regulates various cell-cell interactions through bot
C; Superfamally: neural cell adhesion molecule; fibronectin type III repeat homology; immun
F; 413-475/Domain: immunoglobulin homology < 17Ms,
F; 512-589/Domain: fibronectin type III repeat homology < 3FR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: 168093
R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is the A;Reference number: IS3960; MUID:95347610; PMID:7622062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 KDIQVIVNVPPTIQARQLRVNATAKWAESVVLSCDADGFPDPEISWLKKGEPIEDGE-EK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 INFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 EEIEVNCTAMASKPATTIRW-----FKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 DDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POPVMVTWVRVDDEMPQH----AVLSGP---NLFINNLNKTDNGTYRCEASNIVGKAHS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRK2 delta - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 TDAGEYFCIASNP-IGVDMQAM-YFEVQYAPKIR----GPVVVYTWEGNPVNITCEVFAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 KDVTVIEGEVATISC---QVN---KSDDSVIQLLN----PNRQTIYFRDFRPLKDSRFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 PR-AAVTWFRDGQLLPSSNFSNIKIYSGPTSSSLEVNPDSENDFGNYNCTAINTIGHEFS
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                                                                                                                                                                                                                                                                                                                             Query Match
10.6%; Score 243; DB 2; Length 72
Best Local Similarity 26.5%; Pred. No. 1.9e-09;
Matches 90; Conservative 61; Mismatches 147; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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C;Superfamily: poliovirus receptor; immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTT588G 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: I68093
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Residues: 1-538 < RES>
A, Residues: 1-538 < RES>
C, Crost-references: UNIPROT: Q92692; GB: S79172; NID: C, Genetics:
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Best Local Similarity 22.6'
Matches 111; Conservative
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                      A; Accession: JE0099
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poliovirus receptor homolog precursor - mouse
C;Species: Mus musculus domesticus (western European house mouse)
C;Becies: Mus musculus domesticus (western European house mouse)
C;Becies: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A38211
J, Virol. 66, 2807-2813, 1992
A;Fitle: Molecular Cloning and expression of a murine homolog of the human poliovirus re
A;Reference number: A38211; MUID:92219365; PMID:1560525
A;Fitle: Molecular Cloning and expression of a murine homolog of the human poliovirus reseasion: A38211
A;Molecula type: DNA
A;Residues: 1-467 <MOR>
A;Cross=reference: UNIPROT:P22507; GB:M80206; NID:9199785; PIDN:AA39734.1; PID:9199786
C;Superfemily: poliovirus receptor; immunoglobulin homology
C;Keywords: duplication; glycoprotein; transmembrane protein
F;26-46/Forduct: poliovirus receptor homology #texts
F;26-46/Forduct: poliovirus receptor homology *IRM1>
F;26-334/Domain: signal sequence #status predicted <EXT>
F;26-334/Domain: immunoglobulin homology <IRM1>
F;36-334/Domain: immunoglobulin homology <IRM3>
F;36-334/Domain: inmunoglobulin homology <IRM3>
F;36-334/Domain: inmunoglobulin homology <IRM3>
F;36-4131,174-229,274-320/Disulfide bonds: #status predicted
F;36-131,174-229,274-320/Disulfide bonds: #status predicted
F;312,138,138,315/Binding site: carbohydrate (Asn) (covalent)
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JE0099

neural cell adhesion molecule 1 - African clawed frog

neural cell adhesion molecule 1 - African clawed frog

N/Alterante names: N-CAM 1
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: JE0099
C;Accession: JE0099
C;Accession: Jesyayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMS) as the in A;Title: Molecules: JE0099; MUID: 98204770; PMID: 9535795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQL-----LNFSSS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 LPPTTERVSQVTWQRLDGTVVAAFHPS----FGVDFPNSQFSKDRLSFVRARPETNADLR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELKVSLTNVSISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMIDIQKDTAVEGEEIE 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 IGPOSVAVARCVSTGGRPPARITWISSLGGEAKDTOEPGIQAGTVTIISRYSLVPVGRAD 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 TIIPPPTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVVFA--MLCLL 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QA-----DVGPLVWGAVGGTLLVLLLAGGFLALI 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V------NCTAMASKPATTIRWFKG-NTELKGKSEVEEWSDMYTVTSQLMLKVHKEDD
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Matches 101; Conservative
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g &	108 AKQSTGQDTEAELQDATLALHGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKN-QA 166 150 DIQKDTAVEGEEIEVNCTAMASKPATTIRWFKG-NTELKGKSEVEEWSDMYTVTSQLMLK 208	Qy 349 TTTTILTITDSRAGEEGSIRAVDHAVIGGVVAVVVPAMLCLLIILGRYFARHK 403 :: : : : ; Db 344
යි පි	167 BAQKVTPSQDPTTVALČISKEGRPPARISMLSSLDWBAKETQVSGTLAGTVTVTSRFTLV 226 209 VHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCE 268	RESULT 11 RWHUPD
qq		poliovirus receptor splice form delta precursor – human NiAlernate names: poliovirus receptor H20B C.Species: Home eariers (man)
중 음	269 AIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLMKTDNGTYRCEASNIVGKAHSDYML'328	C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004 C;Accession: A43024; B31496 R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Takeg
ò	YVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	EMBO J. 9, 3217-3224, 1990 A;Title: The poliovirus receptor protein is produced both as membrane-bound and secreted A;Tetle: The poliovirus NUID:91006015; PMID:2170108
a :	345 FVRETENTGGIIAAIIATA 373	A; Accession: A43024 A; Accession: A43024 A; Accession: A200 A; Access
e 6	SYKPPTPKAKLEAQEMPSQLFTLG	A;Cross_references: UNIPROT:P15151; EMBL:X64116 A;Note: 67-Ala was also found
\$ t	430 GQNNSEEKKEYF 441	KiMendelsonn, C.L.; Wimmer, E.; Kacaniello, V.K. Cell 56, 855-865, 1989 A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and expenses and expenses and expenses when the control of th
	TO WORK THE TANK THE TEND THE	A;Accession: Bludge: A30310; NULD:03100920; FNILD:2330243 A;Accession: Bludge: mRNA A;Molecule type: mRNA
RESULT 1 B44194 polioviz	10 rus receptor (clone AGM-delta-1) - green monkev	A;Reldues: 1-66,'A',68-392 <men> A;Cross-references: GB:M24406 C:Comment: The normal function of this receptor is unknown. Membrane-bound and soluble fo</men>
C;Specie C;Date:	se: Cercopithecus aethiops (green monkey, grivet) 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004	
C, Access R, Koike,	. S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.	A;Cross-references: GDB:120324; OMIM:173850 A;Map position: 1943.2-194313.2
A; Title: A; Refere	. 8 second gene for the African green monkey poliovirus receptor that has no puta ence number: A44194; MUID:93059651; PMID:1331508	A; Introns. 2.7/1; 1431; 4431; 4471; 4317; 5317 C; Superfamily: poliovirus receptor; immunoglobulin homology C; Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane prot
A;Accest A;Status A;Molecu	81On: 1844194 8: preliminary 11e type: DNA	F;1-VJ/Domain: signal sequence #starus predicted <210> F;12-392/Product: poliovirus receptor delta #status predicted <mat> F;21-343/Domain: extracellular #status predicted <ext></ext></mat>
A, Residu A, Cross- C, Superf	A;Residues: 1-392 <koi> A;Cross-references: UNIPROT:P32506; GB:S48817 C;Superfamily: poliovirus receptor; immunoglobulin homology</koi>	F;42-125/Domain: immunoglobulin homology <imm1> F;159-223/Domain: immunoglobulin homology <imm2> F;259-314/Domain: immunoglobulin homology <imm3></imm3></imm2></imm1>
Query	Query Match 10.6%; Score 241.5; DB 2; Length 392;	tted <inu> <pre>tted <inu> customic ted</inu></pre> <pre>ttus predicted</pre> <pre>ttus predicted</pre></inu>
Matches	101;	: carbonydrace (ABII)
ેં તે	13 AAAAAAAAPPGIRLELLESAAALIPTGDGONLFTKDVTV-IEGEVATISCQVNK 68	. 6
8 <i>6</i>		14 AAAAAAPGLRLRLLLLFSAAALIPTGDGONLFTKDVTVIEGEVATISC-
qq	:::: : : : : : : : : : : :	2 ARAMAAAWPILIVALIVISWPPUGTGDVVVQAPTQVPGFLGDSVTLPCY
ò	117 SDEGRYPCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEV-NCTAMASK 172	DD 51 LQVPNMEVTHVSQLTWTRHGESGSMAVFHQTQGPSYSESKRLEFVAARLGAELRNASLRM 110
6 B	116 EDEGNYTC-LEVTFPQGSRSVDIWLRVLAKPQN-TAEVQK-VQLTGKEVPVARCVSTGGR 172 173 PATTIRWFKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVT 228	Qy 116ISDEGRYPCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEBIEV-NCT 167
qq	173 PPAHITWHSDLGGMPNTSQAPGFLSGTVTVTSLWILVPSSQVDGKSVTCKVEHESFE 229	11 FOLKVEDBONILCTEVIFFORSKOVDIMLKVERN-IMBVOKT-IMBVOKT-VQLIOBEVERNOV
ð 1		168 STGGRPPAQITWHSDLGGWPNTSQVPGFLSGTVTVTSLWILVPSSQVDGKNVTCKVEHES
g (VHIOMTYPLOGLTREGDALELI
충 名	289 QHAVLSGENLEIANLANTINGIIXCEANILVOAAHSDINLIN 11 VILEETIITIITII 348 288 PPAVAQGAQLLIRPUDKPINTTFICNVTNALGARQAELTVQVKEGPPSEPSGMSSN 343	
		Qy 287 MPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTT 346

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neural cell adhesion molecule long domain form precursor - African clawed frog N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Xenopus laevis (African clawed frog)
R;Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res. 17, 10321-10335, 1989
A;Title: Primary structure and developmental expression of a large cytoplasmic domain for A;Reference number: S09600; MUID:90098871; PMID:2481269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S09600
A;Molecule type: mRNA
A;Residues: 1-1088 «KRI»
A;Crossitues: 1-1088 «KRI»
A;Crossitues: UNIPROT:P16170; EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g21461)
A;Crossitues: the authors translated the codon AAA for residue 970 as Leu
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mole
C;Comment: Several forms of NCAM are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #status predicted
(covalent) #status predicted
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                                                        227 VTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDE 286
                                                                                                                                                                                                             287 MPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 LNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 ISFNEDQSEMTIHHVEKDDEAEYSC-IANNQAGEAEATILLKVYAKPKITYVENKTÄVEL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 EEIEVNCTAMASKPATTIRW-----FKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 DEITLICEA-SGDPIPSITWRTAVRNISSEATTLDGHIVVKEHIRM----SALTLKDIQY 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 DDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 KDIQVIVNVPPTIQARQLRVNATANMAESVVLSCDADGFPDPEISWLKKGEPIEDGE-EK 257
                                                                                                                            228 FEKPOLLTVNLTVYYPPEVSIS-GYDNNWYLGONEA-TLTCDARSNPEPTGYNWSTTMGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 KDVTVIEGEVATISC---QVNKS---DDSVIQLLN----PNRQTIYFRDFRPLKDSRFQL
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                                                                                                                                                                                                                                                                                                                                                                      347 TITITITITITIDSRAGEEGSIRAVDHAVIGGVVAVVVRAMLCLLIILGRYF 399
                                                                                                                                                                                                                                                                                                                                                                                                                  SEHSGMSR---NAIIFLVLGILVF---LILLGIGIYF 365
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Best Local Similarity 26.2%
Matches 89; Conservative
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A;Cross-references: GDB:120324; OMIM:173850
A;Genee: GDB:vR; PVS
A;Cross-references: GDB:120324; OMIM:173850
A;Map position: 19413.2-19413.2
A;Map position: 19413.2-19413.2
A;Map position: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane proc;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane proc;Keywords: algoal sequence #status predicted <81G>F:21-417/Product: poliovirus receptor alpha #status predicted <PVRA>F:21-339;385-417/Product: poliovirus receptor beta #status predicted <PVRB>F:21-319;385-417/Product: poliovirus receptor beta #status predicted <PVRB>F:21-3125/Domain: immunoglobulin homology <!MMI>F:42-125/Domain: immunoglobulin homology
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A;Residues: 1-66,'A',68-417 <MEN>
A;Cross-references: GB:M29535
C;Comment: The normal function of this receptor is unknown. Wembrane-bound and soluble
                                                    334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QVNKSDDSVIQLLNPNR-----QTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVS--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 ----ISDEGRYFCQLYTDPPQESYTT---ITVLVPPRNLMIDIQKDTAVEGEEIEV-NCT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 FGLRVEDEGNÝTC-LFVTFPQGSRSVDIWLRVLAKPON-TAEVOK-VOLTGEPVPMARCV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 AMASKPATTIRWFKGNTELKGKSEVEEW-SDMYTVTSQLMLKVHKEDDGVPVICQVEHPA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTV-----IEGEVATISC- 64
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                                                                                                                        347 TTTTTTTTTTTTTTTGBEGSIRAVDHAVIGGVVAVVFAMLCLLILGRYF
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7:368-41/70main: intracellular #status predicted <INT>
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn)
Query Match 10.5%; Score 240; DB 1; Length 417; Best Local Similarity 25.9%; Pred. No. 1.5e-09; Matches 107; Conservative 54; Mismatches 176; Indels '
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F;259-314/Domain: immunoglobulin homology <IMM3>
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14

Gaps

46;

DB 2; Length 344;

-----VTVNYPPYIS-----EAKGTGVP 234

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C; Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
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                                                                                                                                                                                                                                                                                                                                                                                                              YFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTD-PPQESYTTITVLVP 143
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                                                                                                                                                                                                                                                                                                 29 ILLLFSAAALIPTGDGQNLFTK---DVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTI-
                                                                               Query Match
10.1%; Score 230; DB 2; Length 34
Best Local Similarity 26.2%; Pred. No. 6e-09;
Matches 84; Conservative 53; Mismatches 137; Indels
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C;Species: Gallus gallus (chicken)
C;Species: Julan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42633
R;Yajima, H.; Ohteuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; Ma Biochem. Biophys. Res. Commun. 223, 160-164, 1996
A;Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin re A;Reference number: Z22221; MUID:96254045; PMID:8660363
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A. Neurosci. 15, 2141-2156, 1995
A. Title: Cloning of neurotrimin defines a new subfamily of differentially expressed neurally A;Reference number: 156551; MUID:95198094; PMID:7891157
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                                                                                                                             -OESYTTITYLVPPRNLMIDIQXDTAVE---GEEIEVNCTAMASKPATTIRWFKGNTELK 187
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    372 TDAGEYFCIASNP-IGVDMQAM-YFEVQYAPKIR----GPVVVYTWEGNPVNITCEVFAH 425
                                                                           POPVMVTWVRVDDEMPQH----AVLSGP---NLFINNLNKTDNGTYRCEASNIVGKAHS 324
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C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 156551
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                                                                                                                                                                                                                                           DYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTT
                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-4162 cYAJ>
A;Cross-references: UNIRROT:Q98918; EMBL:D83390; NII
A;Experimental source: breast muscle
C;Keywords: skeletal muscle
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A;Molecule type: mRNA
A;Residues: 1-344 <RES>
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Best Local Similarity 23.99
Matches 86; Conservative
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Q658Q7 Q6MZK6 Q6NUR8 Q6NUR8 Q9NVJ5 Q9D006 Q9D006 Q9DLB9 Q9ULB9 Q9ILB9 Q9ILB9 Q9ILB9 Q9ILB9

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1 MASVVLPSGSQCAAAAAAAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.9%; Score 2280; DB 2; Length 442; Best Local Similarity 99.8%; Pred. No. 2.1e-154; Matches 441; Conservative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.

Zhou Y., Du G., Chen J., Yuan J., Qiang B.;

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, ART132811, AAR65029.1; -.

InterPro; IPR003598; Ig.c2.

InterPro; IPR003585; Neurexin-like.

Fam, PP00047; ig; 2.

SMART; SM00294; 4.1m; 1.

SMART; SM00408; IG.2.

SMART; SP00848; IG. Like; 3.

SCOUENCE 442 AA; 48537 MM; 68183B3238735062 CRC64;
                                                                                                                                                                                                                      01-UUN-2001 (TrEMBLrel. 1.
01-UUN-2001 (TrEMBLrel. 1.
01-OCT-2003 (TrEMBLrel. 2.
Nectin-1ike protein 2.
Name=NBCL2;
PRELIMINARY;
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331.6
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1 MASVVLPSGSQCAAAAAAA .....AIINAEGGQNNSEEKKEYFI
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Q8r5m8
         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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                       361 ITDSRAGEEGTIGAVDHAVIGGVVAVVVPAMLCLLIILGRYFARHKGTYFTHEAKGADDA
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                                                                                  358 ITDSRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL;
MEDLINE=22192378; PubMed=12202822; DOI=10.1126/science.1072356;
Biederer I., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "SynCAM, a Synaptic Adhesion Molecule That Drives Synapse Assembly."; Science 297:1525-1531(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujita E., Alikawa K., Momoi T.;

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AFS39424; AAN01614.1; -..

EMBL; AB18339272; Igsf4a.

R GO; GO:0016021; C:integral to membrane; TAS.

R GO; GO:00056215; C:synaptic vesicle; IDA.

R GO; GO:0005515; P:rotein binding; IPI.

R GO; GO:0007155; P:rotein binding; IPI.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:0007165; P:cell adhesion; IDA.

R GO; GO:000716; P:synaptcgenesis; IDA.

R InterPro; IPR003598; Neurexin-like.

R InterPro; IPR003598; Neurexin-like.

R SWART; SW00294; 4.1m; 1.

R SWART; SW00294; 1.022; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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97.8%; Score 2232.5; DB 2; Length 445;
Best Local Similarity 97.5%; Pred. No. 5.2e-151;
Matches 434; Conservative 2; Mismatches 6; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;
                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Synaptic cell adhesion molecule 1 (RA175 isoform c)
Name=1gst4a; Synonyme=RA175;
                                                                                                                                                                                                                                                                                                              445 AA.
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CETRAIN-129/Svd:

MEDLINE-22256620; PubMed=12242005; DOI=10.1016/S0378-1119(02)00835-1;

MEDLINE-22256620; PubMed=12242005; DOI=10.1016/S0378-1119(02)00835-1;

Rukami T., Satch H., Fujita B., Maruyama T., Fukuhara H.,

Kuramcofii M., Takamcho S., Momio T., Murakami Y.;

"Identification of the Talci gene, a mouse orthologue of the human turn suppressor TSLCI gene.";

Gene 25:7-12(2002).

EMBL; AF434663; AAL86736.1; -.

RMOD; MG:1889272; Igsfau to membrane; TAS.

RO; GO:0016231; C:integral to membrane; TAS.

RO; GO:0016231; C:integral to membrane; TAS.

RO; GO:001515; F:protein binding; IPI.

RO; GO:0000715; P:protein binding; IPI.

RO; GO:000715; P:protein binding; IPI.

RO; GO:000715; P:protein binding; IPI.

RO; GO:000715; P:protein binding; IDA.

RO; GO:000715; P:protein binding; IDA.

RO; GO:000715; P:protein binding; IDA.

RITE-Pro; IPR003589; Reurexin-like.

RITHE-Pro; IPR003589; Neurexin-like.

ROMENT; SMOGO294; 4.1m; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor suprressor in lung cancer 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.2%; Score 2241.5; DB 2
98.0%; Pred. No. 1.2e-151;
iive 1; Mismatches 5;
                                                                                DTAIINAEGGNNSEEKKEYFI 442
                                                                                                   SM00294; 4.1m; 1.
SM00408; IGC2; 1.
E; PS50835; IG LIKE; 3.
CE 445 AA; 48664 MW;
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nes 436; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                    Name=Igsf4a;
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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PROSITE; I
SEQUENCE
                                                                                421
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361 IIDTTATTEPAVHDSRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTY 420
241 EVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPN
                                                                      RWFKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYL
                                                                                                                                                                   EVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPN
                                                                                                                                                                                                                                                                                                                                                           IT-----DSRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTY
                                                                                                                                                                                                                                                              LFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rāttus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC078966; AAH78966.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003598; Ig.
Ffam; PF00047; ig; 3.
SWART; SM00409; IG; 3.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTHEAKGANDAADADTAIINAEGGQNNSEEKKEYFI 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                   407 FTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
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Repolement E., Res. 287:57-66(2003).

Repolement E., Soyama E., Fujita E.,
                                              360
                                                                                                                                                                                                                                                                                                       ITDSRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDA 417
                                                                                                                                                                                                                                                                                                                                  RWFKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYL 237
                                                                                                                BVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPN 297
                                                                                                                                                                                                          LFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTLTI 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 EVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSIS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
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                                                                                                                                                                                                                                     1 MASVVLPSGSQCAAA---AAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEG
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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SMART; SM04081; IG-21.
PROSITE; PS5083; IG LIKE; 3.
SEQUENCE 456 AA; 49787 MW; 3226E866A4BCIC7F CRC64;
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Last annotation update)
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Pred. No. 3.6e-150;
2; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel, 21, 01-JUN-2002 (TrEMBLrel, 21, 01-OCT-2003 (TrEMBLrel, 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.3
Best Local Similarity 95.4
Matches 435; Conservative
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QBR5MB;
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240
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                                                                                                        61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRPQLLNFSSSELKVSLTNVSISDEG 120
                                                                                                                                                       121 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
                                                                                                                                                                                                                                                                                          241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
                                                                                                                                                                                                                                                                                                            241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLF1 300
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                                                                                                                                                                                                                                                                                                                                                            NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTT 359
                                      1 MASVVLPSGSQCAAAAAAAAAPGLRLRILILLFSAAALIPTGDGQNLFTKDVTVIEGEVA 60
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                                                                                                                                                                                                                                                                                                                                                                                 301 NNIAKTDNGTYRCEASNIVGKAHSDYMLYVYDTTATTEPAVHGLTQLPNSAEELDSEDLS
                     MASVVLPSGSQCAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTV1EGEVA
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fulita E., Aikawa K., Momoi T.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB183400; BAD30019.1; -
EMBL; AD1801021; C:integral to membrane; TAS.
GO; GO:0045202; C:synapse; IDA.
GO; GO:000511; C:synaptic vesicle; IDA.
GO; GO:000511; F:protein binding; IPI.
GO; GO:00155; P:callum-independent cell-cell adhesion; IDA.
GO; GO:0007155; P:call adhesion; IDA.
GO; GO:0007416; P:synaptogenesis; IDA.
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91.7%; Score 2093; DB 2; Length 428;
Best Local Similarity 92.6%; Pred. No. 4.5e-141;
Matches 412; Conservative 2; Mismatches 11; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.2.
Pfam; PR00409; IG; 3.
SMART; SM00409; IGc2; 3.
SMART; SM05089; IGC2; 3.
SMART; SM05089; IGC2; 3.
SMOSTTE; PSS0835; IG LIKE; 3.
SEQUENCE 428 AA; 46903 MW; BIODFF1A2B893573 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSIS 120
                                                                                                                                                                                                                                                                                                                                                                                                               LFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPP--TTTTTTTTTTTL 355
                                                                                                                                                                                       EVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSIS 117
                                                                                                                                                                                                                                                         DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTI 177
                                                                                                                                                                                                                                                                                                                          RWFKGNTELKGKSEVBEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --------BSRAGEEGSIRAVDHAVIGGVVAVVF 386
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                                                                                                                                         DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTI
                                                                                                                    1 MASVVLPSGSQCAAA---AAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEG
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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TISSUE=Whole embryo;
Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii
Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
Nagahari K., Sugano S., Isogai T.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AK075502;
EMBL, AK075502;
                                                                                    34;
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                                                                                    8; Indels
                                                     Length
Hypothetical protein.
SEQUENCE 476 AA; 51853 MW; 486A43D37082C8FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50835; IG LIKE; 3. 443 AA; 48648 MW; 046B43AA156F6F64 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PSEC0200.
Homo sapiens (Human).
                                                 Score 2186; DB 2;
Pred. No. 1.2e-147;
1; Mismatches 8;
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InterPro; IPR003598; 19_C2.
InterPro; IPR003585; Neurexin-like.
                                                 95.8%;
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SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGc2; 1.
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                                                                   Best Local Similarity 91.0
Matches 433; Conservative
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SEQUENCE
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SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 417 AA; 45779 MW; 98500180D37845C2 CRC64;
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                                                                                                                                DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVGGEEIEVNCTAMASKPATTI 180
                                                                                                                                                                                                                                                           EVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPN 300
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                                               EVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSIS 117
                                                                                                                                                                           RWFKGNTELKGKSEVBEWSDMYTVTSQLMLKVHKEDDGVPVICQVBHPAVTGNLQTQRYL 237
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                                                                                                                                                                                                                                                                                                                                       ----- 343
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Brain;
MEDLINE-22841094; PubMed=12826663; DOI=10.1074/jbc.M305387200;
MEDLINE-22841094; PubMed=12826663; DOI=10.1074/jbc.M305387200;
Shingal T., Ikeda W., Kakunaga S., Morimoto K., Takekuni K., Itoh Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
Implications of nectin-like molecule-
2/IGSF4/RA175/SGIGSF/TSLC1/SynCAM1 in cell-cell adhesion and transmembrane protein localization in epithelial cells.";
J. Biol. Chem. 278:35421-35427(2003).
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Pujita E., Aikawa K., Momoi T.;

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; A351388; AAQ02381.1; -

R EMBL; AB183401; EAD30020.1; -

R GO; GO:0016021; C:integral to membrane; TAS.

R GO; GO:0045202; C:synapse; IDA.

R GO; GO:0005021; F:protein binding; IPI.

R GO; GO:0007155; F:protein binding; IPI.

R GO; GO:0007155; P:call adhesion; IDA.

R GO; GO:0007155; P:call adhesion; IDA.

R InterPro; IPR00710; Ig-like.

R InterPro; IPR003598; Ig-c2.

R InterPro; IPR003598; Ig-c2.

R Pfam; PR00047; ig; 2.

SMART; SM00294; 4.1m; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-071-2003 (TrEMBLrel. 25, Created)
01-071-2003 (TrEMBLrel. 25, Last sequence update)
25-071-2004 (TrEMBLrel. 28, Last annotation update)
Nectin-like molecule 2 (RAI75 isoform d).
                                                                                                                                                                                                                                                                                                                        417 AA
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01-OCT-2003 (
01-OCT-2003 (
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                                                                                                        1 MASVVLPSGSQCAAA---AAAAAPPGLRLKLLLLLFSAAALIPTGDGQNLFTKDVTVIEG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                      5; Indels
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB094146; BAC66179.1; -.
InterPro; IPR00710; Ig-11ke.
InterPro; IPR003598; Ig_c2.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Secretory isoform of TSLC-1.
Query Match
90.7%; Score 2071.5; DB 2
Best Local Similarity 91.7%; Pred. No. 1.5e-139;
Matches 408; Conservative 1; Mismatches 5;
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237 240

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EVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPN 297
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                                               181 RWFKGNKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYL
                        DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTI
                                                                                                                       RWFKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J; TISSUE=Hippocampus; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900073606 product:immunoglobulin superfamily, member 4, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibbta K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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STRAIN=C57BL/6J; TISSUE=Hippocampus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
MIKEN FANTOM CONSORTIUM;
"FUNCTIONAL ANDOCATION Of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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STRAIN-C57BL/6J; TISSUE-Hippocampus;
The FANTOM Consortium,
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                        118
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MASVVLPSGSQCAAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA 60
                                                                   1 MASAVLPSGSQCAAAAAAAAPPGLKLKLLLLLLLAAAALIPTGDGQNLFTKDVTVIEG
                                                                                                                                           RYFCQLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWF
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0008021; C:synappei; DA.

GO; GO:0008021; C:synappei; DA.

GO; GO:0016338; P:calcium-independent cell-cell adhesion;

GO; GO:0001538; P:calcium-independent cell-cell adhesion;

GO; GO:000116; P:synaptogenesis; IDA.

InterPro; IPRO07110; Ig-like.

PFO0047; IQ; 2.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AB1092414; BAC66173.1; -.
EMBL, AB108402; BAD30021.1; -.
MGD; MGI:1889272; Igsffaa.
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STRAIN=C57BL/6; TISSUE=Spleen cell-derived;
Ito A., Koma Y., Nagano T.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
02-CT-2004 (TrEMBLrel. 28, Last annotation update)
A secretion form of SgIGSF/TSLCI (RALTS isoform e).
Name=Igsfas, Synonyms=RA175, sSgIGSF/STSLC1;
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Pred. No. 5.6e-112;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                               NNLNKTDNGTYRCEASNIVGKAHSDYMLYVY 331
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3; PSS0835, IG LIKE, 3.
E 336 AA, 37155 MW,
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Best Local Similarity 97.9
Matches 327; Conservative
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PROSITE; I
SEQUENCE
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RA Adachi J., Alzawa K., Akahire S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Arakawa T., Hara A., Hayatsu N., Hiraoka T., Kato H.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Sano H., Sasaki D., Shibata W., Shibata Y., Shinaqawa A., Shiraki T.,
RA Sano H., Sasaki D., Shibata W., Shibata Y., Shinaqawa A., Shiraki T.,
RA Sano H., Sasaki D., Shibata W., Shibata Y., Shinaqawa A., Shiraki T.,
RA Sano H., Sasaki D., Shibata W., Hayashizaki Y.,
R. Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RADI, MGI: 1889272; Igsfa.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
ROJ GO:0016021; C:synapsci Losinapsci IDA.
GO; GO:0016338; P:call adhesion; IDA.
GO; GO:0007155; P:call adhesion; IDA.
RICEPIO: IPR00110; Ig-like.
RICEPIO: IPR00110; Ig-like.
RIMERIP ROJ INGO 110; Ig-like.
RIMERIP ROJ INGO 110; Ig-like.
RIMERIP ROJ 110; Ig-like.
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Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1671.5; DB 2; Length 336;
Pred. No. 4e-111;
0; Mismatches 6; Indels 3;
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SEQUENCE 336 AA; 37157 MW; FF887FAF4EFDF120 CRC64;
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STRAIN=C57BL/6J; TISSUE=Hippocampus;
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(TrEMBLrel. 10, 1
(TrEMBLrel. 25, 1
protein 2.
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Matches 325, Conservative
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01-MAY-1999 (
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ID Q922H
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DT 01-MA
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Last sequence update) Last annotation update)

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**MEDLINE=226813149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8; MEDLINE=226813149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8; Fujite E., Soyama A., Momoi T.; "RAI75, which is the mouse ortholog of TSLC1, a tumor suppressor gene in human lung cancer, is a cell adhesion molecule."; Exp. Cell Res. 287:57-66(2003).

Exp. Cell Res. 287:57-66(2003).

EMBL; AB021966; BAA87916.1; -.
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                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                       R MGD; MGI:1889272; Iggfa.

R MGD; MGI:1889272; Iggfa.

R GO; GO:0016021; C:integral to membrane; TAS.

R GO; GO:00045202; C:syrapse; IDA.

R GO; GO:0008021; C:syrapse; IDA.

R GO; GO:0001515; F:protein binding; IPI.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:0007156; P:cell adhesion; IDA.

R GO; GO:0007116; P:syraptcgenesis; IDA.

R InterPro; IPR007110; Ig-like.

R InterPro; IRR003589; Ig-c2.

R InterPro; IRR003589; Neurexin-like.

R SWART; SW00294; 4.1m; 1.

R SWART; SW00408; IGC2; I.

R PROSITE; PSSG0835; IG LIKE; 2.

C SEQUENCE 295 AA; 32509 MW; 9DE9D86F6FF6F488 CRC64;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                  Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF061260; AAC67243.1; -
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Last annotation update)
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98.6%; Pred. No. 8.2e-101;
ilve 1; Mismatches 3;
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Name=Igsfa; Synonyms=ra175c;
Mus musculus (Mouse)
Name=Igsf4a; Synonyms=Necl2;
Mus musculus (Mouse).
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Best Local Similarity 98.6'
Matches 291; Conservative
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SEQUENCE FROM N.A.
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Gaps

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181 LYVYDPPTTIPPPTTTTTTTTTTTTTBAVHDSRAGEEGTIGAVDHAVIGGVVAVVVFA 240
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                    Length 295;
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                                                                                                       Pfan: PF00047; 1g; 1.
SMART; SM00294; 4.1m; 1.
SMART; SM00409; IGC2; 1.
PROSITE; PS50035; IG LIKE; 2.
SEQUENCE 295 AA; 32347 NW; FDD9E8145C6B971B CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adhesion protein RA175B.
                                                                                                                                                                                                                                    Query Match 65.0%; Score 1483; DB 2;
Best Local Similarity 95.9%; Pred. No. 9.7e-98;
Matches 283; Conservative 3; Mismatches 9;
        GO; GO:0007155; P:cell adhesion; IDA.
GO; GO:0007416; P:synaptogenesis; IDA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-2.
InterPro; IPR003585; Neurexin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Igsf4a; Synonyms=ra175b;
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
R MGD; MGI:1889272; Igsf4a.

R GO; GO:0016021; C:integral to membrane; TAS.

R GO; GO:00045202; C:synapse; IDA.

R GO; GO:0008512; C:synapse; IDA.

R GO; GO:0005515; F:protein binding; IPI.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:000716; P:synapcogenesis; IDA.

R GO; GO:000716; P:synapcogenesis; IDA.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003589; Ig-c2.

R InterPro; IRR003589; Neurexin-like.

R SMART; SN00294; 4.1m; 1.

R SMART; SN00409; IGC2; 1.

R PROSITE; PSS6035; IGC2; 1.

R PROSITE; PSS6035; IGC2; 1.

R SRART; SN00408; IGC2; 1.

R SRART; SN00408; IGC2; 1.
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Name=Igsf4a; Synonyms=ra175a;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 306;
                                                                                                                                                                                                                                                                                                                                                         Score 1503.5; DB 2; Length
Pred. No. 3.5e-99;
2; Mismatches 3; Indels
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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KKEYFI 306
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Gaps
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Query Match 61.1%; Score 1394; DB 2; Length 289; Best Local Similarity 91.9%; Pred. No. 2.1e-91; Matches 271; Conservative 3; Mismatches 15; Indels
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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2283 1 MASVVLPSGSQCAAAAAAA.....AIINAEGGQNNSEEKKEYFI 442 2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-622-237-2 Scoring table: Perfect score: Sequence: Searched: Title:

2105692 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:* A_Geneseq_16Dec04:* geneseqp2004s:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Match Length	먑	8	ar TD	Description
100.0 44	42	m	AAB25619	Aab25619 Protein
100.0 442	N	<u>س</u>	AAY94341	Aay94341 Human cel
	2	<u>س</u>	AAY45092	Aay45092 Human lym
100.0 442	N	'n	AAE19887	Human
100.0 442	N	S	ABP62825	Abp62825 Human pol
100.0 442	\sim	9	ADA27144	Human
100.0 442			ADE54238	Human 8
100.0 442			ADE86685	Novel
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σ.		7	ADE61608	Human 8
99.1 440		7	AAY17830	Aay17830 Human PRO
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		4	AAU29040	Human
۲.		9	ABU58416	Human
		9	ABU87964	Abu87964 Novel hum
9.1		9	ABU84279	Abu84279 Human sec
_	\sim	9	ABR66153	Abr66153 Human sec
_		9	ABR65543	Abr65543 Human sec
99.1 440		9	ABU99483	Abu99483 Human sec
1 44	0	9	ABU55930	Abu55930 Human sec
99.1 440	0	9	ABU82722	Abu82722 Human PRO
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99.1 44	0	9	ABR68092	Abr68092 Human sec

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Abu96145	Abu92576	Abo08653	Abo02705	Abr74859	Abr94621	Abu60240	Abu85594	Abu98754	Apu97969	Abu91675	Abu89368	Abu86209	Abu67422	Abu80450	Abr99368	Abr98758	Abo16281	Abr92181	Abo18822
ABU96145	ABU92576	AB008653	AB002705	ABR74859	ABR94621	ABU60240	ABU85594	ABU98754	ABU97969	ABU91675	ABU89368	ABU86209	ABU67422	ABU80450	ABR99368	ABR98758	AB016281 ·	ABR92181	ABO18822
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99.1	99.1	99.1	99.1	99.1	99.1	99.1	1.66	99.1	99.1	1.66	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1
	63	263	2263	2263	2263	2263	2263	2263	2263	2263	2263	2263	2263	2263	2263	2263	2263	2263	2263
2263	52	(A																	

ALIGNMENTS

Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatits; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; crohn's disorder; inflammatory disorder; cardiovascular disorder; coronry arteriosclerosis; myocarditis; meanoma; lymphoma; wound healing; human. Protein encoded by human secreted protein gene #11. AAB25619 standard; protein; 442 AA. (first entry) 21-NOV-2000 AAB25619; RESULT 1 AAB25619

99WO-US025031. WO200029435-A1 Homo sapiens. 27-OCT-1999; 25-MAY-2000.

98US-0105971P. (HUMA-) HUMAN GENOME SCI INC 28-OCT-1998;

Wei Kenny JJ, Moore PA, Ni J, Ruben SM, Olsen HS, Young PE, Greene JM;

WPI; 2000-387742/33.

Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases.

Disclosure; Page 182-183; 803pp; English.

The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAAB06066-AB0623 encode the 12 secreted protein sequences given in AAB35576-B25533. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the

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Location/Qualifiers
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08-MAR-1999;
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   action the control of the control of the control of actions and actions and antiarthitic; antitheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; and antifungal activity. The proteins, polypeptides, agonists and conditions examples of which include: immune disorders e.g. disorders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatory disorders e.g. inflammatory bowel disorders e.g. crohn's disease and nephritis; hyperproliferative disorders such as paraproteinsemias and purpura; cardiovascular disorders e.g. coronary carteriosclerosis and myocardiis; cancer e.g. melanoma and lymphoma. The proteins and polymucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene control of infectious diseases. The human secreted protein gene control of the control of the
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activities of the proteins include: immunosuppressant; anti-inflammatory;
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New human cell surface receptor protein and polynucleotide useful for diagnosis, prevention and treatment of cancer, immune disorders, infection and neuronal disorders.
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J, Azimzai Y, Au-Young
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//label= Immunoglobulin domain
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1. .44
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Matches 442; Conservative
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                     The present sequence is a novel human cell surface receptor protein (HCSRP) designated HCSRP-8. The nucleotide sequence was identified in Incyte Clone 31226 from the CDNA library LUNGNOTO2, which was made from RNA isolated from Lung tissue. A number of Incyte Clones were used to assemble the consensus sequence. BLAST analysis showed that the sequence is homologous to immuno-superfamily protein B12 g3779242. HCSRP and its antagonist are useful for preventing or treating disorders associated with decreased or increased expression or activity of HCSRP. Such disorders include cancers such as leukaemia and melanoma, immune disorders such as rheumatoid arthritis, asthma and atherosclerosis, bacterial and parasitic infections and neuronal disorders such as betthesia. Alzheimer's disease, multiple sclerosis and espilepsy. Polymucleotides encoding HSCRP may be used as hybridisation probes to diagnose these conditions. Anti-HCSRP antibodies may be used as
                                                                                                                                                                                                     antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into contact with cells or tissues expressing HCSRs and for diagnosis of HCSRP-related disorders. HCSRP and its catalytic or immunogenic fragments are useful for drug screening using libraries of
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B7-L1; T cell proliferation; natural killer cell; NK; tumour cell;
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0
                                                                                                                                                                                                                                                                                                          100.0%; Score 2283; DB 3; Length 442; 100.0%; Pred. No. 8.3e-158; ive 0; Mismatches 0; Indels 0
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Claim 1; Page 81-82; 97pp; English
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The present amino acid sequence is the human lymphoid derived dendritic cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic cells and displays homology to adhesion molecules, B-1 and cytoplasmic region of BP-Li. Human LDCAM is expressed in breast, retina, feetal liver, spleen and heart, lung, muscle, placenta, thyroid and lung carcinoma. LDCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and as quality control reagents of LDCAM binding proteins abording spatemic LDCAM may be used for treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for prevention or reducing the effect of congan and bone marrow transplant rejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or
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biological activity, quality control reagent; treatment; inflammation; immune system disorder; autoimmune; viral infection; infectious disease; organ transplant rejection; bone marrow; modulator; immune response.
                                                                                                                                                                                                                                                                                                      39. .442
/label= Mature_human_LDCAM_polypeptide
57. .69
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/note= "N-Glycosylation site"
165. .167
/note= "N-Glycosylation site"
304. .306
/note= "N-Glycosylation site"
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375. .395
/label= Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                       "N-Glycosylation site"
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/label= Extracellular domain
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/label= Cytoplasmic_domain
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'label= Leader_peptide
                                                                                                                                                                                         Location/Qualifiers
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N-PSDB; AAZ50882.
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Length 442; Indels

100.0%; Score 2283; DB 3; 100.0%; Pred. No. 8.3e-158; iive 0; Mismatches 0;

Similarity

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Gaps

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subject. The method comprising contacting a cell component of a proliferating cell with a reagent that detects level of the cell component in the proliferating cell and determining modification in the level of the cell component in proliferating cell as compared with a healthy cell, where modification indicates disorder associated with TSLC1. The method is useful for detecting a cell proliferative disorder (e.g. liver, lung or pancreatic cancer) associated with tumour suppressor lung cancer i (TSLC1) in a subject. The invention is useful in gene therapy and for treating a cell proliferative disorder such as lung cancer funan non-small cell lung cancer), liver cancer (hepatocaellular carcinoma) or pancreatic cancer associated with modification of TSLC1 production, where a reagent which modulates (preferably, increases) TSLC1 level in the cells, is employed. The present sequence is human TSLC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antidiabetic; antiallergic; gene therapy; wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
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                                                                                                                                                                                                                                               Length 442;
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                                                                                                                                                                                                                                            Query Match 100.0%; Score 2283; DB 5; Best Local Similarity 100.0%; Pred. No. 8.3e-158; Matches 442; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1; lung; pancreatic cancer; cell proliferative disorder; cytostatic;
                                    TISCQVNKSDDSVIQLINPNRQTIYFRDFRPLKDSRFQLINFSSSELKVSLTNVSISDEG
                                                                                           TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
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(I), (II) and (III) are useful for diagnostic evaluation of disorders.

(I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
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                                                                                                                                                                                                                                 New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzhaimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
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                                                                                                                                  Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang D, Liu C, Drmanac RT, Wehrman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 2283; DB 5;
100.0%; Pred. No. 8.3e-158;
tive 0; Mismatches 0;
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                                          31-AUG-2001; 2001WO-US027093
                                                                         01-SEP-2000; 2000US-00654935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
                                                                                                                                                                                     2002-583321/62.
                                                                                                        (HYSE-) HYSEQ INC
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                                                                                                                                    Tang YT,
Zhao QA,
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The invention relates to an isolated nucleic molecule that is at least 55% identical to 18 human cDNA sequences representing 12 novel genes encoding secreted proteins or a polymucleotide fragment of the CDNA sequence contained in American Type Culture Collection (ATCC) deposit No. defined in the specification, its species homologue, a variant or allelic variant of the polymucleotide having a polymuclacotide capable of hybridising under conditions the polymuclacotide. Where the polymucleotide having a nucleotide sequence of only A or T readiluse. Also included are recombinant vectors, host cells (for producing the polypeptide), the secreted polypeptide (comprising a sequence that is at least 95% cannot allelic variant or specifically an allelic variant or specifically bind to the polypeptides diagnosing, treating, preventing or ameliorating a medical condition by administering the polypeptide or the polypeptide or ameliorating an activity in a biological assay (by expressing the CDNA sequence and dentifying an activity in a biological assay (by expressing the CDNA sequence in a cell, isolating the supernatant, and detecting an activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
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                                                                                                                                                                                                                                                                                                                                                                       hemostatic; gene therapy; cancer; inflammation; neuroprotective; neurological disorder; blood clotting disorder; food additive; preservative; human; secreted protein.
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                                                                                                                                                                                                                                                                                                                    Human novel secreted protein from gene 11 #3.
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Crocker PR;
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DTAIINAEGGONNSEEKKEYFI 442
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                                                                                                                                           ADA27144 standard, protein; 442
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19-AFR-2000; 2000US-0198407P.
30-OCT-2000; 2000US-0243732P.
18-APR-2001; 2001US-00836353.
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RUBEN S M.
LIU D.
CROCKER P R.
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KENNY J J.
OLSEN H S.
MOORE P A.
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M, Liu D,
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(LIUD/)
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in a biological assay and identifying the protein in the supernatant having the activity). The polypeptides, nucleic acids and antibodies are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation and other immune a disorders, neurological and blood clotting disorders (many examples are given in the specification). The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. The polypeptide, polynucleotide, agonist or antagonist may also be used as a food additive or preservative to increase or decrease storage capabilities, fat content or other intertitional components. The present is a secreted protein of the
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Matches 442; Conservative
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polyneptides or their antibodies. The polynucleotide or the compound that composition comprising the one or more polyneptides or their antibodies. The polynucleotide or the compound to make activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more plany (CCI) and spared nerve injury (SNI) in an animal (e.g. gene presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed contains the sequence data for this patent did not form part of the printed for its in the contains the sequence data for this patent did not form part of the printed contains the contains the c

New composition comprising two or more isolated polypeptides, useful for

Costigan M;

Befort K,

WPI; 2003-268312/26. GENBANK; NP_055148. Woolf C, D'urso D, FARB) BAYER AG

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-033347P.

GEHO) GEN HOSPITAL CORP.

14-AUG-2002; 2002WO-US025765.

27-FEB-2003

preparing a medicament for treating pain in an animal

Claim 1; Page; 1017pp; English.

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181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
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100.0%; Score 2283; DB 7;
100.0%; Pred. No. 8.3e-158;
tive 0; Mismatches 0;
                    Local Similarity 100.
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Human, pain, neuronal tissue, gene therapy, spinal segmental nerve injury, chronic constriction injury, CCI,

segmental nerve injury; c) nerve injury; c)

spared

WO2003016475-A2 Homo sapiens

Human Protein NP_055148, SEQ ID NO 41

(first entry)

29-JAN-2004

ADE54238;

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ADE54238 standard; protein; 442 AA.

240

180 180

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ftp.wipo.int/pub/published_pct_sequences

Sequence 442 AA;

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10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
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   442;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid sequence, or its allelic variant, a fragment of the CDNA sequence, or its fragment, properting or species homologue. The nucleic acid is useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, live disorders such as hepatitis or neural disorders such as Alzheimer's disease. The present sequence represents the amino acid sequence of a novel human secreted protein associated
                                                                                                                           SRAGEEGSIRAVDHAVIGGVVAVVVPAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
                                                                                                     SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA
                                                   nucleic acid molecule, useful for preparing a medicament for venting, treating or ameliorating a medical condition e.g. cancer,
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                                                                                                                                                                                                                                                                                                                                                                                                                                              human; secreted protein; cancer; liver disorder; hepatitis; neural disorder; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wei Y,
                                                                                                                                                                                                                                                                                                                                                                                                             Novel human secreted protein #11 associated protein #1
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Pred. No. 8.3e-158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 136; 380pp; English.
                                                                                                                                                                             442
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liver disorders or neural disorders.
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                                                                                                                                                                           DTAIINAEGGQNNSEEKKEYFI
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99WO-US025031.
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19-APR-2000; 2000US-0198407P
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KENNY J J.
OLSEN H S.
MOORE P A.
WEI Y.
GREENE J M.
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Best Local Similarity
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modulating agent, by contacting an assay system comprising a purified HM polypeptide (human orthologue of genes that modify the p53 pathway in Drosophila) or nucleic acid with a test agent under conditions, where but for the presence of the test agent-biased activity of the assay system. Also included are modulating (M3) a p53 pathway of a cell (comprising cell affective in p53 pathway of a cell (comprising contacting a cell affective in p53 pathway of a cell (comprising contacting a cell affective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid sequence, where p53 function is restored), modulating (M3) a p53 pathway of in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising the sample with a probe for HM comparison; (c) comparing the sample with a probe for HM comparison; (d) contacting the sample with a probe for HM comparison; (e) comparing the results with a control; and (d) determining to identifying modulators of the p53 pathway, and series or disorder prognosis is related the comparison indicates a likelihood disease). (M1) is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where disease or disorder prognosis is related the proliferation of the cell, so that the cell undergoes normal contacting defects in the p53 pathway, such as, angiogenesis, apoptotic or cell proliferation disorders. The present sequence also useful for treating defects in the p53 pathway such as angiogenic, also useful for treating defects in the p53 pathway such as angiogenic, also useful for treating defects. The present sequence
                                                                                                                           invention relates to identifying (M1) a candidate p53 pathway
Example 2; Page 469-470; 678pp; English
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Sequence 442 AA;

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Matches 441; Conservative
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Human p53 modifying protein, SEQ ID 191
ABO07231 standard; protein; 442 AA.
     (first entry)
     13-AUG-2003
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Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; appoptotic disorder; cell proliferation disorder.

Homo sapiens.

WO200299122-A1.

12-DEC-2002

03-JUN-2002; 2002WO-US017382.

05-JUN-2001; 2001US-0296076P. 10-OCT-2001; 2001US-0328605P. 15-FEB-2002; 2002US-0357253P.

(EXEL-) EXELIXIS INC.

Funke RP; Li D, Belvin M, Francis-Lang H, Friedman L, Plowman GD, 2003-156859/15.

N-PSDB; ACD13404

Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in Drosophila.

Example 2; Page 557-559; 678pp; English.

The invention relates to identifying (M1) a candidate p53 pathway

modulating agent, by contacting an assay system comprising a purified HM

CC modulating agent, by contacting an assay system condity the p53 pathway in

Drosophila) or nucleic acid with a test agent under conditions, where but

for the presence of the test agent under conditions, where but

correcting a cell defective in p53 pathway of a cell (comprising

contacting a cell defective in p53 function with a candidate modulator

Also included are modulating (M2) a p53 pathway of a cell (comprising

contacting a cell defective in p53 function with a candidate modulator

that specifically binds to a HM polypeptide comprising an HM amino acid

sequence, where p53 function is restored), modulating (M3) a p53 pathway

in a mammalian cell (comprising contacting the cell with an agent that

specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)

cc adisease in a patient (comprising); (a) obtaining a biological sample

from the patient; (b) contacting the sample with a probe for HM

cxpression; (c) comparing the results with a control; and (d) determining

whether the comparison indicates a likelihood disease). (M1) is useful

for identifying modulators of the p53 pathway. A probe for HM expression

cs useful for diagnosing breast, colon, kidney, lung and ovarian cancer,

contacting applications, where disease or disorder prognosis is related

therapeutic applications, where disease or disorder prognosis is

the p53 function of the cell, so that the cell undergoes normal

cc the p53 function of the cell, so that the cell undergoes normal

cc also useful for reating defects in the p53 pathway of a cell,

the p54 function of the cell, so that the cell undergoes normal

cc also useful for treating defects in the p53 pathway or a cell

cc also useful sorliferation disorders. The present sequence

calso useful sorliferation disorders in the p53 pathway or a cell

cc also useful sorliferation disorders in the p53 pathway or a cell

cc represen

Sequence 442 AA;

Query Match

99.9%; Score 2280; DB 6; Length 442;

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The invention discloses a composition comprising two or more isolated rat or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more or polympeptides or their antibodies. The polymocleotide or the compound that composition a method for identifying a compound useful in treating complypeptides its activity is useful for preparing a medicament for treating pain and a pharmaceutical nerve injury (SNI) in an animal (e.g. gene their activity is useful for preparing a medicament for treating conjury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therespy). The sequence presented is a human protein (shown in Table 2 of therapy) in the sequence data for this patent did not form directly from WIPO at the sequence data for this patent did not form directly from WIPO at the sequence data for this patent did not form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
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   Claim 1; Page; 1017pp; English
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Best Local Similarity 99.8<sup>1</sup>
Matches 441; Conservative
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                                                                 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
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                 0; Indels
99.8%; Pred. No. 1.4e-157; ive 1; Mismatches 0;
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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              Matches 441; Conservative
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GENBANK; AAF69029.
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 Best Local Similarity
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                                                                                                             1 MASVVLPSGSQCAAAAAAAPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
                                                                                                                                                                                                  TISCQVNKSDDSVIQLINPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG
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                                                                                                                                                                        61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG
                                                                                                                                                                                                                                                           121 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF
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                                                                                       1 MASVVLPSGSQCAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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                                                                                                                                                                                                                                                                                                                                                                                                                               241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI
                                                Gaps
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    Length 442;
                              7;
0; Indels
Score 2280; DB 7;
Pred. No. 1.4e-157;
1; Mismatches 0;
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120 120

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61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG
                                                                           RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF
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17-DEC-1997;
18-DEC-1997;
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11-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expression of the polynucleotide sequence the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polyneptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound to method for identifying a compound useful in treating pain and spared nerve injury (SNI) in an animal (e.g. gene therappy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed the specification but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                         Human, pain, neuronal tissue, gene therapy,
spinal segmental nerve injury; chronic constriction injury, CCI,
spared nerve injury; SNI, Chung.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                       Human Protein AAF69029, SEQ ID NO 7528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                             14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                           14-AUG-2002; 2002WO-US025765.
                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
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GENBANK; AAF69029.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 442 AA;
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                                   29-JAN-2004
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 ADE61608;
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                                                                                                        Human;
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Matches
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240
           300
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                                        YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
                                                                                 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTLTITTD 360
                                                                                                                         SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
                                                   241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVWVTWVRVDDEMPQHAVLSGPNLFI
                                                                                          181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
                                                                                                                                                                                                                                                                                                                      Human, PRO protein; tumour necrosis factor family, TNP, cytokine; secreted protein; transmembrane protein; inflammation disorder.
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                                                                                                                                                                 442
                                                                                                                                                                                                                                       AAY17830 standard; protein; 440 AA.
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                                                                                                                                                                            97US-0067411P.
97US-0069378P.
97US-0069334P.
97US-0069425P.
97US-006964P.
97US-006960E.
97US-0069702P.
97US-0069873P.
                                                                                                                                                                                                                                                                                                    Human PRO355 protein sequence.
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98US-0074086P.
98US-0074092P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-371118/31.
N-PSDB; AAX80055.
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9 9

1 MASVVLPSGSQCAAAAAAAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA 1 MASVVL.PSGSQCAAAAAAAAAAPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA

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16-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agents.
                                                                                                                                                                                                                                            Domain
  The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-prolliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
                                                                                                                                                                                                                                                                                               119 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 178
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                                                                                                                                                                                                                                          TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO715; PRO41; PRO313; PRO243; PRO715; PRO341; PRO355; PRO353; PRO351; PRO365; transmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human.
                                                                                                                                                                              Gaps
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Nucleic acids encoding PRO secreted and transmembrane proteins
                                                                                                                                                        Score 2263; DB 2; Length 440;
Pred. No. 2.4e-156;
0; Mismatches 0; Indels 2
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/label= Signal.peptide
9. .15
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                   Claim 12; Fig 27; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB01321 standard; protein; 440
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                                                                                                                                                         99.18;
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                                                                                                                                                                 Best Local Similarity 99.5
Matches 440; Conservative
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                                                                                                                                     Sequence 440 AA;
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New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical and diagnostic
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A, Godowski PJ, Grimaldi CJ, Gurney AL;
, Napier MA, Roy MA, Tumas D, Wood WI;
                                                                                                                                                                                                                                                          /note= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                         /note= "N-myristoylation site"
233. .240
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/note= "N-myristoylation site"
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/note= "N-myristoylation site"
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                                                 /note= "N-glycosylation site"
111. .115
/note= "N-glycosylation site"
"N-glycosylation site"
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/label= Transmembrane domain
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/note= "N-myristoylation
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                                                                                                                             163. .167 / note= "N-glycosylation
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98US-0112850P.
98US-0113296P.
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Gerritsen ME, Goduard
Tr, KIjavin IJ,
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ME, Goddard
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WPI; 2001-602746/68.
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Smith V, Wa
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                                                                                                                                                        30-MAY-2000; 2
02-JUN-2000; 2
05-JUN-2000; 2
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                                                                                                                      KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 238
                                                                                                                                                                                                                              SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 418
                                                                                                                                                                                                                                                                                                                                                                                                                         PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabblt; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prosteat; rectum; cervix; liver; genetic disorder.
                                                                             TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
                                                                                                                                                KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
                                                                                                                                                                                  YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
                                                                                                                                                                                                                     NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTLTIITD 360
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                                        1 MASVVLPSGSQCAAAAAAAPPGLRLRLLLLLFSAAALIPTGDQONLFTKDVTVIEGEVA
                                                         1 MASVVLPSGSQCAAAAAAAPPG--LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
                                                                                                               RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF
                       Gaps
                        7
        Length 440;
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     Score 2263; DB 3;
Pred. No. 2.4e-156;
0; Mismatches 0;
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2000WO-US005841.
2000US-0187202P.
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2000US-0189328P.
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2000US-0191048P.
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2000US-0190828P.
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                       Conservative
              al Similarity
440; Conserv
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21-MAR-2000; 2
21-MAR-2000; 2
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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.

The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adernal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and to screen for modulators of the compounds.
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Wood WI, Zhang Z;
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04-APR-2000; 2000US-0194449F9.
04-APR-2000; 2000US-0194647P.
11-APR-2000; 2000US-0195975P.
11-APR-2000; 2000US-0195975P.
11-APR-2000; 2000US-0196187P.
11-APR-2000; 2000US-0196690P.
11-APR-2000; 2000US-0196820P.
18-APR-2000; 2000US-0198121P.
18-APR-2000; 2000US-0198565P.
25-APR-2000; 2000US-0199569P.
25-APR-2000; 2000US-0199569P.
25-APR-2000; 2000US-0199569P.
25-APR-2000; 2000US-0199569P.
25-APR-2000; 2000US-0199569P.
27-AMY-2000; 2000US-0199664P.
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419 DTAIINAEGGQNNSEEKKEYFI 440	Db 41
1 DTAIINAEGGONNSEEKKEYFI 442	Qy 421
9 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 418	0b 359
1 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420	Qy 361
299 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Db 25
1 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPPTTTTTTTTTTTTTTTTT 360	Qy 301
239 YKPQVHIQMTYPLQGLTREGDALELICEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 298	Db 23
1 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300	Qy 241
179 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 238	Db 17
181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240	9,
119 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 178	Db 1.
121 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180	ογ 1:

Search completed: June 28, 2005, 09:50:06 Job time: 121.548 secs

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US-09-945-587-61

US-09-944-306-61

US-09-944-31-61

US-09-944-61-61

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US-10-176-913-41

US-10-176-913-41

US-10-176-913-41

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JUNIORAL MANIENE Baum, Peter .

TITLE OF INVENTION: Molecules Designated Interpretation of the party of the 
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Sequence 136, App
Sequence 20, Appl
Sequence 11, Appl
Sequence 22, Appl
Sequence 2, Appli
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Sequence 2, Appli
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Sequence 2, Appli
                                                                                                                                                   June 28, 2005, 09:53:58; Search time 112.927 Seconds (without alignments) 1505.131 Million cell updates/sec
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1 MASVVLPSGSQCAAAAAAA.....AIINAEGGQNNSEEKKEYFI 442
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
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21: /cgn2_6/ptodata/2/pubpaa/USIOP_NUBCOMB.pep:*
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-984-130-136
US-09-984-130-136
US-10-302-041-20
US-10-302-041-20
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US-10-303-616-262
US-10-303-616-262
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM protein - protein search, using sw model
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Db 301 NNLAKTONGTRCEASNIVGKAHSDVMLYVZDPPTTITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	MUMBER OF SEQ ID NOS: 149 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 136 LENGTH: 442 TYPE: PRT ORGANISM: Homo sapiens JS-09-984-130-136	Qy 61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120	181 KGNTELKGKSEVEEWSDNYTVTSQLALKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ	241 301 301	Oy 361 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
Qy 121 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWF 180 Db 121 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWF 180 Qy 181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVBHPAVTGNLGTQRYLEVQ 240 Qy 181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVBHPAVTGNLGTQRYLEVQ 240 Qy 241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPWNTWWRVDDBMPQHAVLSGPNLF1 300 Qy 301 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM FILE REFERENCE: 2873-US CURRENT APPLICATION NUMBER: US9/778,187B CURRENT PILING DATE: 2001-02-06 FRIOR APPLICATION NUMBER: PCT/US99/17905 FRIOR APPLICATION NUMBER: US 60/095,672 FRIOR PILING DATE: 1999-08-05 FRIOR FILING DATE: 1998-08-07 NUMBER OF SEQ ID NOS: 10 SEQ ID NO 2 LENGTH: A42 TENGTH: A42 TENGTH: A42 COGANISM: homo sapiens US-09-778-1878-2	Query Match 100.0%; Score 2283; DB 9; Length 442; Best Local Similarity 100.0%; Pred. No. 2.4e-160; Agos 0; Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 MASVVLPSGSQCAAAAAAAAPPGIRIRILLILFSAAALIPTGDGQNLFTKDVTVIEGEVA 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	61 TISCQVNKSDDSVIQLINPNRQTIVFRDFRELKDSRFQLINFSSSELKVSLTNVSISDEG	DD 121 KYFCQLYIDFPQESYTTITVLVPPKNLMIDIQKDITANEGEEIEVNCTAMASKPATITKWF 180 Qy 181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLGTQRYLEVQ 240 DD 181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLGTQRYLEVQ 240	QY 241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300

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Sequence 1, Application US/10403107

Publication No. US20030165974A1

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS

FILE REFERENCE JUH/70-1

CURRENT PILING DATE: 2003-03-28

PRIOR APPLICATION NUMBER: US/09/930,803

PRIOR APPLICATION NUMBER: US/09/930,803

PRIOR APPLICATION NUMBER: US/09/930,803

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PATENTING DATE: 2001-08-15

SEQ ID NO 1.
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CURRENT APPLICATION NUMBER: US/10/302,041
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/778,510
FRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 442
TYPE: PRI
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TYPE: PRT
ORGANISM: Homo sapiens
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US-10-302-041-20
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0; Mismatches 0; Indels
                                                                                                                                                 Sequence 136, Application US/09836353A
Publication No. US20030129685A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PF489P1
CURRENT APPLICATION NUMBER: US/09/836,353A
CURRENT APPLICATION NUMBER: 60/198,407
PRIOR FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR PILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1998-10-28
NUMBER: OF SEQ. ID NOS: 147
SOFTWARE: PATENTIN OF SEQ. 110 NOS: 147
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; Publication No. US20030144478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TILLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 2283; 100.0%; Pred. No. 2.
  421 DTAIINAEGGONNSEEKKEYFI 442
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Best Local Similarity 100.
Matches 442; Conservative
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US-09-836-353A-136
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100.0%; Score 2283; DB 15; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.4e-160;
Matches 442; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                              DB 15; Length 442;
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; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq. Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES;
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
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PRIOR APPLICATION NUMBER: 60/309,261
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 205
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 111
LENGTH: 442
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CORGANISM: Homo sapiens
US-10-015-115-111
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CRGANISM: Homo sapiens
US-10-363-616-262
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US-10-363-616-262
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APPLICANT: Rekuda, Ramesha
APPLICANT: Guo, Xiaojia
APPLICANT: Guo, Xiaojia
APPLICANT: Shimkets, Ramesha
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Raymond J
APPLICANT: Taupier, Raymond J
APPLICANT: Taupier, Raymond J
APPLICANT: Taupier, Raymond J
APPLICANT: Dadigaru, Muralidhara
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-211
CURRENT APPLICATION NUMBER: US/10/015,115
CURRENT PILING DATE: 2000-11-13
FRIOR APPLICATION NUMBER: 60/249,598
FRIOR PELING DATE: 2000-11-13
FRIOR PELING DATE: 2000-11-13
FRIOR PELING DATE: 2001-01-26
FRIOR PELING DATE: 2001-01-26
FRIOR PELING DATE: 2001-01-20
FRIOR PELING DATE: 2001-02-02
FRIOR FILING DATE: 2001-02-04
FRIOR FILING DATE: 2001-02-05
FRIOR FILING DATE: 2001-02-05
FRIOR FILING DATE: 2001-02-05
FRIOR FILING DATE: 2001-02-06
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                                                         Length 442;
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                                                    100.0%; Score 2283; DB 14; 100.0%; Pred. No. 2.4e-160;
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APPLICANT: Shenoy, Suresh G
APPLICANT: Spyrek, Kimberly A
APPLICANT: Serbusen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Guo, Xiaojia
APPLICANT: Geno, Xiaojia
APPLICANT: Gengolii, Esha A
APPLICANT: Shimkets, Richard A
APPLICANT: Taupier, Raymond J
                                                    Query Match 100.
Best Local Similarity 100.
Matches 442; Conservative
     US-10-403-107-1
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| Publication No. US20050058642A1 |
| GENERAL INFORMATION: |
| APPLICANT: GALIBERT, Laurent J. |
| APPLICANT: YAN, Wei |
| TITLE OF INVENTION: ANTACONISTS AND AGONISTS OF LDCAM AND METHODS OF USE |
| TITLE OF INVENTION: ANTACONISTS AND AGONISTS OF LDCAM AND METHODS OF USE |
| TITLE OF INVENTION NUMBER: US/10/898,408 |
| CURRENT APPLICATION NUMBER: 60/490,027 |
| PRIOR FILING DATE: 2003-07-25 |
| NUMBER OF SEQ ID NOS: 13 |
| SOFTWARE: Patentin version 3.2 |
| LENGTH: 442
                                                                                                                                                              181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
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ORGANISM: homo sapiens
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100.0%; Pred. No. 2.4e-160;
iive 0; Mismatches 0;
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Publication No. US20040204568A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
FILE REPERENCE: 2873-US
CURRENT PELING DATE: 2003-07-17
CURRENT FILING DATE: 2003-07-17
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: US/09/778,187B
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: US 60/095,672
PRIOR APPLICATION NUMBER: US 60/095,672
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1908-08-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Version 3.1
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Best Local Similarity 100.
Matches 442; Conservative
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                      241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
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                                                                                           301 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPPTTTTTTTTTTTTTTTTTTTTT
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PtC1
CURRENT PAPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
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US-09-866-028-61
Sequence 61, Application US/09866028
Patent No. US20020058309A1
GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
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Filvaroff, Ellen
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Matches 440; Conservative
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APPLICANT: Botstein, David
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Tumas, Daniel
Wood, William
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ORGANISM: Homo Sapien
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LENGTH: 440
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APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
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Pred. No. 3.9e-160;
1; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/015,115
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR PILING DATE: 2000-11-13
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2001-11-17
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/309,38
PRIOR FILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-08-17
                                                  DTAIINAEGGONNSEEKKEYFI 442
                                                                                                                                                                          ; Sequence 110, Application US/10015115; Publication No. US20030207800A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                            Shenoy, Suresh G
Spytek, Kimberly A
Zerhusen, Bryan D
Patturajan, Meera
Guo, Xiaojia
Kekuda, Ramesha
Gangolli, Esha A
Shimkets, Richard A
Taupier, Raymond J
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Best Local Similarity 99.8
Matches 441; Conservative
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US-10-015-115-110
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59 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 118
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IOR FILING DATE: December 16, 1998
IOR APPLICATION NUMBER: 60/145,222
RIOR FILING DATE: December 22, 1998
RIOR APPLICATION NUMBER: 80/146,222
RIOR APPLICATION NUMBER: 80/146,222
RIOR APPLICATION NUMBER: PCT/1898/15108
RIOR PLILON DATE: December 16, 1998
RIOR PLILON DATE: December 16, 1998
RRIOR APPLICATION NUMBER: 09/216,021
RRIOR APPLICATION NUMBER: 09/216,021
RRIOR RILING DATE: December 21, 1998
RRIOR RILING DATE: December 21, 1998
RRIOR RELICATION NUMBER: 09/24,311
RRIOR APPLICATION NUMBER: 09/254,311
RRIOR APPLICATION NUMBER: PCT/US99/2809
RRIOR RELICATION NUMBER: PCT/US99/2801
RRIOR RELICATION NUMBER: PCT/US00/0414
RRIOR RELICATION NUMBER: PCT/US00/0414
RRIOR RELICATION NUMBER: PCT/US00/0641
RRIOR RELICATION NUMBER: PCT/US00/0650
RRIOR RELICATI
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Pred. No. 7e-159;
0; Mismatches 0;
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Best Local Similarity 99.5
Matches 440; Conservative
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FILE REFERENCE: P5248916 12010-09-26
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR FILING DATE: December 16, 1997
PRIOR PRILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,8702
PRIOR PRILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,8702
PRIOR PRILING DATE: December 17, 1997
PRIOR PRILING DATE: December 18, 1997
PRIOR FILING DATE: December 19, 1998
PRIOR FILING DATE: PEDIUARY 9, 1998
                                                                                                   SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
                                                                                                                                                                                                                      SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 418
                                                                    NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTT 360
                                                                                                                                                                                                                                                                                                             DTAIINAEGGONNSEEKKEYFI 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 61, Application US/09944449
Patent No. US20020102647A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Gerriteen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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APPLICANT: Botstein, David
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Hillan, Kenneth
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61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
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PRIOR APPLICATION NUMBER: 60/113,296
PRIOR PILING DATE: December 22, 1998
PRIOR PILING DATE: December 22, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: September 16, 1998
PRIOR PILING DATE: September 16, 1998
PRIOR PILING DATE: December 1, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 12, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 15, 1999
PRIOR PILING DATE: POTOMER: PCT/US99/12109
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: September 16, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: December 1, 1999
PRIOR PILING DATE: December 1, 2090
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: PEDLUARY 11, 2000
PRIOR PILING DATE: PEDLUARY 22, 2000
PRIOR PILING DATE: PEDLUARY 22, 2000
PRIOR PILING DATE: MARCH 30, 2000
PRIOR PILING DATE: PEDLUARY 28, 2001
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Matches 440; Conservative
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ORGANISM: Homo Sapien
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APPLICANT: Naples, Mary
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, Milliam
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLCI
CURREWY PELLING DATE: 2001-09-26
PRIOR PELLOR DATE: 2001-09-26
PRIOR PELLOR DATE: 2001-09-26
PRIOR PELLOR DATE: December 10, 1997
PRIOR PELLOR DATE: December 11, 1997
PRIOR PELLOR DATE: December 12, 1997
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PRIOR PELLOR DATE: December 16, 1997
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PRIOR PELLOR DATE: December 17, 1997
PRIOR PELLOR DATE: PENDENDER 60/069, 107
PRIOR PELLOR DATE: PENDENDER 100/069, 107
PRIOR PELLOR DATE: PENDENDER 100/07, 440
PRIOR PELLOR DA
             NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTLTILTI
                                              SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
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Patent No. US20020110859A1
GENERAL INFORMATION:
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Grimaldi, Christopher
Gurney, Austin
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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APPLICANT: Botstein, David
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59 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 118
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Pred. No. 7e-159;
0; Mismatches 0; Indels
                                      PRIOR PILIGIO DATE: December 22, 1998

REIOR PELIGIO DATE: December 22, 1998

REIOR PLICATION NUMBER: 60/146,222

REIOR PLING DATE: JULY 28, 1999

PRIOR FLING DATE: December 1, 1998

REIOR PLING DATE: December 1, 1998

REIOR PLING DATE: December 16, 1999

REIOR PLING DATE: December 16, 1999

REIOR PLING DATE: JUNE 22, 1999

REIOR PLING DATE: DECEMBER: PCT/US99/2831

REIOR PLING DATE: PEDCHALY 22, 2000

REIOR APPLICATION NUMBER: PCT/US00/0441

REIOR PLING DATE: REPLAUARY 22, 2000

REIOR APPLICATION NUMBER: PCT/US00/0441

REIOR PLING DATE: REPLAUARY 22, 2000

REIOR APPLICATION NUMBER: PCT/US00/0441

REIOR PLING DATE: MATCH 2, 2000

REIOR REILING DATE: MATCH 3, 28, 2001

REIOR PLING DATE: MATCH 3, 28, 2001

REIOR PLING DATE: MATCH 3, 28, 2001

REIOR REILING DATE: DECEMBER: PCT/US00/2678

REIOR REILING DATE: REPLAUARY 22, 2001

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REIOR REILING DATE: DECEMBER: PCT/US00/2678

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                            LICATION NUMBER: 60/113,296
December 16, 1998
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Best Local Similarity 99.5
Matches 440; Conservative
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CURRENT FILING DATE: 2001-05-26
PRIOR PELING DATE: 2001-05-26
PRIOR PELING DATE: December 3, 1997
PRIOR PLING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 12, 1997
PRIOR PELING DATE: December 12, 1997
PRIOR PELING DATE: December 16, 1997
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PRIOR PELING DATE: December 16, 1997
PRIOR PELING DATE: December 17, 1997
PRIOR PELING DATE: Pecember 18, 1997
PRIOR PELING DATE: Pecember 19, 1998
PRIOR PELING DATE: Pebruary 9, 1998
                                                                                                                                        SRAGEEGSIRAVDHAVIGGVVAVVVPAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
                      DTAIINAEGGONNSEEKKEYFI 442
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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APPLICANT: Botstein, David
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Wood, William
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US-09-944-862-61
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qa	299	299 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPFTTTTTTTTTTTTTTTTTTTTTT	28
ò	361	361 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLILLGRYFARHKGTYFTHEAKGADDAADA 420	20
qq	359	S	18
λō	421	421 DTAIINAEGGONNSEEKKEYFI 442	
qq	419	419 DTAIINAEGGNNSEEKKEYFI 440	
Search o	comple:	Search completed: June 28, 2005, 10:12:35 Job time : 114.927 secs	

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                                                                                          June 28, 2005, 09:43:27; Search time 30.659 Seconds (without alignments) 1076.191 Million cell updates/sec
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Sequence 1, Ap
Sequence 61, A
                                                                                                                                                             US-10-622-237-2
2283
1 MASVVLPSGSQCAAAAAAA......AIINAEGGQNNSEEKKEYFI 442
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Sequence 22,
Sequence 5,
Sequence 5,
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-930-803-1
US-09-866-023-1
US-09-778-510-22
US-08-659-984A-5
US-08-659-984A-1
US-08-659-984A-1
US-08-659-984A-1
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US-08-659-984A-1
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US-08-659-984A-1
US-08-905-311-1
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US-09-906-618-84
US-09-906-7564
US-09-906-7564
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-09-949-016-11380

Sequence 7563, Ap Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6278, Appli Sequence 1, Appli Sequence 3, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 11, Appli Sequence 1168, Appli Appli Sequence 1168, Appli			Length 442; Indels 0; Gaps 0;	SAAALIPTGDGQNLFTKDVTVIEGEVA 60 	FSSSELKVSLINVSISDEG 120 	IEVNCTAMASKPATTIRWF 180 EVNCTAMASKPATTIRWF 180	VEHPAVTGNLQTQRYLEVQ 240	RVDDEMPQHAVLSGPNLFI 300	TTTTTTTTTTTLTILT 360 TTTTTTTTTLTILT
US-09-949-016-7563 US-08-429-742-2 US-09-949-016-11044 US-09-949-016-6278 US-09-949-016-6215 US-09-949-016-6515 US-09-949-016-6515 US-09-949-016-6515 US-09-949-016-6515 US-09-949-016-6861 US-09-949-016-6861 US-09-949-016-6861 US-09-949-016-6861 US-09-949-016-6861 US-09-949-016-6861 US-09-949-016-6861 US-09-949-016-6884 US-09-949-016-6884 US-09-949-016-6884 US-09-949-016-6884 US-09-949-016-6884 US-08-987-867A-17	ALIGNMENTS	n US/09778510 eter Molecules Designated B7L1 44-US 2001-02-07 ER: PCT/US99/17906 1999-08-05, 663 1998-08-07 Ver: 2.0	Score 2283; DB 4; Pred. No. 9e-192; 0; Mismatches 0;	AAAPPGLRLRLLLLLFSAAALIPT 	TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 	RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 	KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 	YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 	NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTILTITTD
10.2 10.2 10.2 10.2 10.2 10.2 10.2 10.2 10.2 10.2 10.2 10.2 10.2 10.2 10.2 10.2 10.2 10.2 10.3		Application Size Size Size Size Size Size Size Size	100.0%; Similarity 100.0%; 2; Conservative	MASVVLPSGSQCAAAAAAAPGLRIRILILIF 					
28 29 30 31 31 32 33 34 33 34 35 20 20 20 40 40 40 40 40 40 40 40 40 40 40 40 40		RESULT 1 US-09-778-510-; Sequence 20, Fatent No. 61 FAPPLICANT: TITLE OF IN. TITLE OF IN. FILE REFERE CURRENT APPL CURRENT APPL FRIOR FILIN FRIOR APPLIC FRIOR FILIN FRIOR FIL	Query Match Best Local S Matches 442	Oy 1	Oy 61	Oy 121 Db 121	Oy 181 Db 181	Qy 241 Db 241	Oy 301 Db 301

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                                                                                                                                                                                                              APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: WOOG, WILLIAM
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P25.48PHC1
CURRENT APPLICATION NUMBER: U5/09/866,028
CURRENT FILING DATE: 2001-05-25
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NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
TYGANISM: Homo Sapien
US-09-866-028-61
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Best Local Similarity 99.5%; Pred. No. 5.1e-190;
Matches 440; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eston, Dan
APPLICANT: Ferrara, Napoleone
                                                                                     Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
                Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
                                                                                                                                                                             Napier, Mary
Roy, Margaret
Tumas, Daniel
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                               APPLICANT:
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Fatent No. 6556493
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: THE VOSHINORI, Muramaki
ITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILLE REFERENCE: JHU1770-1
CURRENT APPLICATION NUMBER: US/09/930,803
CURRENT PILLING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
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                  SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
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SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA
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Patent No. 6642360
GENERAL INFORMATION
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 442; Conservative
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ORGANISM: Homo sapiens
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US-09-866-028-61
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US-09-930-803-1
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APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designat
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
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Patent No. 6512095
GENERAL INFORMATION:
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Best Local Similarity 99.5
Matches 440; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-61
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US-09-778-510-22
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APPLICATION NUMBER: PCT/US99/28313
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  Godowski, Paul
Grimaldi, Christopher
                                              Gurney, Austin
Hillan, Kenneth
                                                                                              Kljavin, Ivar
APPLICANT:
APPLICANT:
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99.5%; Pred. No. 5.1e-190;
iive 0; Mismatches 0;
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                                               PRIOR APPLICATION UNDERS: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: Pebruary 11, 2000
PRIOR FILING DATE: Pebruary 11, 2000
PRIOR PELICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: Pebruary 22, 2000
PRIOR FILING DATE: March 2, 2000
PRIOR PILING DATE: March 2, 2000
PRIOR PLING DATE: March 2, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR PLING DATE: July 28, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: PEBRUARY 28, 2001
LING DATE: December1, 1999
PLICATION NUMBER: PCT/US99/30095
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358 420

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197 LDFRVDRSDDGVAVICRVDHESLNATPQVAMQVLEIHYTPSVKI---IPSTPFPQEGQPL 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 LLFSAAA---LIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFR
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Fatent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Relm, Pamela S.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 39.5%; Score 902; DB 2; L
Local Similarity 44.6%; Pred. No. 1.1e-70;
Nes 194; Conservative 74; Mismatches 137;
                                                                                                                                                                                       15270-002810US
                    APPLICATION NUMBER: US/08/659,984A FILING DATE: 07-UN-1996 CLASSIFICATION: 436 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/485,152 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                               NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFRENCE/DOCKET NUMBER: 1527(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                               LENGTH:
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Patent No. 5942400

GENERAL INFORMATION:

APPLICANT: Anderson, John P.

APPLICANT: Sinha, Sukanto

APPLICANT: Jacobson-Croak, Kirsten L.

TITLE OF INVENTION: Inhibition

NUMBER OF SEQUENCES:

ADDRESSE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Ctr., 8th Floor

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                            Length 423
                                                                                                                                                                                                                                                                              4; Indels
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STATE: Ca.
COUNTRY: USA
ZIP: 9411-3834
COMPUTER READALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OMPUTER: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                       Score 2169; DB 4;
Pred. No. 8.4e-182;
1; Mismatches 4;
                  BR: PCT/US99/17906
1999-08-05
ER: 60/095,663
1998-08-07
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 60/06
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTH NOS: 20
SEQ ID NO 22
                                                                                                                                                                                                                                          95.0%;
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.8°
Matches 418; Conservative
                                                                                                                                                                 TYPE: PRT ORGANISM: Mus musculus
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EYF 423
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US-08-659-984A-5
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                                                                                                                                                   LENGTH: 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 ELTCEAIGKPQPVMVTWVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGK 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.5%; Score 902; DB 3; Length 444; 44.6%; Pred. No. 1.1e-70; Live 74; Mismatches 137; Indels
                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Two Embarcadero Ctr., 8th Floor
San Francisco
California
                                                                                                                                                                                                                                                                                                                                                 15270-002210US
                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,53
                                                                                                    3: Floppy disk
IBM PC compatible
3YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                             NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15;
TELECOMMUNICATION: TELEPHONE: 415-326-2400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       444 amino acids
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Best Local Similarity 44.6
Matches 194; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                     94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-660-531-5
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; Sequence 1, Application US/08659984A

RESULT 8 US-08-659-984A-1

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70 WHELSISVSDVSLSDEGGYTCSLFTMPVKTSKAYLTVLGVPEKPQISGFSSPVMEGDLMQ 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 VNCTAMASKPATTIRWFKGNTELKGKSEVEEWS---DMYTVTSQLMLKVHKEDDGVPVIC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 WVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVVDPPTTI 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 SSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 QVEHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 RVDHESLNATPQVAMQVLEIHYTPSVKI---IPSTPPPQEGQPLILTCESKGKPLPEPVL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 LPTTIIPSLTTATVTTTVAITTSPTTSSIRDPNALAGONGP----DHALIGGIVAV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 PPPTTTTTTTTTTTTLTIIT-------DSRAGEEGSIRAVDHAVIGGVVAV 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               384 VVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYF! 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 GQFPLTQNVTVVEGGTAILTCRVDQNDNTSLQWSNPAQQTLYFDDKKALRDNRIELVRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.2%; Score 895.5; DB 2; Length 45.1%; Pred. No. 3.9e-70; tive 73; Mismatches 130; Indels
                                              APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Ctr., 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                        APPLICANT: Anderson, John P. APPLICANT: Sinha, Sukanto APPLICANT: Jacobson-Croak, Ki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 amino acids
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Query Match
Best Local Similarity 45.1%
Matches 189; Conservative
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REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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INFORMATION:
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                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 SEVEEWSD--MYTVTSQLMLKVHKEDDGVPVICQVEHPAVTG-NLQTQRYLEVQYKPQVH 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 IR---PEPAHPREGOKLLLHCEGRGNPVPQQYVWVKEGSEPPLKMTQESALIFP----F 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 ------HAIIGGIVAFIVFLLILLIFIGHYLIRHKGTYLTHEAKGSDDAPDADT 378
-- DSRAGEEGSIRAVDHAVIGGVVAV 383
                                                                   307 LPTTIIPSLTTATVTTTVAITTSPTTSSIRDPNALAGONGP----DHALIGGIVAV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 PQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG-K 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 IQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMP----QHAVLSGPNLFINN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 LNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTTS 362
                                                                                                                                           384 VVFAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
                                                                                                                                                                               289 INKSDSGTYGCTATSNMGSYTAYFTLNVNDPS---PVPSSSSTY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 DSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 DSSLQWSNPAQQTLYFGEKRALRDNRIQLVSSTPHELSISISNVALADEGEYTCSIFTWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 AAAAAPPGLRLRLLLLFSAAALIPTG----DGQNLFTKDVTVIEGEVATISCQVNKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 APAASP----VPLLLLL--ACSWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCOVKDHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
TITLE OF INVENTION:
FILLE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17806
PRIOR PILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-07
PRIOR FILING DATE: 1999-08-07
NUMBER OF SEQ ID NOS: 22
SOUTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.7%; Score 745.5; DB 4; 39.1%; Pred. No. 5.2e-57; ive 74; Mismatches 137;
       338 PPPTTTTTTTTTTILTIT
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US-09-778-510-6
Sequence 6, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09778510
Patent No. 6312095
GENERAL INFORMATION:
APPLICANT: Baum, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 39.1%
Matches 172; Conservative
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US-09-778-510-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 SSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 VNCTAMASKPATTIRWFKGNTELKGKSEVEEWS---DMYTVTSQLMLKVHKEDDGVPVIC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 QVEHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDALELICEAIGKPQPVMVT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WVRVDDEM--POHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTI 337
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                                                                                                                                                                                                                                                          APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Sinha, Pamela S.
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: Galifornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET UNBER: 15270-002210US
TELECOMMUNICATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                        Sequence 1, Application US/08660531
Patent No. 6221645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-320-272.
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 421 amino acids
TYPE: amino acid
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Best Local Similarity 45.14
Matches 189; Conservative
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                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Chrysl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                           US-08-660-531-1
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT PILING DATE: 2001-07-17
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 PAASLILLILLIF-ACCWAPGGANLSQDDSQPWTSDBTVVAGGTVVLKCQVKDHEDSSLQW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 PGLRLRLLLLLFSAAALIPTG----DGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR PILING DATE: 1999-12-20
PRIOR PLILNG DATE: 1999-12-20
PRIOR PLILNG DATE: 1999-12-20
PRIOR PLILNG DATE: 1999-12-20
PRIOR PLILNG DATE: 2000-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US99/28313
                                            Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
                                                                                                                                                                                                            Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-11-30
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SEQ ID NO 84
LENGTH: 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 LINPURGIIYERDERPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYT 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.4%; Score 739; DB 4; Length 398; 38.6%; Pred. No. 1.9e-56; Live 73; Mismatches 147; Indels
                                         Molecules Designated B7L1
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                                                                                                                                                                      PCT/US99/17906
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Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gao, Wei-Qiang
Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerritsen, Mary E
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
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      Baum, Peter
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ORGANISM: Homo sapien
APPLICANT: Baum,
TITLE OF INVENTION:
FILE REFERENCE:
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243 ---HPREGQKLLLHCEGRGNPVPQQYLWEK-EGSVPPLKMTQESALIFPFLNKSDSGTYG 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.4%; Score 739; DB 4; Length 39: 38.6%; Pred. No. 1.9e-56; ive 73; Mismatches 147; Indels
                PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-30
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Patent No. 668451
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Eaton, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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Best Local Similarity 38.6
Matches 166; Conservative
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US-09-905-125A-84
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                                           PNGKTFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSORIEVLYTPTAMIRPDPP 242
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I. Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
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Grimaldi, Christopher J.
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Hillan, Kerneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Ashkenazi, Avi
Botstein, David
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Eaton, Dan L.
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137 TITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGK-SEVEEW 195
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
ITTLE OF INVENTION: Acide Encoding the Same
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT APLICATION NUMBER: US/09/902,775A
CURRENT APLICATION NUMBER: US/09/902,775A
CURRENT APLICATION NUMBER: CT/08/00/04414
RIOR APLICATION NUMBER: PC/08/00/04414
RIOR APLICATION NUMBER: US/01/02/22
RIOR APLICATION NUMBER: US/01/02/22
RRIOR FILING DATE: 1999-07-28
RRIOR FILING DATE: 1999-07-28
RRIOR APLICATION NUMBER: PC/08/99/20/94
RRIOR FILING DATE: 1999-09-15
RRIOR APPLICATION NUMBER: PC/08/99/20/94
RRIOR FILING DATE: 1999-09-15
RRIOR FILING DATE: 1999-09-15
RRIOR PELING DATE: 1999-09-15
RRIOR PELING DATE: 1999-09-15
RRIOR FILING DATE: 1999-09-15
RRIOR FILING DATE: 1999-09-15
RRIOR FILING DATE: 1999-10-20
RRIOR APPLICATION NUMBER: PCT/08/99/2804
RRIOR FILING DATE: 1999-11-29
RRIOR APPLICATION NUMBER: PCT/08/99/2804
RRIOR FILING DATE: 1999-11-29
RRIOR APPLICATION NUMBER: PCT/08/99/2804
RRIOR APPLICATION NUMBER: PCT/08/99/2804
RRIOR FILING DATE: 1999-11-29
RRIOR APPLICATION NUMBER: PCT/08/99/2809
RRIOR FILING DATE: 1999-11-29
RRIOR FILING DATE: 1999-11-29
RRIOR APPLICATION NUMBER: PCT/08/99/20091
RRIOR APPLICATION NUMBER: PCT/08/99/20099
RRIOR APPLICATION NUMBER: PCT/
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38.6%; Pred. No. 1.9e-56;
tive 73; Mismatches 147; Indels 44; Gaps
                                                                                                                                                   Godowski, Paul J.
Grimaldi, Christopher
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
                                                         Gerber, Hanspeter
Gerritsen, Mary E
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Best Local Similarity 38.6 Matches 166; Conservative
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CRGANISM: Homo sapiens
US-09-902-775A-84
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITILE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-114
CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-09720
PRIOR FILING DATE: 2000-02-22
PRIOR PELICATION NUMBER: PCT/USO0/04414
PRIOR PLICATION NUMBER: US 60/143,048
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
Sequence 84, Application US/09906700
                                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, Christopher
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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183 PNGKTFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTFTAMIRPDPP 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 TITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGK-SEVBEW 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1.9e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
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Job time : 32.659 secs
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version - 2005
GenCore (c) 1993
Copyright (
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OM protein - protein search, using sw model

Run on:

June 28, 2005, 09:42:27; Search time 24.9399 Seconds (without alignments) 1631.912 Million cell updates/sec

Title: Perfect score:

US-10-622-237-4 2197 1 AAPPGLRLKLLLLLLSAAAL.....TAIINAEGGONNSEEKKEYF 423 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote		ď		poliovirus recepto				poliovirus recepto	poliovirus recepto	neural cell adhesi	poliovirus recepto	poliovirus recepto	neurotrimin - rat	elastic titin - hu	connectin/titin -	neuromusculin - fr		neural cell adhesi	50K glycoprotein p	PRR2 alpha - human	opioid-binding pro	opioid-binding cel	surface glycoprote	. adhesion_molecule	perlecan precursor	cell adhesion mole	cell adhesion mole	opioid-binding pro
SUMMARIES	ΩI	T08732	T20992	T43290	HLMSP3	JC4024	A53437	I68093	JE0099	A44194	B44194	IJXENE	RWHUPD	RWHUPA	156551	I38346	T42633	T13669	JE0100	JN0635	JC5519	153960	S03199	JC4025	A45254	JH0506	A38096	B42632	A42632	JC1239
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*	Query	12.3	11.9	11.9	11.2	11.1	11.1	10.9	10.8	10.8	10.7	10.7	10.6	10.6	10.5	10.4	10.3	10.2	10.1	10.1	10.0	10.0	o.	•	9.6	7.6	9.6	٠	9.6	9.5
	Score		261.5	261.5	246.5	244	243	238.5	238	23	234.5	\sim	232.5	232.5	23	228.5	226	225	222	222	220.5	220	217.5	215.5	215.5	214	212	210.5	210.5	209.5
	Result No.	п	7	m	4	ស	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	. 21	22	23	24	25	56	27	28	59

	s-dicerin precurso	cell surface glyco	limbic-system-asso	differentiation an	CD22 homolog/B lym	B-cell adhesion pr	carcinoembryonic a	alcam - human	neogenin - chicken	opioid-binding pro	cell adhesion mole	DM-GRASP precursor	heparan sulfate pr	nephrin - human	connectin 3B - chi	· neural cell adhesi
0.140	675067	I38049	JC4776	149583	A46512	JH0371	A36319	139428	150600	JC1238	C42632	JH0464	S18252	T37190	PN0568	IJHUNG
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	700	646	338	862	898	847	702	583	1443	338	765	587	3707	1241	1323	761
ď	0	9.4	9.4	9.4	9.4	9.4	9.3	9.3	9.5	9.1	9.1	9.1	0.6	6.0	8.9	8.8
9000	6.602	207.5	206.5	206.5	206.5	206	204	203.5	202	200.5	200.5	200	197	196.5	195	193
ć	2	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 2 120992 hypothetical protein F15G9.4a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T20992; T24733

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F;355-374/Domain: transmembrane #status predicted <TMN>
         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                          A; Reference number: Z19929
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Matches
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T43290
hemicentin precursor - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C.Accession: T43290, T20393; T24734
R.Vogel, B.E.; Hedgecock, E.M.
R.Vogel, B.E.; Hedgecock, E.M.
R.Vogel, B.E.; Hedgecock, E.M.
A;Reference number: Z22396
A;Reference number: Z22396
A;Recession: T43290
A;Roccession: T43290
A;Residues: 1-5198 <-VOG>
A;Residues: 1-5198 <-VOG>
A;Residues: 1-5198 <-VOG>
A;References: UNIPROT:O76518; EMBL:AF074901; PIDN:AAC26792.1
R;Sulston, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
A;Accession: T20993
Risulston, J.

submitted to the EMBL Data Library, December 1994

submitted to the EMBL Data Library, December 1994

A; Reference number: 219355

A; Reference number: 219355

A; Residual 120992

A; Residual type: DNA

A; Residuale type: DNA

A; Residuales: 1-515 < WIL>
A; Experimental source: clone F15G9

R; Kershaw, J.

Submitted to the EMBL Data Library, December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4698/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2310 CPA-TGKPEPDITWFKDGEAIHIENIADIIPNGELNG-------NOLKITRIK 2354
                                                                                                                                                                                                                                                                                                                                                                               A, Cross-references: EMBL:247070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a A, Experimental source: clone T09B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 KVSLTNVSISDEGRYFCQLYTDPPQESYT-TITVLVPPRNLMIDIOKD-TAVEGEEIEVN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTAMASKPATTIRWFKG------NKELKGKSEVEEWSDMYTVTSQLMLKVHK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVH---IQMTYPLQGLTREGDAFELTCE 250
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                                                                                                                                                                                                                                                                    A;Reference number: Z19929
A;Accession: T24733
A;Status: pretiminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5175 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 24.6
Matches 87; Conservative
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A, Gene: CESP: F15G9.4a
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HIMSP3

poliovirus receptor homolog precursor - mouse

poliovirus receptor homolog precursor - mouse

poliovirus receptor homolog precursor - mouse

poliovirus muscallus domesticus (western European house mouse)

C;Speciess mas muscallus domesticus (vestern Buropean house ob-Jul-2004

C;Accession: A38211

R;Morrison, M.B.; Racaniello, V.R.

A;Title: Molecular cloning and expression of a murine homolog of the human poliovirus reparece number: A38211; MUID:92219365; PMID:1860525

A;Accession: A38211
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A; Residues: 1-467 < MOR>
A; Cross-references: UNIPROT: PD2507; GB: M80206; NID: g199785; PIDN: AAA39734.1; PID: g199786
C; Superfamily: poliovirus receptor; immunoglobulin homology
C; Reywords: duplication; glycoprotein; transmembrane protein
F; Reywords: duplication; glycoprotein; transmembrane protein
F; Reywords: poliovirus receptor homolog #status predicted < MAT>
F; Ref 467 Product: poliovirus receptor homolog #status predicted < MAT>
F; Ref 47-133 Domain: immunoglobulin homology < IMM1>
F; Ref 7-231 Domain: immunoglobulin homology < IMM2>
F; Ref 7-231 Domain: immunoglobulin homology < IMM2>
F; Ref 7-232 Domain: immunoglobulin homology < IMM3>
F; Ref 7-332 Dom
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A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2911/1; 2967/3; 2931/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2249
A;Molecule type: DNA
A;Residues: 1-5198 <WIL>
A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
A;Experimental source: clone F15G9
R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-5198 <WI2>
A;Cross-references: EMBL:247070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
A;Experimental source: clone T0989
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 KVSLTNVSISDEGRYFCQLYTDPPQESYT-TITVLVPPRNLMIDIQKD-TAVEGEEIEVN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 AIGKPOPVMVTWVRVDDEMPQHAVL----SGPNLFINNLNKTDNGTYRCEASNIVGKAHS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAMASKPATTIRWFKG------NKELKGKSEVEEWSDMYTVTSQLMLKVHK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 EDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVH---IQMTYPLQGLTREGDAFELTCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 VIVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPL----KDSRFQLLNFSSSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2468 DFKVSMLVAPSFDEPNIVRRITVNSGNPSTLHCPAKGSPSPTITWLKDGNAIE 2520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 11.9%; Score 261.5; DB 2; Length 5198; Similarity 24.6%; Pred. No. 1.2e-09; 87; Conservative 65; Mismatches 130; Indels 71:
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: T24734
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A,Cross-references: UNIPROT:P32507; GB:D26107; NID:g475017; FIDN:BAA05103.1; PID:g825507
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R;Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
Biol. Chem. 269, 8431-8438, 1994
A;Title: Amino acid residues on human poliovirus receptor involved in interaction with A;Reference number: A53437; MUID:94179228; PMID:8132569
A;Accession: A53437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIGNLQIQRYLEVQYKPQVHIQMIYPLQGLIREGDAFELICEAIGKPQPVMVTWVRVDDE 268
                                                                                                                                                                                              GKSEV--EEWSDM--YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRY-----LE 220
                                                                                                                                                                                                                                                                                                                                                 VOYKPOVHIQ---MTYPLOGLTREGDAFELTCEAIGKPOPVMVTWVRVDDEMPOHAVLSG 277
                                                                                                                                                                                                                                                                                                                                                                                                                    VOYEPEVTIEGFDGNWYLORMD-----VKLTCKADANPPATEYHWTTLNGSLPKGVEAQN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIIIIDSRAGEEG-TIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFA----RH--KGTYF 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
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C,Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQL-----LNFSSSELKVSLTNVSIS
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                                               QESYTTITVLVPPRNLMIDIQKD-TAVEGEEIEV---NCTAMASKPATTIRWFKGNKELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNLFINN-LNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: C57/BL6, brain
A; Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIP:146667)
C; Superfamily: poliovirus receptor; immunoglobulin homology
F; 47-133/Domain: immunoglobulin homology < IMM
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Best Local Similarity 22.6%;
Matches 90; Conservative
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poliovirus receptor mPVR -
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A; Residues: 1-530 < AOK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEGNYTCEFATFPNGTRRGVTWLRVIAQPEN-----HAEAQEVTIGPQSVAVARCV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMASKPATTIRWFKG-NKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEEPILLPVTLSVRYPPEVSIS-GYDDNWYLGRSEAI-LTCDVRSNPEPTDYDWSTTSGV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTTTTTLTILTITDSRAGEEGTIGAVDHAVIGGVVAVVVPA--MLCLLIILGRYFARHKG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SR-----DVGPLVWGAVGGTLLVLLLAGGFLALILLRGRRRKSPG 384
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A;Gross-references: GDB:583951
A;Map position: 11q23-11q24
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: glycoprotein; transmembrane protein
C;Keywords: glycoprotein; transmembrane proteict
C;Keywords: glycoprotein; transmembrane predicted <SIG>
F;31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F;356-379/Domain: transmembrane #status pradicted <MAT>
                                                                                                                                                                                                                                                                                                                     48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
F;375-467/Domain: intracellular #status predicted <INT>
F;54-131,174-229,274-320/Disulfide bonds: #status predicted
F;128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -NKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQL-----LNFSSSELKVSLTNVSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEGRYFCQLYTDP--PQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEV-----NCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STGGRPPARITWISSLGGEAKDTQEPGIQAGTVTIISRYSLVPVGRADGVKVTCRVEHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDE
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A,Molacule type: mmA
A,Residues: 1-518 <LOP>
A,Residues: 1-518 <LOP>
A,Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
                                                                                                                                                                                                                                                                                                                 PGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEV---ATISCQV------
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421
                                                                                                                                                              DB 1; Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 244; DB 2; Length 518; Pred. No. 1.18-09; 59; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387 TYFTHEAKGADDA------ADADTAIINAEGGONNSEEKKE
                                                                                                                                          11.2%; Score 21.5%; Pred, No. 6.5e-10; Pred, No. 6.5e-10; ive 72; Mismatches 196; Indels -1ve 72; Mismatches 196; Mismatches 196; Mismatches 196; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F,356-379/Domain: transmembrane #status predicted <TMM> F,36,72,82,139,287,308,333/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.1%;
25.1%;
                                                                                                                                                                                              Best Local Similarity 21.63
Matches 101; Conservative
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                                                                                                                                                          Query Match
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A, Accession: JE0099
A; Molecule type: mRNA
A, Residues: 1-725 - KUD>
A; Experimental source: UNIPROT: 073633; DDBJ: AB008162; NID: 93116226; PIDN: BAA25931.1; PID: 9318
A; Experimental source: heart
                                                                                                                                                                                                                                                                                                                                                                                          C;Comment: This protein mediates and regulates various cell-cell interactions through both C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immur F;413-475/Domain: immunoglobulin homology <IMM>
                                                                                                                       as
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R;Koike, S.; 1se, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has A;Reference number: A44194; MUID:93059651; PMID:1331508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 QLLNPNR-----QTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVS-----ISDEGRY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 LNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEIEVNCTAMASKPATTIRWFKGNKE-----LKGKSEVEEWSDMYTVTSQLMLKVHKE 194
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C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 KDVTVIEGEVATISC---QVN----KSDDSVIQLLN----PNRQTIYFRDFRPLKDSRFQL
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                                R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem, Biochhys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of sad-form neural cell adhesion molecules
A;Reference number: JE00099; MUID:98204770; PMID:9535795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 238; DB 2; Length 72
26.2%; Pred. No. 4.5e-09;
ive 61; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;512-589/Domain: fibronectin type III repeat homology <3FR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfemily: poliovirus receptor; immunoglobulin homology C;Keywords: transmembrane protein F;259-314/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 26.29
les 89; Conservative
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A,Molecule type: DNA
A,Residues: 1-417 <KOI>
C; Accession: JE0099
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Matches
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                                                                                                                                                                                                                                                                                                                                        C;Species: However, and the control of the control 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AGAGATGG----IIGGIIAAIIATAVAATGILICR 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 VPGLYISLVTWQRPDAPANHQNV--AAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQDTE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 ICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCKVEHESFEEPALIPVTLSVRYPPEVSIS-GYDDNWYLGRTDA-TLSCDVRSNPEPTGY 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 APPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----ELKVSLTNVSISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMIDIQKDTAVEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QLLNFSSS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 538;
                                     ----AGAGATGG----IIGGIIAAII 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 10.9%; Score 238.5; DB 2; Local Similarity 22.8%; Pred. No. 2.9e-09; les 110; Conservative 63; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----
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no putati

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A,Molecule type: mRNA
A,Residues: 1-1088 «KRI»
A,Cross-references: UNIPROT:P16170; EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g2146
A,Notes: the authors translated the codon AAA for residue 970 as Leu
C,Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol-
C,Comment: Several forms of NCAM are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of a large cytoplasmic domain fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
,219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                              cell adhesion molecule long domain form precursor - African clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POPVMVTWVRVDDEMPQH----AVLSGP---NLFINNLNKTDNGTYRCEASNIVGKAHS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEIEVNCTAMASKPATTIRWFKGNKE-----LKGKSEVEEWSDMYTVTSQLMLKVHKE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEITLICEA-SGDPIPSITWRTAVRNISSEATTLDGHIVVKEHIRM----SALTLKDIQY 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR-AAVTWFRDGQLLPSSNFSNIKIYSGPTSSSLEVNPDSENDFGNYNCTAINTIGHEFS 484
                                                                                                                                                                                                                                                  N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNFSSSELKVSLTNVSISDEGRYPCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;724-1089/Domain: intracellular #status predicted <INT> F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status
                               LTIITDSRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.7%; Score 234; DB 1; Length 10 Best Local Similarity 25.9%; Pred. No. 1.5e-08; Matches 88; Conservative 62; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTT3AG 346
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                                                                                                                                                                                                                                                                                                                                                             RiKrieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res. 17, 10321-10335, 1989
A;fitle: Primary structure and developmental expression
A;Reference number: S09600; MUID:90098871; PMID:2481269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFILVQADTPSS---PAIRKVEPYSSTVMIVFDEPDSTGG
                                                                                                                                                                                                                        N; Alternate names: NCAM-180
                                                                                                                                                                                                                                                                                                                                        C; Accession: S09600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Accession: S09600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
B44194

political seceptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B44194
C
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                                                                                                                                                                                                                                                                            RYLEVOYKPOVHIOMTYPLOGLTREGDAFELTCEAIGKPOPVMVTWVRVDDEMPOHAVLS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FCOLYIDPPOESYTT---ITVLVPPRNLMIDIOKDTAVEGEEIEV-NCTAMASKPATTIR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WFKGNKELKGKSEVEE----WSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQ 216
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                                                   FCQLYTDPPQESYTT---ITVLVPPRNLMIDIQKDTAVEGEEIEV-NCTAMASKPATTIR 160
                                                                                                                                                                                                                                                                                                                                236 VNLTVYYPPEVSIS-GYDNNWYLSQNEA-TLTCDARSNPEPTGYNWSTTMGPLPPFAVAQ 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 LTIITDSRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGT----YFTHE 392
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SQLTWSRHGESGSMAVFHQTQGPNYSEPKRLEFVAARLGTELRDASLRMFGLRVEDEGNY 121
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                                                                                                                                                                                                    | | | :: | | | : | : | : | : | : | CAQLLIRPVDKPINTTFICNVTNALGARQAELTYQVKEGPPSEPS-------
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C;Superfamily: poliovirus receptor; immunoglobul
F;259-314/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 AKGADDAADADTAIINAEGGONNSEEKKE 421
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Best Local Similarity 24.4%;
Matches 100; Conservative 5
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A;Molecule type: L.M. A;Residues: 1-417 <KOI> A;Residues: 1-417 <KOI> A;Crosa-references: UNIPROT:P15151; UNIPROT:Q96BJ1; EMBL:X64116; NID:g35809; PIDN:CAA4547. A;Crosa-references: UNIPROT:P15151; UNIPROT:Q96BJ1; EMBL:X64116; NID:g35809; PIDN:CAA4547. A;Note: 67-Ala was also found A;Note: the gamma form has 331-G1y and lacks residues 332-384 R;Mendelsohn, C.L.; Wimmer, B.; Racaniello, V.R.
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A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Cross-references: GB:N29535
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble fc.
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A;Cross-references: GDB:120324; OMIM:173850
A;Gene: GDB:purces: GDB:120324; OMIM:173850
A;Gene: GDB:120:11; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane proticity. 20/Domain: signal sequence #status predicted <2005
F;11-20/Domain: extracellular #status predicted <2005
F;21-3343/Domain: immunoglobulin homology <1000
F;21-35Domain: immunoglobulin homology <1000
F;259-214/Domain: immunoglobulin homology <1000
F;250-214/Domain: immuno
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75,868-411/Domain: intracellular #status predicted <INTP-
F;586-417/Domain: intracellular #status predicted
F;405-123,166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pre
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Cell 56, 855-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence,
A;Reference number: A90910; MUID:89168426; PMID:2538245
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                                                                                                                                                                                                                                                                                                                                                               poliovirus receptor splice form alpha precursor - human
N;Alternate names: poliovirus receptor H20A
N;Contains: poliovirus receptor beta
C;Species: Homo sapians (man)
C;Bate: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
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343 SRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLIILGRYF 381
                                                                                                  ------GMSRNAIİFLVLGILVF---LILLGIĞIYF 365
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F;159-223/Domain: immunoglobulin homology <IMM2>
F;159-314/Domain: immunoglobulin homology <IMM3>
F;559-314/Domain: immunoglobulin homology <IMM3>
F;344-367/Domain: transmembrane #status predicted <IMM>
F;368-392/Domain: intracellular #status predicted <IMT>
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status px
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A; Cross-references: GB:M24406
A; Cross-references: GB:M24406
C; Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f G; Genetics:
A; Gene: GDB:PVR; PVS
A; Gene: GDB:120134; OMIM:173850
A; Map position: 19413.2
A; Introns: 27/1; 143/1; 242/1; 281/2; 331/1
A; Introns: 27/1; 143/1; 242/1; 281/2; 331/1
C; Superfamily: poliovirus receptor; immunoglobulin homology
C; Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane profile 1: 20/Domain: signal sequence #status predicted <SIG>F; 1-20/Domain: extracellular #status predicted <SIG>F; 21-343/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                poliovirus receptor splice form delta precursor - human
Nalesriade names: poliovirus receptor H20B
C;Alesriade names: poliovirus receptor H20B
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A4304; B31496
R;Kois, HOzie, H; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Title: The poliovirus receptor protein is produced both as membrane-bound and secreted
A,Reference number: S12048, MUID:91006015, PMID:2170108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: A43024
A;Molecule type: DNA
A;Residues: 1-392 < KOI.
A;Coss.references: UNIPROT:P15151; EMBL:X64116
A;Note: 67-Ala was also found
R;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and
A;Reference number: A90910; MUID:89168426; PMID:2538245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 GNKELKGKSEVEEW-SDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIGGMPNTSQVPGFLSGTVTVTSLWILVPSSQVDGKNVTCKVEHESFEKPQLLTVNLTVY 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 YKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTLTITD 342
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Best Local Similarity
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A; Molecule type: mRNA
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A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2q31-2q31
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Job time : 26.9399 secs
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A;Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g101
C;Genetics: .
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242 YPPEVSIS-GYDNNWYLGQNEA-TLTCDARSNPEPTGYNWSTTMGPLPPFAVAQGAQLLI 299
                                                                                                                                              283 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTT
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                                                                                                                                                                                                                                                300 RPVDKPINTTLICNVTNALGARQAELTVQVKE----GPPSEHS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLIILGRYF 381
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                                                                                                                                                                                                                                                                                              85 SSSELKVSLTNVSISDEGRYFCQLYTD-PPQESYTTITVLVPPRNLMIDIQKDTAVEGEE 143
                                                                                                                                                                                                                                                                                                                                               829 VEGTASLEIIRVDMNDAGNFTCRATNSVGSKDSSGALIVQEPPSFVTKPGSKD-VLPGSA 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                888 VCLKSTFQGSTP-LITRWFKGNKELVSGGSCYITKEALESSLELYLV-----KTSD 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 GVPVICOVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQ 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 IEVNCTAMASKPATTIRWFKGNKELKG-----KSEVEEWSDMYTVTSQLMLKVHKEDD 196
                                                                                                                                                                                                      35 TVIEGEVATISCQVNKSDDSVIQ---LLN-----PNRQTIYFRDFRPLKDSRFQLLNF
   Length 7962;
Query Match
10.4%; Score 228.5; DB 2; Length
Best Local Similarity 26.1%; Pred. No. 4.4e-07;
Matches 80; Conservative 55; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1053 IVKESP 1058
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June 28, 2005, 09:38:22; Search time 106.117 Seconds (without alignments) 2041.237 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                  Run on:
```

US-10-622-237-4 2197 Title: Perfect score:

1 AAPPGLRLRLLLLLSAAAL.....TAIINAEGGQNNSEEKKEYF 423 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_03:*.
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

	Description	Q8r411 mus musculu	Q8k3t6 mus musculu	Q8r5m8 mus musculu	Q9by67 homo sapien	Q6ayp5 rattus norv	Q6f3j3 mus musculu	Q7tnll mus musculu	Q8n2f4 homo sapien	Q80vg4 mus musculu	Q9d6e7 mus musculu	Q86wb8 homo sapien	Q9z2h8 mus musculu	Q9qy14 mus musculu	Q9qy16 mus musculu	Q9qy15 mus musculu	Q9qy13 mus musculu	Q8n3j6 homo sapien	Q8izp8 homo sapien	Q6dj83 xenopus tro	_	Q8byp1 mus musculu	Q8bxj7 m mus muscu	_	Q6pfk4 brachydanio	Q7zxx1 xenopus lae	Q66kx2 xenopus lae	Q8nfz8 homo sapien	_	_	homo	Q9y4a4 homo sapien
SUMMARIES	ID	Q8R4L1	Q8K3T6	Q8R5M8	Q9BY67	Q6AYP5	Q6F3J3	Q7TNL1	Q8N2F4	Q80VG4	Q9D6E7	Q86WB8	0922н8	Q9QYL4	O9QYL6 ·	Q9QYL5	Q9QYL.3	Q8N3J6	Q8IZP8	Q6DJ83	Оввго	Q8BYP1	Q8BXJ7	Q8BZP4	Q6PFK4	Q7ZXX1	Q66KX2	Q8NFZ8	Q8R464	Q99N28	Q8N126	Q9Y4A4
	DB	~	7	~	7	~	~	~	~	7	~	~	~	7	7	~	~	~	~	~	N	~	~	~	~	N	N	7	7	7	~	7
	Query Match Length DB	445	445	456	442	476	428	417	443	336	336	333	295	306	295	289	278	435	437	433	404	404	395	395	405	394	390	388	388	396	398	381
de	Query	100.0	8.66	99.1	98.6	97.3	93.2	92.3	92.0	74.2	74.2	73.5	70.4	68.9	68.0	63.9	62.8	40.8	40.7	39.6	39.3	39.1	39.0	38.9	37.6	36.4	36.3	34.9	34.5	33.7	33.3	33.2
	Score	2197	2193	2176.5	2166	2138.5	2048.5	2027	2020.5	1631	1631	1615	1546	1513.5	1493	1404	1380.5	897	895	869.5	864	860	857	854	826.5	800	798.5	766.5	757.5	739.5	732.5	730.5
	Result No.	1	7	m	4	ស	9	7	80	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

	Qesaq, nomo sapien Qemzke homo sapien	Q6nur8 homo sapien O8k1h8 mus musculu	Q9nvj5 homo sapien						Q9jlb7 mus musculu	Q9jlb8 mus musculu	O57349 gallus gall
Q9UJP1	Q6MZK6	Q6NUR8 O8K1H8	Q9NVJ5	Q8BSQ8	900060	Q9JLB9	69NQS3	60ZI8O	Q9JLB7	Q9JLB8	057349
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715.5	413	389	362.5	360.5	337.5	334.5	325.5	323	303.5	303.5	283
32	3 t	32	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	ő	60	120	180
RESULT 1 ORALL Query Match 100.0%; Score 2197; DB 2; Length 445; Best Local Similarity 100.0%; Pred. No. 4.1e-149; Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps	1 AAPPGLRIALLILISAAALIPTGDGQNLPTKDVTVIEGEVATISCQVNKSDDSVIQLLN 	61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDBGRYFCQLYTDBPQESYTTI 	121 TVLVPPRNLMIDIOKOTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM	
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                                                                                                                                                                                                                                                                                                                                       202 YTVISQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDHAVIG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 GVVAVVVFAMLCLLIILGRYFPARKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDHAVIG 360
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   22 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN 81
                                                           262 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
                                                                                                                                                                                                                                                                                                           181 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                                                                                                                                                                                                                                                                                                                               241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Igsf4a; Synonyms=RA175;
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TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 201
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                                                        1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "SynCAM, a Synaptic Adhesion Molecule That Drives Synapse Assembly."; Science 297:1525-1531(2002).
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
REBL; AFSJ9424; AANO1614.1;
REBL; ABL8339429; BAD30018.1;
REBL; ABL8339272; Igsf4a.
RGD; MGI:1889272; Igsf4a.
RGD; GO:0016621; C:integral to membrane; TAS.
RGO; GO:000551; F:protein binding; IPI.
RGO; GO:000551; F:protein binding; IPI.
RGO; GO:000515; F:protein binding; IPI.
RGO; GO:000715; P:calcium-independent cell-cell adhesion; IDA.
RGO; GO:000715; P:calcium-independent cell-cell adhesion; IDA.
RGO; GO:000715; P:calcium-independent cell-cell adhesion; IDA.
RGO; GO:000715; P:cynaptogenesis; IDA.
RGO; GO:000715; P:cynaptogenesis; IDA.
RINTEPPRO; IRR003598; Neurexin-like.
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SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Synaptic cell adhesion molecule 1 (RA175 isoform c)
Name-1gsf4a: Synonyms-RA175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.8%; Score 2193; DB 2;
99.8%; Pred. No. 7.9e-149;
iive 1; Mismatches 0;
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SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGc2; 1.
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EYF 444
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X Brausberg R.L., Fedrigold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Wagner L., Schemen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Logdelland N.B., Farmer A.A., Rubin G.M., Hong L.,

RA Brants S.S., Logdelland N.B., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Logdelland N.B., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

RICHARDS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RILLAID D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

RA Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Generation and initial analysis of more than 15,000 full-length human
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258
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                                                                                                         199 YIVISQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYKLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                                                                                                          EGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
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                                                                                                                                                                                                                                                                            301 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTGEGTIGAVDHAVIG
                                                                            YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 katlus Morygistus (mat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC078966, AHJ78966.1;
Interpro; IPR003599; IG.
Interpro; IPR007110; Ig-like.
Interpro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   476 AA.
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SMART; SM00409; 1G; 3.
SWART; SM00408; 1Gc2; 3.
PROSITE; PS50835; 1G_LIKE; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse cDNA sequences."
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QGAYP5;
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                                                                                                                                                                                                                                         TVLVPPRNLMIDIQKDTAVEGEBIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 201
                                                                                                                                                                                                                                                                                                                                                   YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGKAHSDYMLYVYDPPTTITPTTTTTTTTTTTTTTTTTPPAVHDSRAGEEG 381
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                            AAPPGLRLRLLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN 81
                                                                                                                                PNRQTI Y FRDFRPLKDSRFQLLNFSSSELKVSLTNVSI SDEGRYFCQLYTDPPQESYTTI
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                                                                                                 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
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AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF132811; AAF69029.1; -
InterPro; IPR00110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003585; Neurexin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 3.
SROHENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2166; DB 2;
Pred. No. 6.7e-147;
2; Mismatches 4;
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(TrEMBLrel. 17, I
(TrEMBLrel. 25, I
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417; Conservative
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Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001
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01-OCT-2003
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TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
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                                                                                                                                                                                                                                                                                       142 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
                                                                                                                                                                                                                                                                                                                                                                             262 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNINKTDNGTYRCEASNI
                                                                                      1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                                                                         22 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                                                                                                                     61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
                                                                                                                                                                        PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
                                                                                                                                                                                                                                                                                                                                                           241 EGDAFELTCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C15TBL/6; TISSUE=Brain;
STRAIN=C2541094, PubMed=12826663; DOI=10.1074/jbc.M305387200;
SMIDGINE=25841094, PubMed=12826663; DOI=10.1074/jbc.M305387200;
Shingai T., Ikeda W., Kakunaga S., Morimoto K., Takekuni K., Itoh Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
"Implications of nectin-like molecule-"JGSF4/RAIJ5/SgIGSF/TSLC1/SynCAM1 in cell-cell adhesion and transmembrane protein localization in epithelial cells.";
J. Biol. Chem. 278:35421-35427(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0045202; C:synapse; IDA.
GO; GO:0005021; C:synaptic vesicle; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0016338; P:calcium-independent cell-cell adhesion; IDA.
GO; GO:0007155; P:cell adhesion; IDA.
                 93.2%; Score 2048.5; DB 2; Length 428; 94.3%; Pred. No. 1.7e-138; ive 1; Mismatches 6; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fujita E., Aikawa K., Momoi T.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY35138 AAQ02381.1;
EMBL; AB183401; BAD30020.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Created)
1-OCT-2003 (TrEMBLrel. 25, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Nectin-like molecule 2 (RAI75 isoform d).
               Query Match
Best Local Similarity 94.3
Matches 399; Conservative
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EYF 427
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Q7TNL1
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                                                                                                                                                                                                                                                                            TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 NSAEELDSEDLSDSRAGEEGAIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYF
                                                                                                                                       AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                                                                                                                                                    PNROTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
                                                                                                                                                                                                                                                         TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
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                                                                                                                   1 AAPPGLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                  31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fulita B., Alkawa K., Momoi T.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AB183400; BA230019.1;
EMGJ, AB183400; BA230019.1;
GO; GO:001621; C:isynapse; IDA.
GO; GO:000821; C:synapse; IDA.
GO; GO:000821; C:synaptic vesicle; IDA.
GO; GO:000521; F:protein binding; IPI.
GO; GO:001538; P:call adhesion; IDA.
GO; GO:007155; P:cell adhesion; IDA.
GO; GO:007155; P:synaptogenesis; IDA.
                                                    Length
                                                                                    Indels
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428 AA; 46903 MW; BIODFFIA2B893573 CRC64;
 ll protein.
476 AA; 51853 MW; 486A43D37082C8FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                  DB 2;
                                                 Score 2138.5; DB 2,
Pred. No. 6.9e-145;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 THEAKGADDAADATAIINAEGGONNSEEKKEYF 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THEAKGADDAADADTAIINAEGGONNSEEKKEYF 423
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InterPro; IPR007110; ig-like.
InterPro; IPR003598; ig_c2.
                                                  97.3%;
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SMART; SM00409; IG; 3.
SMART; SM00409; IGc2; 3.
PROSITE; PS50835; IG LIKE
SEQUENCE 428 AA; 46908
                                                                  Best Local Similarity 92.3
Matches 419; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Hypothetical
SEQUENCE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=RA175
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319 VGKAHSDYMLYVYDTTATTEPAVHGLTQLPNSAEELDSEDLSDSRAGEEGSIRAVDHAVI 378
                                                                                                                                                                                                                                                                                                                                                             61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 GGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADATAIINAEGGQNNSEBK 438
                                                                                                                                                                                                                                                                            YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last senotation update)
A secretion form of Sg1GSF/TSLC1 (RAJT5 isoform e).
Name=Igsf4a; Synonyms=RA175, 8Sg1GSF/STSLC1;
Buta musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pujita B., Aikawa K., Momoi T.;
SEQUENCE FROM N.A.
Pujita B., Aikawa K., Momoi T.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB092414; BAC66173.1; -.
R MGD; MGI:188272; Igsf4a.
R GO; GO:0016021; C:integral.
R GO; GO:0045202; C:synaptic vesicle; IDA.
R GO; GO:000812; F:pxotein binding; IPI.
R GO; GO:0016338; P:calcium-independent cell-cell adhesion; IDA.
R GO; GO:0007155; P:calcium-independent
R GO; GO:0007165; P:calcium-independent
R GO; GO:0007165; P:synaptogenesis; IDA.
R GO; GO:0007165; P:synaptogenesis; IDA.
                                                                                                                                                                                      1;
                                                                                                                                   443;
                                                                                                                                DB 2; Length
                                                                                                                                                                                      24; Indels
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STRANT-G57BL/6; TISSUE-Spleen cell-derived;
ILO A., Koma Y., Nagano T.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
           SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 3.
SEQUENCE 443 AA; 48648 MW; 046B43AA156F6F64 CRC64;
                                                                                                                          Query Match 92.0%; Score 2020.5; DB 2
Best Local Similarity '92.9%; Pred. No. 1.8e-136;
Matches 394; Conservative 5; Mismatches 24;
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Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.
Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
Nagahari K., Sugano S., Isogai T.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK075502; BAC11657.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                    Length 417;
                                                                                                                                                                                                                                                                                                                                                       0; Indels
GO; GO:0007416; P:synaptogenesis; IDA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-c2.
InterPro; IPR003598; Neurexin-like.
Pfam; PF00047; ig; 2.
BYART; SM00404; ig; 2.
SWART; SM00408; IG-c2; 1.
PROSITE; PSS0035; IG-LIKE; 3.
SEQUENCE 417 AA; 45779 MW; 98500180D37845C2 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PSEC0200.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                              92.3%; Score 2027; DB 2; 93.4%; Pred. No. 5.7e-137; ive 0; Mismatches 0;
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003598; Neurexin-like.
InterPro; IPR003585; Neurexin-like.
                                                                                                                                                                                                                                                                                                                         Best Local Similarity 93.4%;
Matches 395; Conservative
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SMART; SM00294; 4.1m; 1.
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Q8N2F4;
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336 AA;
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PROSITE; PS50835;
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                                                                                                                                                                                                                                                         AAPPGLRIRLILLILISAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                                                                                                                                                                                                                                                                                                    TVLVPPRNLMIDIQKDTAVEGEBIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
library, clone:2900073G06 product:immunoglobulin superfamily, member
4, full insert sequence.
                                                                                                                                                                                           Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                  Length 336;
                                                                                                                                                                                           0; Indels
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STRALNESSYBL/6J; TISSUE=Hippocampus;
MEDILNE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM COMSOCILUM;
                                                                                                       9EF3D8B8BE5E8F72 CRC64;
                                                                                                                                                74.2%; Score 1631; DB 2; 100.0%; Pred. No. 1e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 A.A.
                                                                                                                                                               100.0%; Prec. ...
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        InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGKAHSDYMLYVY 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||||||||||||||||||||VGKAHSDYMLYVY 334
                                                                                                                                                                   Best Local Similarity 100.
Matches 313; Conservative
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Anno H.,

Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Fururo M.,

Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Fururo M.,

Ra Hanagaki T., Hara A., Hayatsu M., Hiramoto K., Hiraoka T., Hori F.,

Rawai J., Kojima Y., Kono M., Izawa M., Kasukawa T., Kato H.,

Rawai J., Kojima Y., Konon H., Kodda M., Koya S., Kurihara C.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Sana H., Sasaki D., Shibata K., Shibata Y., Shiraki T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagama A., Takahashi F., Tanaka T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagami A., Yoshida K., Yoshino M.,

RA Sogabe Y., Suzuki H., Tagami M., Tagama A., Takahashi F., Tanaka T.,

RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

RA Sogabe Y., Suzuki Y.;

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                                                                                                                 Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Shibata K., Itoh M., "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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MEDLINE=CSTBL/GJ; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=110.101/gr.152600;
MISDLINE=20530913; PubMed=110.1101/gr.152600;
MISDLINE=20530913; PubMed=110.1101/gr.152600;
MISDLINE=20530913; MISDLINE=2053091; MISDLIN
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STRAIN=CS7BL/6J; TISSUE=Hippocampus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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Name=Igsf4a; Synonyms=Nec12;
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Matches 294; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Ito A., Koma Y., Nagano T.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB094146; BAC66178.1; -.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003598; Ig_c2.
Ffam; PR00047; ig; 2.
SMART; SM00409; IGc2; 1.
PROSITE; PS50835; IGG2; 1.
SROGUENCE 333 AA; 36915 MW; D7C1102F46D08492 CRC64;
                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Secretory isoform of TSLC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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Pred. No. 1.4e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.5%; Scor.
99.0%; Pred. No. ....
0; Mismatches
                                                                                                                                                                                                                                                                          333 AA
                                                                                                                                                                                                                                                                          PRT;
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Q922H8;
Q1-MAX-1999 (TrEMBLrel. 10, C)
01-MAX-1999 (TrEMBLrel. 10, L)
01-OCT-2003 (TrEMBLrel. 25, L)
Nectin-like protein 2.
                                                                                                           VGKAHSDYMLYVY 313
                                                                                                                                   URKAHSDYMLYVY 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.0
Matches 310; Conservative
                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                              Name=sTSLC-1;
                                                                                                           301
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086WBB
AC Q86WB
AC Q86WB
DT 01-JU
DT 0
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Q922H8
ID Q9Z2H
AC Q9Z2H
DT 01-MA
DT 01-MA
DT 01-MC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYM 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYVYDPPTTIPPPTTTTTTTTTTTTILTIITDSRAGEEGTIGAVDHAVIGGVVAVVVFA 369
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                                                                                                                                                                                                     DEQUENCE FROM N.A.

2. A Lanu Y., Du G., Chen J., Yuan J., Qiang B.;

2. Submitted (ARR-1998) to the EMBL/GenBank/DDBJ databases.

3. Submitted (ARR-1998) to the EMBL/GenBank/DDBJ databases.

3. Roj. MG1.188272; Igsta.

3. Roj. GO:0015201; C:integral to membrane; TAS.

4. Roj. GO:0016212; C:synapse; IDA.

5. Roj. GO:00045202; C:synapse; IDA.

6. Roj. GO:00045202; C:synapse; IDA.

7. Roj. GO:00016338; P:calcium-independent cell-cell adhesion; IDA.

7. Roj. GO:0007155; P:call adhesion; IDA.

7. Roj. GO:0007155; P:call adhesion; IDA.

8. Roj. GO:0007155; P:call adhesion; IDA.

9. 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adhesion protein RATJ5C.
Name=158f4a; Synonyms=ral75C;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.4%; Score 1546; DB 2; L 100.0%; Pred. No. 1.1e-102; Live 0; Mismatches 0;
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Gaps

189

249

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PROURNUE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8; MEDILINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8; Medical E., Soyama A., Momoi T.;

"Rai75, which is the mouse ortholog of TSLC1, a tumor suppressor gene in human lung cancer, is a cell adhesion molecule.";

Exp. Cell Res. 287:55-66(2003).

Exp. Cell Res. 287:55-6(2003).

EMGD; MGI:1889272; Igg64a.

GO; GO:0016021; C:synaptic vesicle; IDA.

GO; GO:0016215; C:synaptic vesicle; IDA.

GO; GO:0016515; P:protein binding; IPI.

GO; GO:00155; P:protein binding; IPI.

GO; GO:00155; P:protein binding; IPA.

GO; GO:00155; P:sprotein independent cell-cell adhesion; IDA.

GO; GO:0015838; P:calcium-independent cell-cell adhesion; IDA.

GO; GO:0015838; P:calcium-independent cell-cell adhesion; IDA.

GO; GO:0015838; P:protein independent cell-cell adhesion; IDA.

GO; GO:0015838; P:calcium-independent cell-cell adhesion; IDA.

GO; GO:0015838; P:calcium-independent cell-cell adhesion; IDA.

GO; GO:0001585; P:protein independent cell-cell adhesion; IDA.

GO; GO:0001585; P:protein independent cell-cell adhesion; IDA.

GO; GO:0001585; P:protein independent cell-cell adhesion; IDA.

GO; GO:000585; P:protein independent cell-cell adhesion; IDA.

GO; GO:0007155; P:protein independent cell-cell adhesion; IDA.

GO; GO:000585; P:protein independent cell-cell adhesion; IDA.

GO; GO:000585; P:protein independent cell-cell adhesion; IDA.

GO:0007155; P:protein independent cell-cell adhesion; IDA.

GO:0007155; P:protein independent cell-cell adhesion; IDA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALELTC 120
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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       GO; GO:0007155; P:cell adhesion; IDA.

GO; GO:0007416; P:synaptogenesis; IDA.
InterPro; IPR00310; Ig-11ke.
InterPro; IPR00358; Neurexin-like.
InterPro; IPR00358; Neurexin-like.
Pfam; PF00047; ig; 1.
SMART; SM00294; 4.1m; 1.
SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGC2; 1.
PROSITE; PS08385; IGC2; 1.
SROSITE; PS08385; IG LIKE; 2.
SEQUENCE 295 AA; 32347 MW; FDD9E8145C6B971B CRC64;
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SMART; SW00294; 4.1m; 1.
SMART; SW00408; IGC2; 1.
PROSTIE; PS50835; IG LIKE; 2.
SEQUENCE 289 AA; 31811 MW; 8D1B836D0565AEA4 CRC64;
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0.1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
0
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96.6%; Pred. No. 6.8e-99;
tive 2; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Igsf4a; Synonyms=ral75b;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 96.64
Matches 284; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adhesion protein RA175B.
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Q9QYL5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAIGKPOPVWVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYM 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTT318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML 60
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R MGD; MGI:1889272; Igsf4a.

R GO; GO:0016021; C:integral to membrane; TAS.

R GO; GO:0015202; C:syrapse: IDA.

R GO; GO:0008512; C:syrapse: IDA.

R GO; GO:0008515; F:protein binding; IPI.

R GO; GO:0015318; P:calcium-independent cell-cell adhesion; IDA.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:0007156; P:syraptcogenesis; IDA.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003589; Ig-C2.

R InterPro; IRR003589; Neurexin-like.

R SMART; SM00294; 4.1m; 1.

R SMART; SM00408; IGC2; 1:

R PROSITE; PSS6035; IG LIKE; 2.

SEQUENCE 306 AA; 33522 MW; A4CE37B0F23554D5 CRC64;
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Name=Igsfa; Synonyms=ra175a;
Mus muscules (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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Search completed: June 28, 2005, 09:53:50 Job time : 107.117 secs

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	Copyright	GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	
protein -	protein - protein search, using sw model	using sw model	
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1442.016 Million cell updates/sec Run

US-10-622-237-4

2197 1 AAPPGIRLRLLLLLLSAAAL.....TAIINAEGGQNNSEEKKEYF Perfect score:

BLOSUM62 Sequence:

Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* A_Geneseq_16Dec04:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		df			SUMMARIES		
Result		Query					
No.	Score	Match	Length	BB	CI CI	Description	
	2197	100.0	423	m	AAY45093	Aay45093 Mouse lym	E
7	2169	98.7	442	m	AAB25619	Aab25619 Protein e	Φ
٣	2169	98.7	442	m	AAY94341		-
4	2169	98.7	442	m	AAY45092	Aay45092 Human lym	E
ι,	2169	98.7	442	Ŋ	AAE19887	Aae19887 Human tum	E
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10	2166	98.6	442	9	ABO07196	Abo07196 Human p53	m
11	2166		442	9	AB007231	Abo07231 Human p53	
12	2166	98.6	442	7	ADE61605	Ade61605 Human Pro	o
13	2166	98.6	442	7	ADE61608	Ade61608 Human Pro	o
14	2149	97.8	440	~	AAY17830	Aay17830 Human PRO	o
15	2149	97.8	440	ო	AAB01321		o.
16	2149	97.8	440	4	AAU29040	Aau29040 Human PRO	Q
17	2149	97.8	440	9	ABU58416	Abu58416 Human PRO	Q
18	2149	97.8	440	9	ABU87964	Abu87964 Novel hum	Ē
19	2149	97.8	440	9	ABU84279	Abu84279 Human sec	ŭ
20	2149	97.8	440	9	ABR66153	Abr66153 Human sec	ပ္
21	2149	97.8	440	9	ABR65543	Abr65543 Human sec	ņ
22	2149	97.8	440	9	ABU99483	Abu99483 Human sec	ņ
23	2149		440	9	ABU55930	Abu55930 Human sec	Ö
24	2149	97.8	440	9	ABU82722	Abu82722 Human PRO	Q
25	2149	97.8	440	9	ABU89843	Abu89843 Novel hum	Ē

Abr68092 Human sec	Abu96145 Novel hum	Abu92576 Human sec	Abo08653 Human sec	Abo02705 Human sec	Abr74859 Human sec	Abr94621 Human sec	Human	Abu85594 Human PRO	Abu98754 Novel hum	Novel	Abu91675 Novel hum	Human	Abu86209 Human sec	Abu67422 Human sec	Human	Abr99368 Human sec	Abr98758 Human sec	Abol6281 Human sec	Abr92181 Human sec
ABR68092	ABU96145	ABU92576	ABO08653	ABO02705	ABR74859	-	ABU60240	ABU85594	ABU98754	ABU97969	ABU91675	ABU89368	ABU86209	ABU67422	ABU80450	ABR99368	ABR98758	ABO16281	ABR92181
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ALIGNMENTS

Lymphoid derived dendritic cell adhesion molecule; LDCAM; mouse; B7-1; B7-11; T cell proliferation; natural killer cell; NK; tumour cell; biological activity; quality control reagent; treatment; inflammation; immune system disorder; autonimmune; viral infection; infectious disease; organ transplant rejection; bone marrow; modulator; immune response. Mouse lymphoid derived dendritic cell adhesion molecule. AAY45093 standard; protein; 423 AA. 31-MAY-2000 (first entry) AAY45093; AAY45093

147. .149 /note= "N-Glycosylation site" 286. .288 "N-Glycosylation site" "N-Glycosylation site" /note= "N-Glycosylation site" 'note= "N-Glycosylation site" "N-Glycosylation site" Location/Qualifiers 1. .356 /label= Extracellular_domain 357. .377 /label= Transmembrane_domain 378. .423 /label= Cytoplasmic_domain . . . 292 /note= "N .97 49. .51 /note= " 83. .85 'note= Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Key Domain Mus sp Domain Domain

WO200008158-A2

99WO-US017905. 05-AUG-1999; 17-FEB-2000

98US-0095672P 07-AUG-1998;

(IMMV) IMMUNEX CORP.

21-NOV-2000 (first entry)

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The present amino acid sequence is the mouse lymphoid derived dendritic cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic cells and displays homology to adhesion molecules, B7-1 and cyroplasmic region of B7-L1. Mouse LDCAM is found on whole embryo, testes, triple negative cells murine splenic and lymph node CD8+, S49.1 and dendritic cells. LDCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and as quality control reagents of LDCAM binding proteins. LDCAM may be used for treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells or
                                                                                                                         molecules designated LDCAM are capable of altering or modulating T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevention or reducing the effect of organ and bone marrow transplant rejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells on
                                                                                                                                                                                                  Claim 7; Page 46-47; 44pp; English.
  Baum PR, Fanslow WC;
                                                   WPI; 2000-205712/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells bearing B7L-1
                                                                           N-PSDB; AAZ50883
                                                                                                                         Novel molecule cell function.
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Sequence 423 AA;

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240
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                                                                                                                       PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
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                                                                  1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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                                                                                                                                                                                                               YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                    AAPPGLRLRLLLLLLSAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                          Gaps
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Length 423;
100.0%; Score 2197; DB 3; Length
100.0%; Pred. No. 2.5e-151;
iive 0; Mismatches 0; Indels
                          423; Conservative
Query Match
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Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer,
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                                           Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAPPGLRIRLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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Pred. No. 2.9e-149;
1; Mismatches 4; Indels C
                                                                                                                                                                                                                                                                          Moore PA,
                    Protein encoded by human secreted protein gene #11.
                                                                                                                                                                                                                                                                          Kenny JJ,
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 182-183; 803pp; English.
                                                                                                                                                                                                                                                                          Olsen HS, Young PE,
                                                                                                                                                                                                                                                                                                                                                               wounds, and infectious diseases.
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Best Local Similarity 98.8
Matches 418; Conservative
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                                                                                                                                                               WO200029435-A1.
                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                         27-OCT-1999;
                                                                                                                                                                                                                               28-OCT-1998;
                                                                                                                                                                                   25-MAY-2000,
                                                                                                                                                                                                                                                                                     Greene
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AAB25619 standard; protein; 442 AA.

AAB25619;

RESULT 2
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AC AAB2

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WO200028032-A2
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07-DEC-1998;
08-MAR-1999;
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                                                          EGDAFELTCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
                                                                                        VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTGAVDHAVIG 360
                                                                                                       378
                                                                                                                     GVVAVVVFAMLCLLILGRYPARHKGTYFTHEAKGADDAADDAIINAEGGONNSEEKK 420
                                                                                                                            Human; HCSRP; cytostatic; antiarthritic; antirheumatic; antiasthmatic; immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic; neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma; rheumatoid arthritis; aethma; atherosclerosis; akathesia; Alzheimer's diseases; multiple sclerosis; epilepsy.
                                                                   TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
                             YTVTSQLMLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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label= Immunoglobulin_domain
                                                                                                                                                                                                                                                   Human cell surface receptor protein #8.
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/label= Signal_peptide
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label= HCSRP-8
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The present sequence is a novel human cell surface receptor protein (HCSRP) designated HCSRP-8. The nucleotide sequence was identified in Incyte Clone 312266 from the cDNA library LUNGNOTO2, which was made from Incyte Clone substance. A number of Incyte Clones were used to assemble the consensus sequence. BLAST analysis showed that the sequence is homologous to immuno superfamily protein B12 31779242. HCSRP and its antagonist are useful for preventing or treating disorders associated with decreased or increased expression or activity of HCSRP. Such disorders include cancers such as leukaemia and melanoma, immune disorders unclude cancers such as leukaemia and atherosclerosis, bacterial and parasitic infections and neuronal disorders such as athematoid arthritis, asthma and atherosclerosis, bacterial and parasitic infections and neuronal disorders such as athematoid arthritis, asthma and atherosclerosis, colymples and polymuleotides encoding HSCRPs may be used as hybridisation probes to disponse these conditions. Anti-HCSRP antibodies may be used as magnosists, as a targeting or delivery mechanism for bringing pharmaceutical agents into contact with cells or tissues expressing HCSRP and for diagnosis of HCSRP-related disorders. HCSRP and its catalytic or immunogenic fragments are useful for drug screening using libraries of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAPPGLRIKILLILIFSAAALIPIGGGONLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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                                                                /note= "potential phosphorylation site"
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/label= Immunoglobulin_domain
note= "potential phosphorylation site"
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                                                                                                                                                                                                                                                                                   'note= "potential glycosylation site"
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Pred. No. 2.9e-149;
1; Mismatches 4;
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/label= Transmembrane_domain
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98US-00206647.
99US-0123404P.
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N-PSDB; AAA27051.
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99WO-US017905
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                                                                                                                                                                                                                                                                                                                                                                                             Lymphoid derived dendritic cell adhesion molecule; LDCAM; human, B7-1, B7-Li, T cell proliferation; natural killer cell; NK; tumour cell; biological activity; quality control reagent; treatment; inflammation; immune system disorder; autoimmune; viral infection; infectious disease; organ transplant rejection; bone marrow; modulator; immune response.
                                 TVLVPPRNLMIDIQKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM
                                                                                                                                                                             YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                                                                                                                                                  PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
                                                                                     TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
                                                                                                                                                         YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                                                                                                                               EGDAFELTCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
                                                                                                                                                                                                                                                                                                       VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTGAVDHAVIG
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/note= "N-Glycosylation site"
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/note= "N-Glycosylation site"
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/note= "N-Glycosylation site"
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/label= Extracellular_domain
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/label= Transmembrane_domain
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/label= Cytoplasmic_domain
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/label= Leader_peptide
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WO200008158-A2

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The present amino acid sequence is the human lymphoid derived dendritic cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic cells and displays homology to adhesion molecules, B7-1 and cytoplasmic region of B7-L1. Human LDCAM is expressed in breast, retina, foetal liver, spleen and heart, lung, muscle, placenta, thyroid and lung carcinoma. LDCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and sequentially control reagents of LDCAM binding proteins. LDCAM may be used for treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for treating the effect of organ and bone marrow transplant rejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
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molecules designated LDCAM are capable of altering or modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 TVLVPPRNLMIDIOXDTAVEGEBIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 YTVTSQLMLXVHKEDDGVPVICQVEHPAVTGNLQTQRYLLEVQYXPQVHIQMTYPLQGLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.7%; Score 2169; DB 3; 98.8%; Pred. No. 2.9e-149; ive 1; Mismatches 4;
                                                                                                              Claim 7; Page 42-43; 44pp; English.
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Best Local Similarity 98.8
Matches 418; Conservative
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The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABQ93288-ABQ93332). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
(I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral
                                                                                                                                                                                                                  VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTGAVDHAVIG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, vulnerary, dermatological, neuroprotective, nootropic, cancer, antiparkinsonian; immunostimulant, cytostatic; immunosuppressive, antidiabetic; antiallergic; gene therapy; wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
                                                        YTVTSQLMLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQXKPQVHI QMTYPLQGLTR
                                                                                                                                                  319 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTDSRAGEEGSIRAVDHAVIG
                                                                                                                                                                                                                                                                                                                                            379 GVVAVVVPAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK
                             YTVTSQLMLKVHKBDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                         EGDAFELTCEA1GKPQPVMVTWVRVDDEMPQHAVLSGPNLF1NNLNKTDNGTYRCEASN1
                                                                                                                                                                                                                                                                                                                   361 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 262; 284pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ren F, Zhang J,
Wehrman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou P, Xue AJ,
iu C, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP62825 standard; protein; 442 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sclerosis, diabetes and allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-AUG-2001; 2001WO-US027093.
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Wang D, Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-583321/62.
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Zhao QA,
                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for detecting cell proliferative disorder associated with tumour suppressor lung cancer 1 (TSLC1) in a subject. The method comprising contacting a cell component of a proliferating cell with a reagent that detects level of the cell component in the proliferating cell and determining modification in the component in proliferating cell as compared with a healthy cell, where modification indicates disorder associated with a healthy cell, where modification indicates disorder associated with TSLC1. The method is useful for detecting a cell proliferative disorder (e.g. liver, lung or pancreatic cancer) associated with tumour suppressor lung cancer (TSLC1) in a subject. The invention is useful in gene therapy and for treating a cell proliferative disorder such as lung cancer (human non-small cell lung cancer), liver cancer (hepatocellular cancin cancer cancer cancer (hepatocellular carcinoma) or pancreatic cancer associated with modification of TSLC1 production, where a reagent which modulates (preferably, increases) TSLC1 level in the cells, is employed. The present sequence is human TSLC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
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                                                                                                                                                                                                                                                                                            Human; hepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1;
liver; lung; pancreatic cancer; cell proliferative disorder; cytostatic;
gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting cell proliferative disorder associated with tumor suppressor lung cancer (TSLC) 1 in subject, comprises contacting proliferating cell of subject with reagent detecting TSLC1 and detecting modification in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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                                                                                                                                                                                                                                                                 Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.7%; Score 2169; DB 5; 98.8%; Pred. No. 2.9e-149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 49-50; 59pp, English.
                                                                                                                    AAE19887 standard; protein; 442 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-2001; 2001WO-US025690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-AUG-2000; 2000US-0225264P
                                                                                                                                                                                                                  (first entry)
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Matches 418; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-241913/29.
  441
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EYF
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                  18-JUN-2002
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                                                                                                                                                                   AAE19887;
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                                                                                                                                                                                                                TVLVPPRNIMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM 198
                                                                                                                                                                                                                                                                                              GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK 438
                                                                                                                                                             PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
                                                                                                                                                                                                     IVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
                                                                                                                                                                                                                                                                                                                          VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTILTITDSRAGEEGTIGAVDHAVIG 360
                                                                                                                                                                                                                                                                                                                                                                  GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK 420
                                                                                                                       09
                                                                                                                                           78
sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                       YTVTSQLMLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHI QMTYPLQGLTR
                                                                                                                                   AAPPGLRLRLLLLLRSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                                                                                                                                         PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
                                                                                                                                                                                                                                                                                  EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
                                                                                                                       1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                                                                                                                                                                                                            YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; antiinflammatory; immunomodulator; neuroprotective; hemostatic; gene therapy; cancer; inflammation; immune disorder; neurological disorder; blood clotting disorder; food additive;
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0
                                                                               98.7%; Score 2169; DB 5; Length 442; 98.8%; Pred. No. 2.9e-149;
                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human novel secreted protein from gene 11 #3.
                                                                                                  1; Mismatches
                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preservative; human; secreted protein
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19-APR-2000; 2000US-0198407P.
30-0CT-2000; 2000US-0243792P.
18-APR-2001; 2001US-00836353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-2001; 2001US-00984130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                   Matches 418; Conservative
                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         EYF 423
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                                                           Seguence 442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003055231-A1.
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The invention relates to an isolated nucleic molecule that is at least CC 95% identical to 18 human cDNA sequences representing 12 novel genes encoding secreted proteins or a polymucleotide fragment of the cDNA sequence contained in American Type Culture Collection (ATCC) deposit No. defined in the specification, its species homologue, a variant or allelic variant of the polymucleotide having a polymucleotide capable of hybridising under conditions the polymucleotide, where the polymucleotide having a polymucleotide capable of hybridising under conditions the polymucleotide, where the polymucleotide having a mucleotide sequence of only A or T residues. Also included are recombinant vectors, host cells (for producing the polympeptide), the secreted polymeptide (comprising a sequence that is at least 95% included are recombinant vectors, host cells (for producing the polympeptide), the coretin, variant, allelic variant or species homologue), antibodies that specifically bind to the polympeptides, domain, epitope, full-length coretin, variant, allelic variant or species homologue), antibodies that specifically bind to the polympeptides, diagnosing, treating, preventing or medical condition and activity in a biological assay (by expressing the collection or a succeptibility to a captuence in a cell, isolating the supernatant in the supernatant and an ectivity.) The polympeptides, nucleic acids and antibodies are useful for diagnosing a pathological condition, for preventing, treating, or amelication or a pathological and blood clotting disorders (many examples are disorders). munological probes for differential identification of the creaticition mapping. The polypeptides and antibodies are useful for chromosome identification, The mucleic acids are also useful for restriction mapping The polypeptides and antibodies are useful for chromosome identification. The mucleic acids are also useful for restrictional propes for decrease storage capabilities, fat content or other nutricional components. The polypeptides and a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Greene JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Wei Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 72; 454pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Young PE, Kenny JJ, O'
M, Liu D, Crocker PR;
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Matches 418; Conservative
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NI J.
YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
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GREENE J M.
                                                                                                                                                                                                                                                                          RUBEN S M.
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or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates
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                                                                                                                           EGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 318
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                                                                                                                                                                                   GVVAVVVFAMLCLLIIGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK 438
The invention discloses a composition comprising two or more isolated rat
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                                                             YTVTSQLALKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                                                                      VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTGAVDHAVIG
                                                                                                           EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
                                                                                                                                                                                                                                  GVVAVVVFAMLCLLI ILGRYFARHKGTYFTHEAKGADDAADADTAI INAEGGONNSEEKK
                                               YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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                                                                                                                                                                                                                                                                                                                                                                                                       ADE54238 standard; protein; 442 AA.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in reating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that polypeptides or their antibodies. The polynucleotide or the compound that collypeptides or their antibodies. The polynucleotide or the compound that polypeptides is activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene the sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK 420
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 442;
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98.7%; Score 2169; DB 7;
Best Local Similarity 98.8%; Pred. No. 2.9e-149;
Matches 418; Conservative 1; Mismatches 4;
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The invention relates to an isolated nucleic acid sequence, or its allelic variant, a fragment of the cDNA sequence, or its fragment, domain, epitope or species homologue. The nucleic acid is useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, liver disorders such as hepatitis or neural disorders such as Alzheimer's disease. The present sequence represents the amino acid sequence of a novel human secreted protein associated
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                                                                                                                                                                                                                                                                                       New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g. cancer,
                                                                                                                                                                                                                          Greene JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.7%; Score 2169; DB 8;
98.8%; Pred. No. 2.9e-149;
iive 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 136; 380pp; English
                                                                                                                                                                                                                         Olsen HS,
                                                                                                                                                                                                                                                                                                                 liver disorders or neural disorders.
                                                 98US-0105971P.
99WO-US025031.
2000US-0198407P.
                        18-APR-2001; 2001US-00836353
                                                                                                                                                                                                                       Young PE, Kenny JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418; Conservative
                                                                                                               YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
WEI Y.
GREENE J M.
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Best Local Similarity
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19-APR-2000;
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10-JUL-2003
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                                                                                                                                                                   (WEIY/) (GREE/) (RUBE/)
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antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.
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                                                                                                                                                                                                                                                                                                       Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
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                                                                                                                                                                                                                                           Human p53 modifying protein, SEQ ID 156.
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                                                         ABO07196 standard; protein; 442 AA
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15-FEB-2002; 2002US-0357253P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-156859/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                              13-AUG-2003
                                                                                                                     ABO07196;
RESULT 10
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The invention relates to identifying (M1) a candidate p53 pathway conductanting an assay system comprising a purified HM education agent, by contacting an assay system comprising a purified HM p03 pathway in polypeptide (human orthologue of genes that modify the p53 pathway in Drosophila) or nucleic acid with a test agent under conditions, where but activity, and detecting a test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell defective in p53 function with a cell (comprising contacting at each activity of the assay system. CC contacting a cell defective in p53 function is restored), modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide comprising and diagnosing (M4) a disease in a patient (comprising: (a) obtaining a biological sample comparison; (b) contacting the sample with a probe for HM expression of identifying modulators of the p53 pathway. A probe for HM expression contently in a patient, where the cancer has greater than 25 % expression level. In a patient, where the cancer has greater than 25 % expression level. Modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, of a cell, thus restoring the p53 pathway of a cell, thus restoring M3) are useful for modulating the p53 pathway of a cell, thus restoring the p53 pathway such as angiogenic, also proliferation or progression through the cell cycle. (M2) and (M3) are useful for treating defects in the p53 pathway such as angiogenic, also useful for treating defects in the p53 pathway such as angiogenic, apoptotic or cell proliferation disorders in the p53 pathway such as angiogenic, appoptotic or cell proliferation disorders in the p53 pathway such as angiogenic.

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                                                                                                                                                                                                                                     GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADDAIINAEGGQNNSEEKK 438
                                                                                                                                                                            YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR 258
                                                                             78
                                                                                                                                                                                                                                                                                                                                                                                                               Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.
                                                                                                                                                           YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYELQGLTR
                                                                         AAPPGLRLRLLLLLFSAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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                                                             1 AAPPGLRLRLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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represents a human p53 pathway modifying protein
                               6; DB 6;
4.8e-149;
                              98.6%; Score 2166; I 98.6%; Pred. No. 4.8e ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID 191
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10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
                                                                                                                                                                                                                                                                                                                                                                                                Human p53 modifying protein,
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                                              Conservative
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                                    al Similarity
417; Conser
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               Sequence 442 AA;
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The invention relates to identifying (M1) a candidate p53 pathway condulating agent, by contacting an assay system comprising a purified HM collypeptide (human orthologue of ganes that modify the p53 pathway in Drosophila) or nucleic acid with a test agent under conditions, where but contrologue activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator contacting a cell defective in p53 function with a candidate modulator contacting a cell defective in p53 function with a candidate modulator contacting a cell defective in p53 function with a candidate modulator contacting the cell with a mammalian cell (comprising contacting the cell with a mapped or a disease in a patient (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) contacting the sample with a probe for HM expression; (C) comparison indicates a likelihood disease). (M1) is useful comparison indicates a likelihood disease). (M1) as useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. (C) in a patient, where disease or disease or disease or cell the p53 pathway, such as, angiogenesis, apoptotic or cell conditations, where disease or disease prognosis is related to proliferation of sorders (G) cancer). Another two new methods (M2 and C) the p53 function of the cell, so that the cell undergoes normal condition or prograssion through the cell undergoes normal condition or prograssion through the cell undergoes normal calso useful for treating defects in the p53 pathway of a cell, cancer also useful for treating defects in the p53 pathway of a cell, calculating defects in the p53 pathway of a cell, calculating defects in the p53 pathway of a cell, calculating defects in the p53 pathway such as angiogenic, also useful for treating defects in the p
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Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in Drosophila.
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                                                                                                                                                                                                                               678pp; English
                                                                                                                                                                                                                               Example 2; Page 557-559;
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139 TVLVPPRNLMIDIQRDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM 198
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                        Query Match

98.6%; Score 2166; DB 7;
Best Local Similarity 98.6%; Pred. No. 4.8e-149;
Matches 417; Conservative 2; Mismatches 4;
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
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GENBANK; AAF69029.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying a negent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polyneptides or their antibodies. The polynucleotide or the compound the composition of pain and a pharmaceutical composition comprising the one or more polynetides is activity is useful for preparing a medicament for treating pain and a sparal segmental nerve injury (SNI)) in an animal (e.g. gene context) in the sequence data for this patent did not form part of the printed the specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form directly from WIPO at the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                          chronic constriction injury; CCI;
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                                                                                                                                                                                                                                                                                                                                            Human Protein AAF69029, SEQ ID NO 7525
                                                                                                                                                                                   ADE61605 standard; protein; 442 AA.
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spared nerve injury; SNI; Chung.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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standard; protein; 440 AA.

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more isolated rat
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preparing a medicament for treating pain in an animal
              two
              invention discloses a composition comprising
                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
       Claim 1; Page; 1017pp; English.
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Sequence 442 AA;

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138
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Length 442;
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98.6%; Score 2166; DB 7;
98.6%; Pred. No. 4.8e-149;
tive 2; Mismatches 4;
            Best Local Similarity 98.6
Matches 417; Conservative
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RESULT. 14 AAY17830

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The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-prolliferative and immunosuppressive activity. The proteins and polyjvucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
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                                                                                                                    Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
secreted protein; transmembrane protein; inflammation disorder.
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Pred. No. 8.2e-148;
1; Mismatches 4;
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                                                                                                                                                                                                                                                                                                  970S-0069278P-
970S-0069334P-
970S-0069425P-
970S-0069694P-
970S-006960P-
970S-0069870P-
970S-0069870P-
970S-0069873P-
                                                                                        Human PRO355 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.8%;
Best Local Similarity 98.3%;
Matches 416; Conservative
                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
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                                                                                                                                                                 Homo sapiens
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16-DEC-1997;
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New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptors/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human nucleic acids encoding secreted and transmembrane polypeptides,
designated as PRO polypeptides, useful as pharmaceutical and diagnostic
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HB, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
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98.3%; Pred. No. 8.2e-148;
iive 1; Mismatches 4;
                       "N-myristoylation site"
                                     428. .432
/note= "N-myristoylation
430. .434
/note= "N-glycosylation s
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98US-0112850P.
98US-0113296P.
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Matches 416; Conservative
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Hillan KJ, Kljavin IJ,
                     'note=
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N-PSDB; AAA49563.
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                                                                                                                                                YTVTSQLMLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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/note= "Tyrosine kinase phosphorylation site"
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/note= "Tyrosine kinase phosphorylation site"
365. .371
/note= "N-myristoylation site"
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'note= "N-myristoylation site"
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/note= "N-myristoylation site"
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/note= "N-glycosylation site"
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/note= "N-glycosylation site"
306. .310
/note= "N-glycosylation site"
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/label= Signal peptide
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/label= Transmembrane
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99. .103
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-778-187B-2
US-09-984-130-136
US-09-836-353A-136
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US-09-778-1878-4
US-10-302-041-22
US-10-622-237-4
US-10-615-115-112
US-10-015-115-112
                                                                                                                                                                                                                                                                                                                                     of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       1717557 segs, 384547976 residues
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                                                                     protein search, using sw model
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Maximum DB seq length: 200000000
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US-10-302-041-20

US-10-403-107-11

US-10-015-115-111

US-10-015-115-111

US-10-015-115-111

US-10-018-115-10

US-10-984-408-21

US-09-944-457-61

US-09-944-457-61

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US-09-944-49-61

US-09-944-43-61

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FION: Molecules Designated B7L1
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US-09-944-822-61
US-09-943-784-61
US-09-943-684-61
US-10-052-586-34
US-10-174-590-34
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US-10-174-591-34
US-10-175-737-34
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Fatent No. US2002016468611
GENERAL INFORMATION:
APPLICANT:
BAUM, Peter
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR PAPLICATION NUMBER: BCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 22
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Best Local Similarity 100.
Matches 423; Conservative
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-22
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Sequence 22, Agrication US/10302041

Sequence 22, Sequence 22, Sequence 22, Sequence 22, Sequence 22, Sequence 22, Sequence 22, Sequence 22, Sequence 22, Sequence 23, Sequence 24, Sequence 24, Sequence 25, Sequence 26, Sequence
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Best Local Similarity 100.0
Matches 423; Conservative
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US-10-302-041-22
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  TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
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                                                                                                  YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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Sequence 4, Application US/09778187B

Patent No. US20020168712A1

GENERAL INFORMATION

APPLICANT: Baum, Peter R.

APPLICANT: Baum, Peter R.

TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM

FILE REPERBURE: 2873-US

CURRENT FILING DATE: 2801-02-06

PRIOR APPLICATION NUMBER: PCT/US99/17905

PRIOR APPLICATION NUMBER: DCT/US99/17905

PRIOR APPLICATION NUMBER: US 60/095,672

PRIOR PILING DATE: 1999-08-07

NUMBER OF SEQ. ID NOS: 10

SOSTWARE: Patentin version 3.1
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Publication No. US20050058642A1
GENERAL INFORMATION:
APPLICANT: GALIBERT, LAURENT J.
APPLICANT: YAN, Wei
TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
FILE REFERENCE: 3467-A2
CURRENT APPLICATION NUMBER: US/10/898,408
CURRENT FILING DATE: 2004-07-23
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Sequence 4, Application US/1062237

Publication No. US20040204568A1

GENERAL INFORMATION:

APPLICANT: Baum, Peter R.

APPLICANT: Baum, Peter R.

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/622,237

CURRENT APPLICATION NUMBER: US/09/778,187B

PRIOR APPLICATION NUMBER: US/09/778,187B

PRIOR APPLICATION NUMBER: US/09/778,187B

PRIOR APPLICATION NUMBER: US/09/778,187B

PRIOR FILING DATE: 1099-08-05

PRIOR FILING DATE: 1998-08-05

PRIOR FILING DATE: 1998-08-07

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 4

LENGTH: 423
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ORGANISM: mus musculus
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Best Local Similarity
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Publication No. US20030207800A1
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/490,027
PRIOR FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 423
                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 423; Conservative 0;
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APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
PEPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
                                                                                                           TYPE: PRT
CRGANISM: mus musculus
US-10-898-408-4
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TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of TITLE OF INVENTION: Using the Same TITLE OF INVENTION: Using the Same TITLE OF INVENTION: Using the Same CURRENT APPLICATION NUMBER: US/10/015,115 CURRENT PILING DATE: 2002-09-23 PRIOR PEDICATION NUMBER: 60/249,598 PRIOR FILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/24,240 PRIOR FILING DATE: 2001-01-26 PRIOR FILING DATE: 2001-01-26 PRIOR FILING DATE: 2001-02-06 PRIOR FILING DATE: 2001-02-06 PRIOR FILING DATE: 2001-02-06 PRIOR FILING DATE: 2001-02-16 PRIOR FILING DATE: 2001-07-31 PRIOR PRIO
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US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. US20020164686A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
               Padigaru, Muralidhara
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; ORGANISM: Mus musculus
US-10-015-115-113
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100.0%; Pred. No. 1.3e-153;
ive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR FILING DATE: 2001-01-26
PRIOR PELING DATE: 2001-01-26
PRIOR PELING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR PLILING DATE: 2001-02-16
PRIOR PLING DATE: 2001-07-10
PRIOR PLING DATE: 2001-07-10
PRIOR PLING DATE: 2001-07-10
PRIOR PLING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 205
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 112
LENGTH: 445
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Publication No. US20030207800A1
GENERAL INFORMATION:
APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Sernusen, Bryan D
APPLICANT: Sertusen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Guo, Xiaojia
APPLICANT: Guo, Xiaojia
APPLICANT: Guimete, Ramesha
APPLICANT: Teunis Ramesha
APPLICANT: Taupier, Raymond J
APPLICANT: Li, Li
APPLICANT: Li, Li
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Best Local Similarity 100.0
Matches 423, Conservative
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US-10-015-115-112
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EYF 444
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79 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 138
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                                                  Score 2169; DB 9;
Pred. No. 1.5e-151;
1; Mismatches 4;
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Pred. No. 1.5e-151;
1; Mismatches 4;
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Publication No. US20030055231A1
GENERAL INFORMATION:
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Best Local Similarity 98.8%;
Matches 418; Conservative
                                                  Query Match 98.7%;
Best Local Similarity 98.8%;
Matches 418; Conservative
; ORGANISM: homo sapiens
US-09-778-187B-2
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Pred. No. 1.5e-151;
1; Mismatches 4;
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Patent No. US20020168712A1
GENERAL INPORMATION:
APPLICANT: Baum, Peter R.
TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
FILE REFERENCE: 2873-US
CURRENT APPLICATION NUMBER: US/09/778,187B
CURRENT FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: DCT/US99/17905
PRIOR APPLICATION NUMBER: US 60/095,672
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Version 3.1
   Molecules Designated B7L1
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
FRIOR APPLICATION NUMBER: PCT/US99/17906
FRIOR FILING DATE: 1999-08-05
FRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
                                                            1999-08-05
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.8%;
Matches 418; Conservative
                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapien
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US-09-778-187B-2
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TYPE: PRT
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Db 199 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLIR 258 QY 241 EGDAFELTCEAIGKPQPVWTWYRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300 L	RESULT 12 US-10-302-041-20 Sequence 20, Application US/10302041 Publication No. USG0030144478A1 Publication No. USG0030144478A1 Publication No. USG0030144478A1 Publication No. USG0030144478A1 Sequence 20, Application No. USG0030144478 Sequence 20, Application No. USG003014442 Sequence 20, Application No. USG003014444 Sequence 20, Application No. USG003014444 Sequenc	Qy 121 TVLVPPRNIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
	LYVYDPPTTITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Query Match 98.7%; Score 2169; DB 10; Length 442; Best Local Similarity 98.8%; Pred. No. 1.5e-151; Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0; Qy 1 AAPPGIRELILILSAAALIPTGDGONETKOVTHIGGEVATISCQNNKSDDSVIQLIN 60 Db 19 AAPPGIRELILILESAAALIPTGDGONETKOVTHIGGEVATISCQNNKSDDSVIQLIN 78 Qy 61 PNRQTIYFRDFRENCORFOLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTT1 120 Db 79 PNRQTIYFRDFRENCORFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTT1 138 Qy 121 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRMFKGNKELKGKSEVEEWSDM 180 Db 139 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRMFKGNKELKGKSEVEEWSDM 198 CQY 131 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRMFKGNTELKGKSEVEEWSDM 198 CQY 131 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRMFKGNTELKGKSEVEEWSDM 198 CQY 131 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRMFKGNTELKGKSEVEEWSDM 198

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APPLICANT: Guo, Xiaojia APPLICANT: Guo, Xiaojia APPLICANT: Guo, Xiaojia APPLICANT: Kekuda, Ramesha APPLICANT: Kekuda, Ramesha APPLICANT: Kekuda, Ramesha APPLICANT: Shimkets, Richard APPLICANT: Shimkets, Richard APPLICANT: Taupier, Raymond J APPLICANT: Taupier, Raymond J APPLICANT: Li, Li, Li, Muralidhara TTLLE OF INVEWTION: Proteins, Polynucleotides Encoding Them and Methods of TTLLE OF INVEWTION: Using the Same TTLLE OF INVEWTION: Using the Same TTLLE OF INVEWTION: Using the Same FILE REFERENCE: 21402-21

CURRENT APPLICATION NUMBER: 60/248,153

PRIOR PLICATION NUMBER: 60/249,598

PRIOR PLICATION NUMBER: 60/264,240

PRIOR PLICHOR DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/264,240

PRIOR PLICATION NUMBER: 60/264,240

PRIOR PLICHOR DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/269,562

PRIOR PLICHOR DATE: 2001-07-16

PRIOR PLICHOR DATE: 2001-07-31

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    Shenoy, Suresh G
Spytek, Kimberly A
Zerhusen, Bryan D
                                                              Patturajan, Meera
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Matches 418; Conservative
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                                                                                                                                                                                            Sequence 1, Application US/10403107

Publication No. US20030165974A1

GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: TOSHINORI, Muramaki
TITLE OF UNUSWITON: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILE REFERENCE: JHU1770-1
CURRENT APPLICATION NUMBER: US/10/403,107
CURRENT PILLING DATE: 2003-03-28
PRIOR FILING DATE: 2001-08-15
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
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Best Local Similarity 98.8
Matches 418; Conservative
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ORGANISM: Homo sapiens
                                                            EYF 423
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US-10-015-115-111
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                                                                   US-10-363-616-262

Sequence 262, Application US/10363616

Publication No. US20040044181A1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NOWEL NUCLEIC ACIDS AND POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/10/363,616

CURRENT APPLICATION NUMBER: 08/654,935

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 490

LENGTH: 442
                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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439 EYF 441
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                                                                  TITLE OF INVENTION: Molecules Designated FILE SPERIERS. 2844-08.
CURRENT APPLICATION NUMBER: US/09/778,510 CURRENT FILING DATE: 2001-02-07 PRIOR APPLICATION NUMBER: 199-08-05 PRIOR FILING DATE: 1998-08-05 PRIOR FILING DATE: 1998-08-07 PRIOR FILING DATE: 1998-08-07 SOFTWARE: PARIOR PRIOR FILING DATE: 1998-08-07 SOFTWARE: SEQ ID NOS: 22 SOFTWARE: Patentin Ver. 2.0
                                                                    Baum, Peter
Tron: Molecules Designated
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1999-08-05
Sequence 22, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
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GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK
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                                                                                                                                                                               TITLE OF INVENTION:

FILE REPRENCE:
CURRENT APPLICATION:
MOLECULES Designated B7L1
FILE REPRENCE:
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
FRIOR APPLICATION NUMBER:
FRIOR FILING DATE: 1999-08-05
FRIOR FILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE:
PATENT PROSECULES DESIGNED TO NUMBER OF SEQ ID NOS: 22
SOFTWARE:
PATENT PROSECULES DESIGNED TO NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2169; DB 4;
Pred. No. 1.7e-184;
1; Mismatches 4;
                                                                                                                                            ; Sequence 20, Application US/09778510; Patent No. 6512095; GENERAL INFORMATION; APPLICANT: Baum, Peter
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US-09-930-803-1
'Sequence 1, Application US/09930803
'Patent No. 6596493
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    98.7%;
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Best Local Similarity 98.8
Matches 418; Conservative
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapien
                                                                            423
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EYF 441
                                                   EYF 423
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                                                                                                                   RESULT 2
US-09-778-510-20
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APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
                 APPLICANT: REEVES, ROGER
APPLICANT: YOSHINORI, Muramaki
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: JHU1770-1
CURRENT APPLICATION NUMBER: US/09/930,803
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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Grimaldi, Christopher
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GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrara, Napoleone
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Gerritsen, Mary
Goddard, Audrey
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Matches 418; Conservative
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Hillan, Kenneth
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Tumas, Daniel
Wood, William
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                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT:
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FILING DATE: February 22,
     REFERENCE: P2548P1C1
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APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PICI CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
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                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                           Length 440;
                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                       Score 2149; DB 4;
Pred. No. 9.9e-183;
1; Mismatches 4;
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Patent No. 6734288
GENERAL INFORMATION:
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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Best Local Similarity 98.3
Matches 416; Conservative
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                                                                                                                                                                TYPE: PRT
CRGANISM: Homo Sapien
US-09-866-028-61
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EYF 439
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US-09-944-457-61
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CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: US/09/944,457

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 06/069,334

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: DECEMBER 16, 1997

PRIOR PLING DATE: PEDINGY 5, 1998

PRIOR PLING DATE: PEDINGY 25, 1998

PRIOR PLING DATE: PECEMBER 16, 1999

PRIOR APPLICATION NUMBER: POT/US99/126, 21

PRIOR PRIUME DATE: PECEMBER 16, 1999

PRIOR PRIUME DATE: PECEMBER 16, 1999

PRIOR PRIUME DATE: PECEMBER 16, 1999

PRIOR PRIUME DATE: PECE
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PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR PLILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
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FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/USO0/08439
FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/USO0/14042
FILING DATE: May 22, 2000
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APPLICATION NUMBER: PCT/US00/04414
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70 DFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNL 129 | : | : | : | : | : | | | | | | |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 ELTCEAIGKPQPVMVTWVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 ILITCESKGKPLPEPVLWIXDGGELPDPDRMVVSGRELNILFLNKIDNGTYRCEAINTIGQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 TIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADAAIINA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 LLLSAAA---LIPTGDGONLFTKDVTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 LMLKVHKEDDGVPVICQVEHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 41.1%; Score 904; DB 2; Length 44 Best Local Similarity 44.7%; Pred. No. 5.8e-72; Matches 194; Conservative 74; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08660531

Patent No. 6221645

GENERAL INFORMATION:

APPLICANT: Chryaler, Susanna M.S.

APPLICANT: Sinha, Sukanto

APPLICANT: Reim, Pamela S.

TITLE OF INVENTION: Beta-Secretase

NUMBER OF SEQUENCES: 21

CORRESPONDEES: 11

CORRESPONDEES: Townsend and Crew LLP
от-док: US/08/659,984A
07-JUN-1996
N: 436
                              APPLICATION NUMBER: US/08/659,984A
CLASSIPICATION NUMBER: US/08/659,984A
CLASSIPICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-07N-1995
ATTORNEY/AGENT INFORMATION:
NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REPERONCE/DOCKET NUMBER: 15270-00281
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                                                                                                                                                                                        TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 EGGQNNSEEKKEYF 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || | |:|||||||
430 EGSQVNAEEKKEYF 443
               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-659-984A-5
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US-08-660-531-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRXLEVQXKPQVHIQMTYPLQGLTR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PINQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVLVPPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQBSYTTI 120
                                                                                                                                                                                                                                                                                                                                                                                                                      19 AAPPG--LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN 76
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                                                                                                                                                                                                                                                                                                                                      Gaps
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| Patent No. 5942400 |
| GENERAL INFORMATION: |
| APPLICANT: Anderson, John P. |
| APPLICANT: Sinha, Sukanto |
| TITLE OF INVENTION: Assays for Detecting Beta-Secretase |
| TITLE OF INVENTION: Inhibition |
| NUMBER OF SEQUENCES: 21 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Townsend and Townsend and Crew LLP |
| STREET: TWO Embarcadero Ctr., 8th Floor |
| CITY: San Francisco |
| STATE: California
                                                                                                                                                                                                                                                                                            Length 440;
                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                          Score 2149; DB 4;
Pred. No. 9.9e-183;
1; Mismatches 4;
        PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
SEQ ID NO 61
                                                                                                                                                                                                                                                                                            97.8%;
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.3
Matches 416; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                            ; ORGANISM: Homo Sapien
US-09-944-457-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94111-3834
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US-08-659-984A-5
                                                                                                                                                                                     LENGTH: 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 DFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWS---DMYTVTSQ 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMLKVHKEDDGVPVICQVEHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDAF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELICEAIGKPOPVMVTWVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 ILTCESKGKPLPEPVLWTKDGGELPDPDRMVVSGRELNILFLNKTDNGTYRCEATWTIGQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 TIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINA 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 LLLQAAASKNKVKGSQGGFPLTQNVTVVEGGTAILTCRVDQNDNTSLQWSNPAQQTLYFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 LLLSAAA---LIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.1%; Score 904; DB 3; Length 444; 44.7%; Pred. No. 5.8e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74; Mismatches 136; Indels
                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 AHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTILTIT-
Two Embarcadero Ctr., 8th Floor
                                                                                                                                                                                                                                                                                                                                                        15270-002210US
                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                               NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REFRENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGGQNNSEEKKEYF 423
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EGSQVNAEEKKEYF 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 444 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 44.73
Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                  San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                           FILING DATE:
                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-660-531-5
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RESULT 8 US-08-659-984A-1 ; Sequence 1, Application US/08659984A

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86 SSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 WHELSISVSDVSLSDEGQYTCSLFTMPVKTSKAXLTVLGVPEKPQISGFSSPVMEGDLMQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 VNCTAMASKPATTIRWFKGNKELKGKSEVEEWS---DMYTVTSQLMLKVHKEDDGVPVIC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 WVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTI 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 WIKDGGELPDPDRMVVSGRELNILFLNKTDNGTYRCEATWIIGGSSAEYVLIVHDVPWTL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             320 PPPTTTTTTTTTTTTLTILTIIT-------DSRAGEEGTIGAVDHAVIGGVVAV 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 LPTIIPSLITATVITITVAITISPITSAITSSIRDPNALAGQNGP----DHALIGGIVAV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 QVEHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 GQFPLTQNVTVVEGGTAILITCRVDQNDNTSLQMSNPAQQTLYFDDKKALRDNRIELVRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 GONLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYF
||| || || : :|||| ||||||| |:|||||||
APPLICANT: Anderson, John P.
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
ATTORNEY/AGENT INFORMATION:
NAME: Heelin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
40.7%; Score 893.5; DB 2;
Best Local Similarity 45.0%; Pred. No. 4.6e-71;
Matches 188; Conservative 73; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                      ZIP: 94111-3834
COMPUTER READABLE FORM:
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     -DSRAGEEGTIGAVDHAVIGGVVAV 365
                                                                  307 LPTIIPSLTTATVTTTVAITTSPTTSATTSSIRDPNALAGONGP----DHALIGGIVAV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 YFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPP 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 RNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKG-KSEVEEWSD--MYTV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247
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                                                                                                                                                                                                 366 VVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEEKKEYF 423
                                                                                                                                                                                                                                                   11 LLLLLLACSWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQWSNPAQQTL
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TITLE OF INVENTION: Molecules Designated B7L1
TITLE OF INVENTION: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT PILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR PILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
NUMBER OF PALENTIN VONS: 22
SOFTWARE: PALENTIN VEY: 2.0
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38.8%; Pred. No. 2.6e-57;
tive 73; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09778510 Patent No. 6512095
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US-09-778-510-6
Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Sec
     320 PPPTTTTTTTTTILTILT
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Best Local Similarity 38.8
Matches 165; Conservative
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SEQ ID NO 4
LENGTH: 398
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US-09-778-510-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 QVEHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVT 261
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363 VVFVTLCSIFLLGRYLARHKGTYLTNEAKGAEDAPDADTAIINAEGSOVNAEEKKEYF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 GONLFTKDVTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
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45.0%; Pred. No. 4.6e-71;
ive 73; Mismatches 130; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREEF: Two Enbarcadero Ctr., 8th Floor STRTE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGRAT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111.3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         Sequence 1, Application US/08660531
Patent No. 6221645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
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Matches 188; Conservative
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                              RESULT 9
US-08-660-531-1
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Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                 Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
                                                              Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 38.3
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 VGKAHSDYMLYVYDPPTTIPPPFTTTTTTTTTTTTTTTTTTTTTTTGARGEEGTIGAVDHAVIG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 PPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGK-SEVEEWSD--MY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----- HAIIG 334
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                                                                                                                                                                                                                                                                                                                                                                                                                  TIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLV 124
                                                                                                                                                                                                                                                                                                                                                10 LLLLLLSAAALIPTG-----DGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQ
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                               33.3%; Score 732.5; DB 4; Length 398; 38.3%; Pred. No. 9e-57; ive 74; Mismatches 144; Indels 43
               Molecules Designated B7L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 MGSYKAYYILMVNDPS---PVPSSSSTY-----
                        CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1998-08-05
PRIOR PILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 6
                                                                               PCT/US99/17906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 84, Application US/09907794A Patent No. 6635468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Eaton, Dan L.
APPLICANT: Firara, Napoleoné
APPLICANT: Firara, Napoleoné
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 38.33
Matches 162; Conservative
Baum, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard, A.
                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapien
                 TILE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                 LENGTH: 398
                                                                                                                                                                                                                                                 JS-09-778-510-6
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69 TLYFGEKRALRDNRIQLVTSTPHELSISISNVALADEGEYTCSIFTMPVRTAKSLVTVLG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LLLLLLSAAALIPTG-----DGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQ
                                                         and Transmembrane Polypeptides and Nucleic
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38.3%; Pred. No. 9e-57;
live 74; Mismatches 144;
                                                                                                               TITLE REPERINCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-03

PRIOR PRIO
TITLE OF INVENTION: Acids Encoding the Same
```

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125 PPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGK-SEVEEWSD--MY 181
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Pred. No. 9e-57;
                       PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-06
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PRIOR PLILING DATE: 1999-12-06
PRIOR PLICATION NUMBER: PCT/US99/3099
PRIOR PLILING DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-07
PRIOR PLILING DATE: 1999-12-07
PRIOR PLILING DATE: 1999-12-07
PRIOR PLILING DATE: 1999-12-07
PRIOR PLILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc.
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
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38.3%;
   FILING DATE: 1999-10-05
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Best Local Similarity 38.3
Matches 162; Conservative
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TVTSQLMLKVHKEDDGVPVICQVEHPAVTG-NLQTQRYLEVQYKPQVHIQMTYPLQGLTR 240
                                                                                                                               241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
                                                                                                                                                                 -----HAIIG 334
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CURRENT APPLICATION NUMBER: US/09/905,125A

CURRENT FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: US/09/905,125A

PRIOR PILING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-08

PRIOR PELING DATE: 1999-07-08

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PRIOR PELING DATE: 1999-09-08

PRIOR PELING DATE: 1999-09-13

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APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
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Grimaldi, Christopher J.
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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EYF 397
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65 TIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLV 124
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PPPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28664
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PELING DATE: 1999-12-02
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CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
                                                                                              Godowski, Paul J.
Grimaldi, Christopher
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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Best Local Similarity 38.3
Matches 162; Conservative
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SEQ ID NO 84
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-84
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PPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGK-SEVEEWSD--MY 181
                                                                                                                                                                     246 EGQKILILHCEGRGNPVPQQYLWEK-EGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSN 304
                                                                                                                                                                                                                        361 GVVAVVVFAMLCLLILILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK 420
                                                                                                                                                                                                                                                                                                                        ------HAIIG 334
                         182 TVTSQLMLKVHKEDDGVPVICQVEHPAVTG-NLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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                                                                                                                                                                                                                                                 305 MGSYKAYYTLNVNDPS---PVPSSSSTY----
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PLING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
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CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
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Grimaldi, Christopher
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Gerber, Hanspeter
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Mather, Jennie P.
Pan, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 LILILILFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQWSNPAQQ 68
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PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-30
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US-09-906-700-84
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Search completed: June 28, 2005, 09:55:53 Job time : 31.341 secs

ribosomal protein	υ	sex-determining pr		hypothetical prote	hypothetical prote	prophage pi2 prote	heat-shock 27K pro	ž	hypothetical prote	promastigote surfa	te D		hypothetical prote	-	pecifi	protein	dihydrolipoamide S	probable phosphodi	methyl-CpG-binding	zip protein precur	probable membrane	related to protein	male-specific doub	dihydrolipoamide S	probable MAP kinas	prot	guanylate cyclase,	hypothetical prote	muscarinic acetylc	hypothetical prote	fragile X mental r	ein -	gene serrate prote	hypothetical prote	1-phosphatidylinos	probable nuclear a	gene hindsight pro	hypothetical prote	probable laminin a		ij	N	D D	ø	e o	ø,	parsin, ovary-matu
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ALIGNMENTS
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RESULT 1

T26880
hypothetical protein Y43F8C.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26880
R;Ainscough, R.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z20279
A;Reference number: Z20279
A;Reference number: DAZ
A;Reference number: DAZ
A;Reference number: DAZ
A;Residus: preliminary; translated from GB/EMBL/DDBJ
A;Residus: 1108 cwll.
A;Residus: 1108 cwll.
A;Cross-references: UNIPROT:09XWN0; EMBL:AL032637; PIDN:CAA21621.1; CESP:Y43F8C.9
A;Genelics:
A;Gene: CESP:Y43F8C.9
A;Introns: 40/3

Query Match

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3.4%; Score 15; DB 2; Length 108;
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probable WRKY-type DNA binding protein At2g38470 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein T19C21.4 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date. 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004 C;Accession: T02498; D84805 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,

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promastigote surface antigen P2 (clone 4.6) precursor - Leishmania major (fragment)
C.Species: Leishmania major
C.Species: Leishmania surface antigen derived from a multigenic family.
J. Biol. Chem. 266, 24477-24484, 1991
A.Title: Variants of a Leishmania surface antigen derived from a multigenic family.
A.Reference number: A41710; MUID:92105105; PMID:1761547
A.Reference number: A41710; MUID:92105105; PMID:1761547
A.Residues: L-327 - AMURA
A.Residues: Diocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage
F;1-299/Product: promastigote surface antigen P2 (fragment) #status predicted -RPSA>
F;300-327/Domain: carboxyl-terminal propeptide #status predicted -CTP>
F;299/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asp) (in mature form).
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C.Species: Caenorhabditis
R.Chissoe, S.
Submitted to the EMBL Data Library, July 1995
A.Description: The sequence of C. elegans cosmid EEED8.
A.Reference number: Z18428
A.Reference number: Z18428
A.Reference number: Z18428
A.Reference number: A.Reference of C. elegans cosmid EEED8.
A.Reference number: S1922
A.Reference nu
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100.0%; Pred. No. 6.9e-05;
.ive 0; Mismatches 0; Indels
                                                                                     Indels
                                 Pred. No. 3.4e-06; 
; Mismatches 0;
100.08; Pre-
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Best Local Similarity 100.
Matches 14; Conservative
                                 Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                           339 PPTTTTTTTTTT
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A;Molecule type: mRNA
A;Residues: 1-518 <MIC>
A;Cross_references: UNIPROT:043753; EMBL:Z18952; NID:g18319; PIDN:CAA79477.1; PID:g18320
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A;Molecule type: DNA
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v 100.0%; Pred. No. v...
o; Mismatches
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A;Reference number: $15811
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A;Residues: 1-141,'I',143-780,'E',782-885,'GY'
A;Cross-references: EMBL:X51478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459 TTTTTTTTTTI 472
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Best Local Similarity 100.0
Matches 14; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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;Molecule type: DNA
;Residues: 1-889 <LEI>
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C;Species: Dianthus caryophyllus (clove pink)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 819252
R;Park, K.Y.; Drory, A.; Woodson, W.R.
Bjant Mol. Biol. 18, 377-386, 1992
A;Title: Molecular cloning of an 1-aminocyclopropane-1-carboxylate synthase from senesci
A;Reference number: 819252; MUID: 92119258; PMID:1731995
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C;Species: Dianthus caryophyllus (clove pink)
C;Species: Dianthus caryophyllus (clove pink)
C;Date: 0.2-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S31442
R;Michael, M.Z.
R;Michael, 
submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.
A;Reference number: Z14676
A;Refectesion: T02498
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-512 <ROU>
A;Residues: 1-512 <ROU>
A;Residues: L-512 <ROU>
A;Residues: L-512 <ROU>
A;Experimental source: cultivar Columbia
R;Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X; Kaul, S; Rounsley, S.D.; Shea, M; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Macrman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Only Eisen, Mature 402, 761-768, 1999
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C.Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C;Keywords: carbon-sulfur lyase; ethylene biosynthes1s; phosphoprotein; pyridoxal phosph
F;276/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A,Reference number: A84420; MUID:20083487; PMID:10617197
A,Accession: D84805
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-512 <STO>
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100.0%; Pred. No. 0.00011;
Live 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.00011;
ive 0; Mismatches 0; Indels
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A;Map position: 2
A;Introns: 74/3; 143/3; 321/2; 375/2
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Matches 14; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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A;Residues: 1-516 <PAR>
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A; Status: preliminary
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S31442
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rep protein - slime mold (Dictyostellum discoideum) plasmid Ddp2
C.Species: Dictyostellum discoideum
C.Species: Dictyostellum discoideum
C.Species: 28-Sep-1990 #sequence revision 28-Sep-1990 #text_change 09-Jul-2004
C.Accession: A35679; S14202; S15811
R.Leiting, B.; Lindner, I.J.; Noegel, A.A.
Mol. Cell. Biol. 10, 3727-3736, 1990
A.Title: The extrachromosomal replication of Dictyostellum plasmid Ddp2 requires a cis-a-A.Reference number: A35679; MUID:90287164; PMID:2192261
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;7itile: The sequence and organization of Ddp2, a high-copy-number nuclear plasmid of Di;Reference number: S14202; WUID:91172902; PMID:2077544
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R;Barnes, D.A.; Bonnin, A.; Huang, J.X.; Gousset, L.; Wu, J.; Gut, J.; Doyle, P.; Dubrem Mol. Biochem. Parasitol. 96, 93-110, 1998
A;Title: A novel multi-domain mucin-like glycoprotein of Cryptosporidium parvum mediates A;Reference number: Z20989; MUID:99066935; PMID:9851610
C;Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C;Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph-
F;278/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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C;Species: Cryptosporidium parvum
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                   Gaps
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A;Residues: 1-141,'I',143-353,'A',355-780,'E',782-885,'GY' <SLA2>
A;Cross-references: EMBL:X51478; NID:g7307; PIDN:CAA35843.1; PID:g7308
C;Genetics:
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100.0%; Pred. No. 0.00011;
ative 0; Mismatches 0; Indels
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merozoice surface antigen - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium
C;Species: S3310
R;Ramasamy, R.; Ranasinghe, C.
submitted to the RMIL Data Library, November 1993
A;Description: Cycle ds DNA sequencing of a malaria parasite protein from infected blood
A;Description: S39310
A;Reference number: S39310
A;Status: preliminary
A;Residues: 1-278 «RAM»
A;Residues: 1-278 «RAM»
A;Residues: 1-278 «RAM»
A;Residues: 1-278 «RAM»
C;Superfamily: Epstein-Barr Virus nuclear antigen
C;Superfamily: Epstein-Barr Virus nuclear antigen
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C.Species: Plasmodium falciparum
C.Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C.Accession: A45632
A.Fitle: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2)
A.Riberence number: A45632; MUID:92178286; PMID:1542312
A.A.A.Contens: KR1916
                                                                                                                                                             A;Accession: T26868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: NNA
A;Essidues: 1-245 - WNLS
A;Cross-references: UNIPROT:09XWP2; EMBL:AL032637; PIDN:CAA21609.1; CESP:Y43F8C.5
A;Experimental source: clone Y43F8C
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26868
R;Ainscough, R.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z20279
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Best Local Similarity 100.0
Matches 13; Conservative
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Best Local Similarity
Matches 13; Conserv
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A;Molecule type: DNA
A;Residues: 1-274 <MAR>
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A;Gene: CESP:Y43F8C.5
A;Introns: 69/3; 163/2
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Aug-2004
C;Accession: B5688
R;Engle, M.J.; Alpers, D.H.
Cin. Chem. 38, 2506-2509, 1992
A;Title: The two mRNAs encoding rat intestinal alkaline phosphatase represent two distint A;Reference number: A56888; MuID:93092310; PMID:1458592
A;Accession: B5688
      A,Cross-references: UNIPROT:096503; EMBL:AF068065; NID:94063041; PID:94063042; PIDN:AAC9
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S01358
salivary glue protein sgs-3 precursor - fruit fly (Drosophila simulans)
C;Species: Drosophila simulans
C;Species: Drosophila simulans
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S01358, A29888
A;Marrin, C;H:; Mayeda, C;A:; Meyerowitz, E.M.
J. Mol. Biol. 201, 273-287, 198
A;Ritle: Evolution and expression of the Sgs-3 glue gene of Drosophila.
A;Reference number: S01358; MUID:88332966; PMID:3138416
A;Accession: S01358
A;Accession: Compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Experimental source: duodenal mucosa
A.Note: sequence extracted from NCBI backbone (NCBIN:121249, NCBIP:121252)
C.Superfamily: Alkaline phosphatase
C.Keywords: intestine; membrane protein; phosphoric monoester hydrolase
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                                                                                                                               Gaps
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                                                               Query Match 3.2%; Score 14; DB 2; Length 1832; Best Local Similarity 100.0%; Pred. No. 0.00031; Matches 14; Conservative 0; Mismatches 0; Indels
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A,Cross-references: FlyBase:FBgn0012853
A,Cross-references: FlyBase:FBgn0012853
C,Superfamily: salivary glue protein
F,1-23/Domain: signal sequence #status predicted <SIG>
F,24-217/Product: salivary glue protein sgs-3 #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ?.9%; Score 13; DB 2; Length 67; Local Similarity 100.0%; Pred. No. 0.00016; les 13; Conservative 0; Mismatches 0; Indels
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T26868
hypothetical protein Y43F8C.5 - Caenorhabditis elegans
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A,Residues: 1-217 <MAR>
A,Cross-references: UNIPROT:P13729
                                                                                                                                                                                                                    373 PITITITITIT 386
                                                                                                                                                                                      340 PITITITITIT 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-67 <ENG>
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Matches
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A;Residues: 1-519 <WIL>
A;Cross-references: UNIPROT:Q09592; EMBL:Z46935; PIDN:CAA87049.1; GSPDB:GN00020; CESP:Ml(
A;Experimental source: clone M106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alkaline phosphatase (EC 3.1.3.1) - rat
NiAlternate names: phytase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S18408; S17576
B;Strom, M.; Krisinger, J.; DeLuca, H.F.
B;Ochim. B;ophys. Acta 1090, 299-304, 1991
A;Title: Isolation of a mRNA that encodes a putative intestinal alkaline phosphatase reg
A;Reference number: S18408, WUID:92062729; PMID:1954251
A;Accession: S18408
A;Status: preliminary
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A;Note: the correct sequence of residues 144-160 is shown in Fig. 2; the corresponding c R;Yang, W.J.; Matsuda, Y.; Sano, S.; Masutani, H.; Nakagawa, H.
Biochim. Biophys. Acta 1075, 75-82, 1991
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23739
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A;Introns: 47/2; 110/3; 185/2; 231/2; 270/2; 321/2; 347/3; 411/3; 452/3
C;Superfamily: Caenorhabditis elegans hypothetical protein M106.2
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A;Introns: 40/1; 110/3; 141/2; 219/3; 393/1
C;Superfamily: probable zinc metalloproteinase T04G9.2
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
2.9%; Score 13; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 13; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 0.00091;
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                                                                   A, Accession: T20658
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
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A;Molecule type: DNA
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submitted to the EMBL Data Library, December 1994
A;Reference number: Z19792
A;Accession: T23739
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     R;Percy, C.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19307
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Matches 13; Conservative
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A;Residues: 1-551 <STR>
                                                                                                                                                                                                                                                               A; Gene: CESP: F09E8.6
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A;Accession: T22023
A;Accession: T22023
A;Status: PT22023
A;Status: DNA
A;Residues: 1-284 <WIL>
A;Cross-references: UNIPROT:Q20202; EMBL:Z69792; PIDN:CAA93666.1; GSPDB:GN00028; CESP:F4
A;Experimental source: clone F40E10
C;Genetics:
A;Gene: CESP:F40E10.5
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A;Cross-references: EMBL:AF045635; PIDN:AAC02556.1; GSPDB:GN00022; CESP:C05G6.3
A;Experimental source: strain Bristol N2; clone C05G6
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32949
                                                                                                                                                                                                                                                          hypothetical protein F40E10.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T22023
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20658
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                                0; Indels
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A, Description: The sequence of C. elegans cosmid C05G6.
A), Reference number: Z21252
A, Accession: T32949
A, Status: preliminary; translated from GB/EMBL/DDBJ
Best Local Similarity 100.0%; Pred. No. 0.00054; Matches 13; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, February 1996
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A;Introns: 34/3; 76/2; 141/3; 183/3; 240/3
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A;Gene: CESP:C05G6.3
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A,Gene: CESP: F55D12.5
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A;Reference number: 219385
A;Reference number: 219385
A;Accession: T21175
A;Cosestion: T21175
A;Molecule type: DNA
A;Residues: 1-651 <WIL>
A;Experimental source: Clone F20G4
B;McMurray, A.
A;Title: Purification and characterization of phytase from rat intestinal mucosa. A;Reference number: $17576; MUD:91370007; PMID:1654110
A;Accession: $17576
A;Accession: $17576
A;Molecule type: protein
A;Residues: $20-29 < YAN>
A;Note: 10-Val was also found
C;Superfamily: alkaline phosphatase
C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: T32661
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-560 <HEN>
A;Cross-references: EMBL:AF039047; PIDN:AAB94223.1; GSPDB:GN00023; CESP:KIID12.1
A;Experimental source: strain Bristol N2; clone K11D12
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A, Reference number: Z19606
A, Accession: T22735
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Residues: 1-651 < WIZ>
A, Residues: 1-651 < WIZ>
A, Residues: EMBL: Z75542; PIDN: CAA99864.1; GSPDB: GN00019; CESP: F55D12.5
A, Experimental source: clone F55D12
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein K11D12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 K3-C;Baccession: T32661 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 K3-C;Baccession: T32661 #special for the EMBL Data Library, December 1997 A;Description: The sequence of C. elegans cosmid K11D12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 20
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A;Map position: 5
A;Introns: 5/3; 48/3; 90/3; 127/3; 149/3; 190/1; 207/1; 233/3; 264/1; 480/1
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Matches 13, Conservative
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C; Species: Runinococcus flavefaciens
C; Species: Runinococcus flavefaciens
C; Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C; Accession: S51592
R; Zhang, J.X.; Martin, J.; Flint, H.J.
Mol. Genet. 25-5, 260-264, 1994
A; Title: Identification of non-catalytic conserved regions in xylanases encoded by the x, A; Reference number: S51892; MuID:95115675; PMID:7816035
A, Accession: S51592
A, Accession: S51592
A, Accession: S51592
A, Accession: S51592
A, Residues: 1-781 < ZHA>
A, Residues: 1-781 < ZHA>
A, Residues: 1-781 < ZHA>
A, Cross-references: UNIPROT:052753; EMBL: Z35226; NID:9516273; PIDN:CAA84537.1; PID:951627.
F, C2295 Domain: endo-1, 4-beta-xylanase homology < XXL.
F, 2239 Domain: Thermotoga xylanase A amino-terminal repeat homology < TXA>
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A;Molecule type: mRNA
A;Residues: 1-831 <AUB>
A;Cross-references: UNIPROT:015756; EMBL:AF020409; NID:g2425146; PID:g2425147
A;Experimental source: strain AX4
C;Genetics:
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession T08611
R;Aubry, L.; Firtel, R.A.; Iranfar, N.
submitted to the EMBL Data Library, August 1997
                                                                                                                                                                       Gaps
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A;Map position: 1
A;Introns: 29/2; 54/3; 93/3; 180/2; 236/1; 264/2; 471/3; 486/3; 583/3
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2.9%; Score 13; DB 2; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                       Length 651;
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Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                Query Match 2.9%; Score 13; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0;
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A;Accession: T08611
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phospholipase C - yeast (Candida albicans)
C;Species: Candida albicans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18257
R;Bennett, D.E.; Mccreary, C.E.; Coleman, D.C.
Microbiology 144, 55-72, 1998
A;Title: Genetic characterization of a phospholipase C gene from Candida albicans: presentiation: T18257
A;Reference number: Z18844; MUID:98129081; PMID:9467900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Roides: 1-1099 - BEN>
A;Cross-references: UNIPROT:013433; EMBL:Y13975; NID:g2462981; PIDN:CAA74308.1; PID:g246
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P;566-726/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
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Cispecies: Mus musculus (house mouse)
Cjate: 02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 15-Jun-2001
CjAccesion: JE0120
RiHaidaris, C.G.; Medzihradsky, O.F.; Gigliotti, F.; Simpson-haidaris, P.J.
DNA Res. 5, 77-85, 1998
A;Title: Molecular characterization of mouse Pneumocystis carinii surface glycoprotein A
A;Reference number: JE0120; MUID:98344138; PMID:9679195
                                                                                                                                                                                                                                    R;Wada, M.; Nakamura, Y.
DNA Res. 1, 163-168, 1994
A;Title: NGS gene cluster encoding major cell surface glycoproteins of rat Pneumocystis
A;Reference number: JC2299; MUID:96051989; PMID:8535973
A;Accession: JC2300
                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-1083 <WAD>
A;Cross-references: UNIPROT:Q12075; GB:D31909; GB:D17441; NID:g559718; PIDN:BAA06705.1;
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                                                                                                                                                        C;Species: Pneumocystis carinii
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
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C;Keywords: glycoprotein
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                                                                                                                            glycoprotein MSG100 - Pneumocystis carinii
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A;Residues: 1-1282 <HAI>
A;Cross-references: GB:AF143102
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                                                                                                                            cell surface
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JC2217
major surface glycoprotein 5 - Pneumocystis carinii
C.Species: Pneumocystis carinii
C.Species: Pneumocystis carinii
C.Species: B-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C.Accession: JC2217
R.Kitada, K.; Wada, M.; Nakamura, Y.
DNA Res. 1, 57-66, 1994
A,Title: Multi-gene family of major surface glycoproteins of Pneumocystis carinii: full-A;Recession: JC2217; MulD:96051981; PMID:7584029
A,Accession: JC2217
A;Molecule type: mRNA
A;Residues: 1-1076 <RIT>
A;Cession: JC2217
A;Molecule type: mRNA
A;Residues: 1-1076 <RIT>
A;Cross-references: UNIPROT:Q01830; DDBJ:D21827; NID:g425784; PIDN:BAA04851.1; PID:d1005
C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100
C;Keywords: glycoprotein
F;245,471,574,804,837/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $12519

Glutactin - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Species: Drosophila melanogaster

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: $12519

C;Accession: $12519

Biological Drosophila Drosophila basement membrane-related glycoprotein with seque A;Reference number: $12519; MUID:90214632; PMID:2108864
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1023 <OLS>
A;Cross-references: UNIPROT:P33438; EMBL:X53286; NID:g297084; PIDN:CAA37380.1; PID:g2970
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A;Expertimental source: strain AX3
C;Genetics:
A;Gene: spnA
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100.0%; Pred. No. 0.0016;
cive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0017;
iive 0; Mismatches 0; Indels
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R; Aubry, L.; Firtel, R.A.
submitted to the EMBL Data Library, August 1997
A; Reference number: Z16454
A; Accession: T08606
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-975 cAUB>
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 13; Conservative
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C;Species: Dictyostelium discoideum
C;Saccession: S71628; S78068
R;Schuster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I.
EMBO J. 15, 3880-3889; 1996
A;Title: The hybrid histidine kinase DokA is part of the osmotic response system of Dict, A;Title: The hybrid aliatidine kinase DokA is part of the osmotic response system of Dict, A;Taccession: S71628
A;Taccession: S71628
A;Stacus: nucleic acid sequence not shown
A;Molecule type: DNA
A;Stacus: uncleic acid sequence not shown
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q23901; EMBL:X96869
A;Experimental source: strain AX2; substrain 214
R;Schuster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I.
Submitted to the EMBL Data Library, March 1996
A;Description: The hybrid histidine kinase DokA is part of the osmotic response system of A;Reference number: S78068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: modulates cell response to changes in osmolarity; involved in spore formating typeyments, shown the spore formating spore formating spore formating the spore formation the sponse regulator homology <RRH2>
F;1520-1629/Domain: response regulator homology <RRH2>
F;1568/Binding site: phosphate (Asp) (covalent) #status predicted
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A;Status: preliminary; not compared with conceptual translation
A;Status: 1-1737 GEIS.
A;Status: 1-1737 GEIS.
A;Cross-references: UNIPROT:O9TW28; GB:AF090533; NID:g5714395; PIDN:AAD47903.1; PID:g5714.
A;Experimental source: strain AX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RiGeissler, H.; Schwarz, B.C.; Soldati, T.
submitted to GenBank, September 1998
A; Description: Identification of two novel and highly divergent myosins in Dictyostellium A; Reference number: A59235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 2 - slime mold (Dictyostelium discoideum)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S78068
A;Molcaule type: DD.
A;Residues: 1-149,'E',151-219,'TRVLKLIQSTNNWIYWY',238-1671 <SCW>
A;Ccoss_references: EMBL:X96869; NID:g1237201; PIDN:CAA65612.1; PID:g1237202
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C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A59235
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100.0%; Pred. No. 0.0025;
tive 0; Mismatches 0; Indels
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F;62-874/Domain: myosin motor domain homology #status atypical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1053 Trititititi 1065
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Best Local Similarity 100.0
Matches 13; Conservative
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T17456
cell surface protein DTFA - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T17456
R;Ginger, R.S.; Drury L.; Bader, C.; Zhukovskaya, N.V.; Williams, J.G.
Development 125, 3343-3352, 1998
A;Title: A novel Dictyostelium cell surface protein important for both cell adhesion and A;Reference number: Z18798; MUID:98359946; PMID:9693138
A;Reference number: Z18798; MUID:98359946; PMID:9693138
A;Refatus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1402
A;Residues: 1-1402
A;Residues: 1-1402
A;Residues: UNIPROT:096668; EMBL:AF102575; NID:94063399; PIDN:AACS
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C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100
C;Keywords: glycoprotein
F;248,612,717,779,1063/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 30

Thirdo's

Chitinase (EC 3.2.1.14) - yellow fever mosquito

C;Species: Aedes aegypti (yellow fever mosquito)

C;Date: 20.5ep-1999 #sequence_revision 20.5ep-1999 #text_change 09-Jul-2004

C;Accession: T14075

R;de la Vega, H; Specht, C.A.; Liu, Y.; Robbins, P.W.

Insect Mol. Biol. 7, 233-239, 1997

A;Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosophila.

A;Reference number: Z17872

A;Accession: T14075
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2.9%; Score 13; DB 2; Length 1402;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                  Length 1282;
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A;Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: dtfA
C;Function:
A;Description: involved in the cell adhesion and cell sorting
                                                                                                                                               Query Match
2.9%; Score 13; DB 2; I
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 13; Conservative 0; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-1635 <DEL>
                                                                                                                                                                                                                                                                                                                                                                  1158 Tritritritii 1170
                                                                                                                                                                                                                                                                                              341 TTTTTTTTTT 353
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Matches 13; Conservative
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C;Accession: A54843
R;Choi, K.W.; Benzer, S.
Cell 78, 125-136, 1994
A;Title: Rotation of photoreceptor clusters in the developing Drosophila eye requires th A;Reference number: A54843; MUID:94306509; PMID:8033204
A;Accession: A54843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolox (Xeywordse: alternative splicing; ATP F;Xeywordse: alternative splicing; ATP F;38-301/Domain: protein kinase homoloyy «KIN» F;46-54/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homeocic protein smox-2, engrailed-like - fluke (Schistosoma mansoni)
C;Species: Schistosoma mansoni
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Aug-2004
C;Accession: S33640, S27841
R;Webster, P.J.; Mansour, T.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: FlyBase: FBgn0011817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:Y57A10A.i
A;Introns: 8/3; 54/3; 112/3; 151/1
                                                                    134 rrrrrrrrrrr 145
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Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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A; Residues: 1-477 < CHO>
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                                                 C. Accession: T18273

Mol. Cell. Biol. 15, 5645-5656, 1995

Mol. Cell. Biol. 15, 5645-5656, 1995

A. Title: A phosphatidylinositol (PI) Kinase gene family in Dictyostelium discoideum: Bic A, Accession: T18273

A, Accession: T18273

A, Accession: T18273

A, Molecule type: mRNA

A, Residues: 1-1858 < ZHO>

A, Cross-references: UNIPROT:P54674; EMBL:U23477; NID:g733521; PID:g733522; PIDN:AAA85722
C;Genetics:
A, Gene: PIK2

C, Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 34
S05358
Sypotherical protein (clone AAC1) - slime mold (Dictyostelium discoideum) (fragment)
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Species: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: S05358
S;Shaw, D.R.; Richter, H.; Glorda, R.; Ohmachi, T.; Ennis, H.L.
Mol. Gen. Genet. 218, 453-459, 1989
A;Title: Nucleotide sequences of Dictyostelium discoideum developmentally regulated cDNA
A;Reference number: S05355; MUD:90066348; PMID:2511421
A;Accession: S05358
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A;Molecule type: DNA
A;Residues: 1-342 <GAT>
A;Cross-references: UNIPROF;Q22902; EMBL:U64858; PIDN:AAB18288.1; GSPDB:GN00023; CESP:C1
A;Experimental source: strain Bristol N2; clone C16D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P14195; EMBL:X16525; NID:g7172; PIDN:CAA34532.1; PID:g930011
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C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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100.0%; Pred. No. 0.0027;
cive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0054;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.7%; Score 12; DB 2; Length 183;
100.0%; Pred. No. 0.0032;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: T29557
R;Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid C16D9.
A;Reference number: Z20640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 715 TTTTTTTTTT 727
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Best Local Similarity 100.
Matches 13; Conservative
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Matches 12; Conserv
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Best Local Similarity
Matches 12; Conserv
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A; Residues: 1-183 < SHA>
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A;Introns: 59/2; 316/3
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A;Cross-references: UNIPROT:Q9NA83; EMBL:AL117195; NID:e1549729; PIDN:CAB55014.1; CESP:Y.
A;Experimental source: clone Y57A10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C;Accession: T31631
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hypothetical protein Y57A10A.i - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-458 <WIL>
                                                                                                                               submitted to the EMBL Data Library, September 1999
A;Reference number: 221048
A;Accession: T31631
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.7%; Score 12; DB
100.0%; Pred. No. 0.0
ive 0; Mismatches
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C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004 nemo, form I - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster

A;Cross-references: UNIPROT:Q23993; GB:U12009; NID:g515669; PIDN:AAA21124.1; PID:g532558

ö Gaps ö Length 477; Indels 2.7%; Score 12; DB 2; Le 100.0%; Pred. No. 0.0071; ive 0; Mismatches 0;

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A; Gene: CESP: K08E3.6
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A;Title: Conerved classes of homeodomains in Schistosoma mansoni, an early bilateral me A;Reference number: S33640; MUID:92399260; PMID:1356008
A;Accession: S33640
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-524 <WEB>
A;Cross-references: UNIPROT:Q26601; EMBL:S44191; EMBL:M85305; NID:g161103; PIDN:AAA29929
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C;Superfamily: Alkaline phosphatase
C;Keywords: intestine; phosphoprotein; phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-530 cGAT>
A;Cross-references: UNIPROF:O61209; EMBL:AF040646; PIDN:AAB94986.1; GSPDB:GN00020; CESP:A;Experimental source: strain Bristol N2; clone H17B01
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C;Species: Mus musculus (house mouse)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 16-Aug-2004
C;Accession: B36307
R;Manes, T.; Glade, K.; Ziomek, C.A.; Millan, J.L.
Genomics 8, 541-554, 1990
A;Title: Genomic structure and comparison of mouse tissue-specific alkaline phosphatase
A;Reference number: A36307, MUID:91139124, PMID:2286375
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32812
R;Gattung, S.; Maggi, L.
R;Gattung, S.; Maggi, L.
A;Bestription: The sequence of C. elegans cosmid H17B01.
A;Reference number: Z21227
A;Reference number: Z21227
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C,Superfamily: homeobox homology
C,Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;424-480/Domain: homeobox homology <HOX>
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A;Gene: CESP:H17B01.2
A;Map position: 2
A;Introns: 42/3; 58/1; 173/3; 268/2; 308/2; 340/1; 364/2; 387/3
                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.7%; Score 12; DB 2; Length 524; Best Local Similarity 100.0%; Pred. No. 0.0077; Matches 12; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0078;
tive 0; Mismatches 0; Indels
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1es 12; Conservative
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A; Residues: 1-559 <MAN>
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Matches
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-680 wMIL-
A;Cross-references: UNIRROT:093374; EMBL:Z79598; PIDN:CAB01865.1; GSPDB:GN00028; CESP:C44
A;Experimental source: clone C4444
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A;Reference number: Z19743
A;Accession: T21954
A;Accession: T21954
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-681 < WIL>
A;Cross-references: UNIPROT:Q9XUS9; EMBL:Z81568; PIDN:CAB04593.1; GSPDB:GN00021; CESP:K06
A;Experimental source: clone K08E3
C;Genetics:
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regulatory protein CRAC - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Species: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: A54796
R;Insall, R; Kuspa, A.; Lilly, P.J.; Shaulsky, G.; Levin, L.R.; Loomis, W.F.; Devreotes, A;Insall, R; Kuspa, A.; Lilly, P.J.; Shaulsky, G.; Levin, L.R.; Loomis, W.F.; Devreotes, A;Ittle: CRAC, a cytosolic protein containing a pleckstrin homology domain, is required f
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                                                                                                                                                                                                                            hypothetical protein C44H4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19939
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23454
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A;Introns: 26/3; 74/3; 122/3; 216/3; 364/3; 589/3
                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, August 1996
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A;Introns: 36/1; 73/2; 237/3; 361/3; 612/3
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259 TTTTTTTTT 270
341 TTTTTTTTT 352
                              341 TTTTTTTTT 352
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A;Accession: T19939
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C;Accession: T30546
R;Mei, Q.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A.
Rifect. Immun. 66, 4268-4273, 1998
A;Title: Characterization of major surface glycoprotein genes of human Pneumocystis cariu. A;Reference number: Z17905; MUID:98380374; PMID:9712777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)

laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)

C;Species i Drosophila melanogaster

C;Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004

C;Accession: S28399; S18253

R;Kusche-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, L.I.; Fessler, J.H.

B;Kusche-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, L.I.; Fessler, J.H.

A;Title: Laminin A chain: expression during Drosophila development and genomic sequence.

A;Reference number: S28399; MUID:93049203; PMID:1425586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :Molecule type: nucleic acid
:Residues: 1-3712 <KUS>
:Cross-references: UNIPROT:Q00174; GB:M96388; NID:g157799; PIDN:AAA28662.1; PID:g157800
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Biol. Chem. 266, 22899-22904, 1991
Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struct: Reference number: S18253; MUID:92078147; PMID:1744083
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A;Experimental source: f.sp. hominis
                                                                                                                                                                                                                                                                                                  2,Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Jun-2001
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Residues: 1762-3712 <GAR>
:Cross-references: EMBL:M75882; NID:g157797; PIDN:AAA28661.1; PID:g157798
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.0.0.013;
0; Indels
                                                                                                                                                                                                                                 major surface glycoprotein - Pneumocystis carinii (fragment)
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100.0%; Pred. No. 0.0
ive 0; Mismatches
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Best Local Similarity 100.
Matches 12; Conservative
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                    A,Accession: A54796
A;Status: preliminary
A;Ratus: preliminary
A;Ratus: preliminary
A;Ratus: Draininary
A;Ratus: 1.698 clNS>
A;Cross-references: UNIPROT:P35401; GB:U06228; NID:g641960; PIDN:AAA61782.1; PID:g456398
C;Genetics: 11/3; 153/1
C;Superfamily: Dictyostelium regulatory protein CRAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xylanaee, beta(1,3-1,4)-glucanase - Ruminococcus flavefaciens
C;Species: Ruminococcus flavefaciens
C;Species: Ruminococcus flavefaciens
C;Species: Ruminococcus flavefaciens
C;Accession: 436910
R;Flint, H.J.; Martin, J.; McPherson, C.A.; Daniel, A.S.; Zhang, J.X.
J. Bacteriol. 175, 2943-2951, 1993
A;Title: A bifunctional enzyme, with separate xylanase and beta(1,3-1,4)-glucanase domain A;Reference number: A36910; MUID:93259938; PMID:8491715
A;Accession: A36910
A;Status: preliminary
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A;Experimental source: strain Bristol N2; clone C12D12
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A;Introns: 48/1; 86/3; 137/1; 172/3; 224/3; 253/1; 287/3; 328/2; 454/1; 487/3; 692/1
C;Superfamily: Epstein-Barr virus membrane antigen gp350
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R;Nhan, M: Hawkins, J. Bankins, J. Bankitted to the EMBL Data Library, March 1996  
A;Description: The sequence of C. elegans cosmid C12D12.  
A;Reference number: Z20656
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100.0%; Pred. No. 0.011;
ive 0; Mismatches 0; Indels
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A;Reference number: A54796; MUID:94375528; PMID:8089184
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 TTTTTTTTT 352
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Best Local Similarity 100.
Matches 12; Conservative
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Matches 12; Conserva
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A; Residues: 1-825 < NHA>
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A; Residues: 1-802 <FLI>
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probable auxin-induced protein, 50455-50036 [imported] - Arabidopsis thaliana (c)species: Arabidopsis thaliana (mouse-ear cress)

C;Bate: 02-Var-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D66417
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Hughes, B.; Huizar, L.

A;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.; Li, J.H.; Li, J.H.; Li, Y.; Lin, X.Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Praser, C.M.; White, Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Accession: D86417
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Cypothetical protein SA2097 [imported] - Staphylococcus aureus (strain N315)

Cypecies: Staphylococcus aureus

Cypecies: Staphylococcus aureus

Cypecies: Staphylococcus aureus

Cypecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

Cypeciesion: C90029

Cypecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

Cypecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

Cypecies: 10-May-2002

Cypecies: 10-May-2002

Cypecies: 10-May-2003

Cypecies: 10-May-2004

Cypecies: 10-May
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C;Accession: T28561
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C;Superfamily: Caenorhabditis elegans hypothetical protein Y9D1A.2
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Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lennard, N.
submitted to the EMBL Data Library, September 1999
A;Reference number: 220233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.5%; Score 11; DB 100.0%; Pred. No. 0.0; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-164 <WIL>
A;Cross-references: EMBL:AL110480; P1
A;Experimental source: clone Y24F12A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.5
Best Local Similarity 100.
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-139 <STO>
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NyAlternate names: ankyrin G
Syspecies: Home sapiens (man)
Cyspecies: Home sapiens (man)
Cyspecies: Home sapiens (man)
Cyspecies: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
CyAccession: A55575
CyAccession: A55575
CyAccession: A55575
Ayrore 2352-2359, 1995
Ayritle: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the ax
Ayreference number: A55575; MUID:95138209; PMID:7836469
                           F;2698-3712/Domain: G < DOMG.
F;2698-3712/Domain: repeat G1 < RG1>
F;2698-3048/Domain: repeat G2 < RG2>
F;3049-3223/Domain: repeat G3 < RG3>
F;3049-3223/Domain: repeat G3 < RG3>
F;3049-3228/Domain: repeat G4 < RG4>
F;3079-3208/Domain: repeat G4 < RG4>
F;3134-3228/Domain: repeat G4 < RG4>
F;3134-3228/Domain: repeat G4 < RG4>
F;3134-3228/Domain: repeat G5 < RG5>
F;1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,3
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-4377 <KOR>
A;Cross-references: UNIPROT:Q12955; GB:U13616; NID:g608024; PIDN:AAA64834.1; PID:g608025
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C,Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C;Keywords: alternative splicing; peripheral membrane protein
F;73-105/Domain: ankyrin repeat homology <ANOL>
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Pred. No. 0.046;
0; Mismatches 0; Indels
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100.0%; Pred. No. c...
... 0; Mismatches
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Fil39-171/Domain: ankyzin repeat homology cAN03>
Fil20-20/Domain: ankyzin repeat homology cAN03>
Fil20-20/Domain: ankyzin repeat homology cAN04>
Fil20-23/Domain: ankyzin repeat homology cAN06>
Fil20-29/Domain: ankyzin repeat homology cAN06>
Fil20-23/Domain: ankyzin repeat homology cAN06>
Fil20-32/Domain: ankyzin repeat homology cAN08>
Fil20-33-35-Domain: ankyzin repeat homology cAN08>
Fil20-33-365/Domain: ankyzin repeat homology cAN09>
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F;2116-2697/Domain: I/II, heptad repeats <DOM2>
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A;Cross-references: GDB:424503; OMIM:600465
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Matches 12
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A;Residues: 1-373 <AND>
A;Cross-references: EMBL:U55854; PIDN:AAA98013.1; GSPDB:GN00020; CESP:C04G6.2
A;Experimental source: strain Bristol N2; clone C04G6
                                                                                                                                                                                                                                                                                                                                                                   Galivary glue protein sgs-3 precursor - fruit fly (Drosophila yakuba)
C;Species: Drosophila yakuba
C;Species: Drosophila yakuba
C;Date: 30-5ep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S01360; C30360; C3036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Ictalurus punctatus (channel catfish)
C;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: FlyBase:FBgn0013172
C;Superfamily: salivary glue protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-263/Product: salivary glue #rotein sgs-3 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.5%; Score 11; DB 2; Length 263; 100.0%; Pred. No. 0.036; ative 0; Mismatches 0; Indels
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A;Introns: 33/3; 85/3; 143/1; 179/1; 226/2; 263/1; 310/2
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A;Cross-references: UNIPROT:P13728
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RAD 23B protein - channel catfish
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les 11; Conserv
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A: Mole genome sequencing of meticillin-resistant Stapylococcus aureus.
A:Reference number: A89758; MUD:21311952; PMID:11418146
A;Accession: C90029
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1.166 cKUR>
A;Cross-references: UNIPROT:099RW9; GB:BA000018; PID:gl3702104; PIDN:BAB43396.1; GSPDB:GC;Genetics:
A;Genetics:
A;Genetics:
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merozoite surface antigen 2 [imported] - malaria parasite (Plasmodium falciparum) (fragm merozoite surface antigen 2 [imported] - malaria parasite (Plasmodium falciparum) (fragm C;Species Plasmodium falciparum)

C;Species 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004

C;Accession: T46896

R;Prescott, N.; Stowers, A.W.; Cheng, Q.; Bobogare, A.; Rzepczyk, C.M.; Saul, A.

Mol. Biochem. Parasitol. 63, 203-212, 1994

A;Title: Plasmodium falciparum genetic diversity can be characterized using the polymorp

A;Reference number: Z24128; MUID:94277144; PMID:8008018
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AMOLecule type: DNA
A,Residues: 1-208 <PRE>
A,Cross-references: UNIPROT:Q25949; EMBL:L19048; NID:g438839; PIDN:AAC37195.1; PID:g4388
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A;Experimental source: clone Y24F12A
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C;Species: Caenorhabditis elegans
C;bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C;Accession: T26560
R;Lennard, N.
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C;Superfamily: Caenorhabditis elegans hypothetical protein Y9D1A.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: MSA-2
A;Map position: 2
C;Superfamily: Epstein-Barr virus nuclear antigen
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Best Local Similarity 100.
Matches 11; Conservative
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Matches 11; Conserv
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A;Status: preliminary
A;Molecule type: mRNA
A;Resdues: 1-525 «STA>
A;Status: 1-525 «STA>
A;Coss-treferences: UNIPROT: P17955; GB:X52583; NID:957640; PIDN:CAA36813.1; PID:957641
B;D'Onofrio, M.; Starr, C.M.; Park, M.K.; Holt, G.D.; Haltiwanger, R.S.; Hart, G.W.; Hanc
Proc. Natl. Acad. Sci. U.S.A. 85, 9595-9599, 1988
A;Title: Partial cDNA sequence encoding a nuclear pore protein modified by O-linked N-ace
A;Reference number: A31762; MUID:89071743; PMID:3200844
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R;Cordes, V.; Waizenegger, I.; Krohne, G.

Bur. J. Cell Biol. 55, 31-47, 1991

A;Title: Nuclear pore complex glycoprotein p62 of Xenopus laevis and mouse: cDNA cloning A;Reference number: A56573; MUID:92007945; PMID:1915419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nuclear pore glycoprotein p62.
         A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992 C;Superfamily: octopamine receptor type I
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norregicus (Norway rat)
C;Date: 09-Nov-1990 #sequence revision 09-Nov-1990 #text_change 09-Jul-2004
C;Accession: A35596; A31762; I55336; S11666
R;Starr, C.M.; D'Nonfrio, M.; Park, M.K.; Hanover, J.A.
J. Cell Biol. 110, 1861-1191, 1990
A;Title: Primary sequence and heterologous expression of nuclear pore glycop
A;Reference number: A35596; MUID:90277705; PMID:2190987
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C;Species: Mus musculus (house mouse)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
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J. Biol. Chem. 266, 11980-11985, 1991
A;Title: The gene encoding rat nuclear pore glycoprotein p62 is intronless.
A;Reference number: ISS3336; MUID:91268076; PMID:2050692
                                                                                                                                                                                                  Gaps
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A;Residues: 370,'FR',373-525 <DON>
A;Cross-references: GB:J04143; NID:g623564; PIDN:AAA60741.1; PID:g623565
A;Experimental source: hepatic
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100.0%; Pred. No. 0.065;
ive 0; Mismatches 0; Indels
                                                                                                                                      Length 484
                                                                                                                               Query Match 2.5%; Score 11; DB 2; Best Local Similarity 100.0%; Pred. No. 0.061; Matches 11; Conservative 0; Mismatches 0
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C, Keywords: coiled coil; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nuclear pore glycoprotein p62 - rat
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Conservative 0
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Matches 11; Conserv
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S58868
G protein-coupled receptor GCR1 - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Accession: S58868; S58869
R;Vanden Broeck, J; Vulsteke, V; Huybrechts, R; De Loof, A.
J. Neurochem. 64, 2387-2395, 1995
A;Title: Characterization of a cloned locust tyramine receptor cDNA by functional expres
A;Reference number: S58868; MUID:95279966; PMID:7760020
A;Recession: S58868
A;Status: preliminary
A;Rolecule type: mRNA
A;Residues: 1-484 <VANA
A;Cross-references: UNIPROT:Q25321; EMBL:X69520; NID:g871404; PIDN:CAA49268.1; PID:g8714
A;Molecule type: mRNA
A;Residues: 1-307, 'D', 309-338,'K', 340-484 <VA2>
A;Cross-references: EMBL:X69521; NID:g871406; PIDN:CAA49269.1; PID:g871407
Riliu, Z.; Li, P.; Kocabas, A.; Karsi, A.; Ju, Z.
Biochem. Biophys. Res. Commun. 289, 317-324, 2001
A;Title: Microsatellite-containing genes from the channel catfish brain: Evidence of tri
A;Contents: Brain
A;Accession: JC7783
A;Accession: JC7783
A;Accession: JC7783
A;Accession: JC7783
A;Residues: 1-385 < LIU>
A;Coss-references: UNIPROT:Q?LZR8
C;Comment: This protein with a polythreonine tract, has importance in the nucleotide exc
C;Genetics: A;Gene: rad23b
A;Introns: 76/3
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-415 <BLA>
A,Cross-references: UNIPROT: Q9GZH9; EMBL:AF026212; PIDN:AAB71300.1; GSPDB:GN00028; CESP:
A,Experimental source: strain Bristol N2; clone F52G3
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C'Jaces 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 09-Jul-2004
C'Accession: T32467
R'Blanchard, M.; Gattung, S.; Sansone, J.
submitted to the EMBL Data Library, September 1997
A'Description: The sequence of C. elegans cosmid F52G3.
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A;Map position: X
A;Introns: 31/1; 49/1; 104/1; 117/1; 220/1; 241/2; 307/1; 370/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%; Score 11; DB 2; Length 385;
100.0%; Pred. No. 0.05;
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114 TTTTTTTT 124
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Length 569;

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C, Accession: 847277
R; Thaele, R.; Lucin, P.; Schneider, K.; Koszinowski, U.
Submitted to the EMBL Data Library, February 1994
A; Reference number: 847277
A; Accession: 847277
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-569 < TTA>
A; Residues: 1-569 < TTA>
A; Coss-references: UNIPROT: Q83183; EMBL: X77798; NID: g535195; PIDN: CAA54825.1; PID: g5351
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A;Experimental source: clone T05C12
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C;Species: Ceenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24505
                                               gp88 protein - murine cytomegalovirus
C,Species: murine cytomegalovirus, murine herpesvirus 1
C,Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
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A;Introns: 28/3; 48/3; 103/3; 156/3; 192/3; 249/3; 408/3; 495/3; 623
C;Superfamily: Caenorhabditis elegans hypothetical protein T05C12.4
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A;Molecule type: DNA
A;Residues: 1-649 <WIL>
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Best Local Similarity 100.
Matches 11; Conservative
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Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cipate: 18-Uul-2001 #sequence_revision 18-Uul-2001 #text_change 09-Uul-2004
Cipaccesion: A98199
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A98199
A;Status: preliminary
A;Residues: 1-558 <HAY>
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A;Cross-references: UNIPROT:Q63850; GB:S59342; NID:g236260; PIDN:AAB19953.1; PID:g236261
A;Note: sequence extracted from NCBI backbone (NCBIN:59342, NCBIP:59343)
C;Comment: The amino end of this protein contains O-linked N-acetylglucosamine additions
C;Keywords: glycoprotein; nuclear membrane; peripheral membrane protein
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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100.0%; Pred. No. 0.065;
tive 0; Mismatches 0
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100.0%; Pred. No. 0.068;
iive 0; Mismatches 0
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Pred. No. 0.068;
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C;Accession: A45155
R;Hauser, F.; Hoffmann, W.
B.iol. Chem. 267, 24620-24624, 1992
A;Title: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C.1 A;Reference number: A45155; MUID:93077556; PMID:1447205
A;Accession: A45155
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A;Residues: 1-662 <HAU>
A;Residues: 1-662 <HAU>
A;Cross-treferences: UNIPROT:Q05049; GB:L02115; NID:g214147; PIDN:AAA74725.1; PID:g951460
F;162-207/Domain: trefoil homology <TRF!>
F;307-347/Domain: trefoil homology <TRF2>
F;354-394/Domain: trefoil homology <TRF2>
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
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Length 649;
2.5%; Score 11; DB 2; Length 649
100.0%; Pred. No. 0.078;
ive 0; Mismatches 0; Indels
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Gispecies: Archaeoglobus fulgidus
Cispecies: Archaeoglobus fulgidus
Cispecies: Archaeoglobus fulgidus
Cispate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cisate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Riklenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Wosse, C.R.; Venter, J.C.
A;Ritle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A;Reference number: A69250; MUID:98049343; PMID:9389475
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C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
C;Accession: T18775
R;Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
A;Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Biol A;Reference number: Z06411
A;Accession: T18775
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A.Residues: 1-1093 <ZHO>
A.Cross-references: UNIPROT:P54677; EMBL:U23479; NID:g733527; PID:g733528; PIDN:AAA85725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-816 <KLE>
A;Cross-references: UNIPROT:028331; GB:AE000968; GB:AE000782; NID:g2689291; PIDN:AAB89306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: EMBL:U20864; NID:g669026; PID:g669033; PIDN:AAC46666.1; CESP:F32A5.2
A,Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: CESP:F32A5.2
A;Introns: 23/1; 58/3; 102/3; 136/2; 277/2; 380/2; 422/1; 502/1; 580/2; 648/1; 935/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: C69493
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F32A5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.5%; Score 11; DB 2; Length 816; Best Local Similarity 100.0%; Pred. No. 0.094; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.5%; Score 11; DB 2; Length 977; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Riballey, A. submitted to the EMBL Data Library, July 1995 A;Description: The sequence of C. elegans cosmid F32A5. A;Reference number: Z18482 A;Accession: T16232 A;Staus: preliminary; translated from GB/EMBL/DDBJ
                                                 hypothetical protein AF1948 - Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 PTTTTTTTT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 PITITITITI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338 PPPTTTTTT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 ppprirrrrrr 367
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A; Residues: 1-977 < PAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: T16232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypotherical protein ZC13.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T25.07
R;Bradshaw, H.
R;Brads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Genetics:
A,Gene: CESP:ZC13.3
A,Map position: X
A;Introns: 19/3; 52/2; 86/1; 169/1; 301/1; 365/1; 401/3; 506/2; 528/2; 553/1; 639/1; 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-770 <WIL>
A;Cross-references: UNIPROT:Q20908; EMBL:Z74473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:F5
A;Experimental source: clone F56H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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hypothetical protein F56H9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Data Library, June 1996
R;Burton, J.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19618
A;Reference number: Z19618
A;Accession: T22808
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                         Score 11; DB 2; Length 662;
Pred. No. 0.079;
0; Mismatches 0; Indels
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100.0%; Pred. No. 0.086;
tive 0; Mismatches 0; Indels
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A;Gene: CESP:F56H9.1
A;Map position: 5
A;Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2
                                                                                                                                                                  Query Match 2.5%; Score 11; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
F;526-566/Domain: trafoil homology <TRF4>
F;573-613/Domain: trafoil homology <TRF5>
F;621-661/Domain: trafoil homology <TRF6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.5
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                340 PTTTTTTTT 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 TTTTTTTTT 351
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Best Local Similarity
Matches 11; Conserva
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C; Genetics:

RESULT 68

Gaps

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C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 151382
R;Jasoni, C.L.; Walker, M.B.; Morris, M.D.; Reh, T.A.
R;Jasoni, C.L.; Walker, M.B.; Morris, M.D.; Reh, T.A.
A;Title: A chicken achaete-scute homolog (CASH-1) is expressed in a temporally and spati:
A;Reference number: 151382; MUID:95324365; PMID:7600956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                larval glue protein Lgp-1 precursor - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Accession: A60095; S50126; S44060
R;Swida, U.; Lucka, L.; Kress, H.
Development 108, 269-280, 1990
A;Title: Glue protein genes in Drosophila virilis: their organization, developmental con.
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A; Molecule type: DNA
A; Molecule type: J-23
A; Molecule type: J-24
A; Molecule type: Act a 1219, 576-580, 1994
A; Molecule type: Act a 1219
A; Molecule typ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT: Q90575; EMBL: U01339; NID: 9401726; PIDN: AAC59658.1; PID: 94017
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C;Species: Drosophila melanogaster
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: salivary glue protein
C;Keywords: glycoprotein; salivary gland; tandem repeat
C;Reywords: glycoprotein; salivary gland; tandem cepeat
F;1-23/Domain: slignal sequence #status predicted csIG-
F;43-86;94-104/Region: 11-residue repeats (T-T-T-T-T-T-T-T-T)
F;105-160/Region: 8-residue repeats (T-T-T-T-T-T-T-P)
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                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-219 <JAS>
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100.0%; Pred. No. 0.27;
trive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.3%; Score 10; DB 2;
100.0%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: FlyBase:Dvir/Lgp1
A;Cross-references: FlyBase:FBgn0010305
A;Map position: X16A
                                              - chicken
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Best Local Similarity 100.0
Matches 10, Conservative
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Matches 10; Conservative
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                                                 chaete-scute homolog
                                                                                                                                                                                                                                                                                                                                             A; Accession: I51382
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D64237

hypothetical protein MG338 - Mycoplasma genitalium
C;Species: Mycoplasma gentalium
C;Species: Mycoplasma gentalium
C;Species: Mycoplasma gentalium
C;Species: Mycoplasma gentalium
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: D64237
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
R;Fraser, C.M.; Venter, J.C.
Science 270, 397-403,
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reseince: D64237
A;Science 270, 397-403,
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-1271 cTTGR>
A;Cross-references: UNIPROT:P47580; GB:U39716; GB:L43967; NID:g1046037; PID:g1046042; TI
C;Genetics:
A;Genetics:
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N;Alternate names: protein T20K14_210
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51538
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mewsubmitted to the Protein Sequence Database, August 2000
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                                                                                                           2.5%; Score 11; DB 2; Length 1093; 100.0%; Pred. No. 0.12; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.14;
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100.0%; Pred. No. 0.17;
lve 0; Mismatches 0; Indels
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A;Experimental source: cultivar Columbia; BAC clone T20K14
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100.0%; Pre-
                                          C;Keywords: phosphotransferase
                                                                                                                                                                                        11; Conservative
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A;Molecule type: DNA
A;Residues: 1-127 <SAT>
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A;Introns: 97/3
A;Note: T20K14_210
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A;Note: PIK4
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C; Accession: A03329
R; Garfinkel, M.D.; Pruitt, R.E.; Meyerowitz, E.M.
J. Mol. Biol. 168, 765-789, 1983
A; Title: DNA sequences, gene regulation and modular protein evolution in the Drosophila A; Title: DNA sequences, gene regulation and modular protein evolution in the Drosophila A; Reference number: A92904; MUID:83294545; PMID:6411930
A; Molecule type: DNA
A; Residues: 1-307 cGAR>
A; Cross-references: UNIPROT: P02840; GB:X01918; NID:g8581; PIDN: CAA25994.1; PID:g603989
C; Comment: This protein is produced by third-instar larvae.
C; Genetics:
A; Gene: sgs-3
A; Cross-references: FlyBase: FBgn0003373
A; Matrons: 10/1
C; Superfamily: salivary glue protein
C; Keywords: salivary gland; tandem repeat
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Search completed: June 28, 2005, 10:21:26 Job time : 32.5711 secs

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SEQUENCE FROM N.A.

C TISSUB-Whole embryo;
A Cat T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
A Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
A Nagahari K., Sugano S., Isogai T.;
Submitterd (MAR-2012) to the EMBL/GenBank/DDBJ databases.
EMBL, AK07550; BGT1657.1;
R Genew; HGN0:5951; IGSF4.
R InterPro; IPR003598; Ig_c2.
R InterPro; IPR003598; Neurexin-like.
R SMART; SM00294; 4.1m; 1.
R SMART; SM02094; 4.1m; 1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                        Length 442;
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                                                                                                                                                                                              Indels
SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 3.
SEQUENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OMA-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PSEC0200.
Homo sapiens (Human)
                                                                                                                                   Score 341; DB 2; L
Pred. No. 1.3e-310;
0; Mismatches 1;
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                                                                                                                                        77.1%;
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Best Local Similarity 99.8
Matches 441; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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     29bjq7
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SEQUENCE FROM N.A.
Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF13811, AAF69019.1;
InterPro; IPR003110; Ig-11ke.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Neurexin-like.
PF00047; ig; 2.
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Last annotation update)
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07YUQ3

07Y
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Q861L5
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Q658Q7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Noctin-like protein 2.
Name=NECL2;
Homo sapiens (Human).
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241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
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                                         YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Project.

In Submittee (JUL-2004) to the EMBL/GenBank/DDBJ databases.

Result, AB092414; BAC66173.1; ---

REMBL; AB183402; BAD30021.1; ---

REMBL; AB183402; BAD30021.1; ---

REMBL; AB183402; Igsf4a.

REMBL; AB183402; Igsf4a.

ROG; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016021; C:integral to wemicle; IDA.

ROG; GO:0008021; C:synaptic vesicle; IDA.

ROG; GO:000512; F:protein binding; IPI.

ROG; GO:000155; F:protein binding; IPI.

ROG; GO:000155; F:protein binding; IPA.

ROG; GO:000155; F:protein adhesion; IDA.

ROG; GO:000155; F:protein adhesion; IDA.

ROG; GO:000155; F:protein adhesion; IDA.

ROG; GO:000715; F:protein adhesion; IDA.

RINGERPO; IRR007110; III-like.

RINGERPO; IRR007359; IG-12.
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STRAIN=CSFBL/6; TISSUB=Spleen cell-derived;
Ito A., Koma Y., Nagano T.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 2.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG LIKE; 3.
SEOUENCE 336 AA; 37155 MW; 9EF3D8B8BESE8F72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 28, Last annotation update)
A secretion form of SgIGSF/TSLC1 (RA175 isoform e).
Name=1gsf4a; Synonyme=RA175, sSgIGSF/sTSLC1;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                              301 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVY 331
                                                                                                                                                                       NNLNKTDNGTYRCEASNIVGKAHSDYMLYVY 331
                                                                                                                                                                                                                                                                                                                                                                                                              336 AA.
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                                                                                                                                        1 MASVVLPSGSQCAAAAAAAAPGLRLRLLLLLFSAAALIPTGGGQNLFTKDVTVIEGEVA 60
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                                                                                                 1 MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                      0; Indels
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB094146; Bac66179.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Ffam; PF00047; Ig; 2.
SWART; SM004009; Ig-2; 1.
PROSITE; PS0835; IG LIKE; 3.
SEQUENCE 333 AA; 36915 MW; D7C1102F46D08492 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Secretory isoform of TSLC-1.
100.0%; Pred. No. 3.5e-302; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYD 332
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                               Matches 332; Conservative
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Homo sapiens (Human).
   Best Local Similarity
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Query Match
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Adachi J., Aizawa K., Akhinza T., Arai A., Aono H.,
Adachi J., Aizawa K., Akhira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akhira S., Fukunishi Y., Furuno M.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Sogabe Y., Suzuki A., Nishi K., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Saaki D., Shibata K., Shibata Y., Shiraaka T.,
A Sogabe Y., Suzuki H., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
B. Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; MG13775; BSAB28988:1; -
BMGD; MG1:1889272; Igsféd.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
RO; GO:0008021; C:synaptic vesicle; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

C STRAIN=C57BL/6J; TISSUE=Hippocampus;
MEDLINE=C57BL/6J; TISSUE=Hippocampus;
MEDLINE=C57BL/6J; TISSUE=Hippocampus;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
A Shibata K., Itoh M., Aizawa K., Nagaoka S., Isashiro H., Itoh M.,
A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakagudi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
TRIKEN integrated sequence analysis (RISA) system-384-format
Esquencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRANTE-CS7BL/6J; TISSUE=Hippocampus;
MEDLINE=CS7BL/6J; TISSUE=Hippocampus;
MEDLINE=CS7BL/6J; PubMed=11042159, DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C59BL/6J; TISSUE-Hippocampus;
MEDLINE=99579253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
  CDNA, RIKEN full-length enriched
                       library, clone:2900073G06 product:immunoglobulin superfamily, member
4, full insert sequence.
                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE-Hippocampus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Hippocampus;
The FANTOM Consortium,
musculus adult male hippocampus
                                                                                  Mus musculus (Mouse)
                                                                 Name=Igsf4a;
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94 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
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STRAIN=CS7BL/6; TISSUE=Brain;
MEDLINE=22841094; PubMed=1282663; DOI=10.1074/jbc.M305387200;
MEDLINE=22841094; PubMed=12826663; DOI=10.1074/jbc.M305387200;
Shingai T., Ikeda W., Kakunaga S., Morimoto K., Takekuni K., Itoh S., Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
"Implications of nectin-like molecule-
2/IGSF4/Ra175/SgIGSF/TSLC1/SynCAM1 in cell-cell adhesion and
Lransmembrane protein localization in epithelial cells.";
J. Biol. Chem. 278:35421-35427(2003).
                                                                                                                                                                                                                                                                                Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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0
GO, GO:0005515; F:protein binding; IPI.

GO; GO:0016338; P:calcium-independent cell-cell adhesion; IDA.

GO; GO:00074155; P:cell adhesion; IDA.

GO; GO:0007415; P:synaptogenesis; IDA.

InterPro; IPR003598; Ig_c2.

InterPro; IPR003598; Ig_c2.

SMART; SM00409; IGc2; 1.

PROSITE; PSS0835; IG_LIKE; 3.

SROUGENCE 336 AA; 37157 MW; FF887FAF4EFDF120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60; 60:0016021; C:integral to membrane; TAS.
60; 60:0045202; C:synapse; IDA.
60; 60:0008021; C:synapse; IDA.
60; 60:0008515; F:protein binding; IPI.
60; 60:0015318; P:calcium-independent cell-cell adhesion; IDA.
60; 60:0007155; P:cell adhesion; IDA.
60; 60:0007155; P:cell adhesion; IDA.
                                                                                                                                                                                                                                      Length 336;
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98500180D37845C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-007-2003 (TrEMBLrel. 25, Created)
1-007-2003 (TrEMBLrel. 25, Last sequence update)
25-007-2004 (TrEMBLrel. 28, Last annotation update)
Nectin-like molecule 2 (RA175 isoform d).
                                                                                                                                                                                                                                    33.9%; Score 150; DB 2; Le
100.0%; Pred. No. 1.1e-131;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003585; Neurexin-like.
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SMART; SM00294; 4.1m; 1.
SMART; SM0049; IGC.; 1.
SEQUENCE PS50835; IG LIKE; 3.
SEQUENCE 417 AA; 45779 MW;
                                                                                                                                                                                                                                                                                Matches 150; Conservative
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                                                                                                                                                                                                                                                            Local Similarity
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94 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
                                                                                                                                                                    MEDLINE-22192378; PubMed=12202822; DOI=10.1126/science.1072356;
Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,
Sudhof T.C.;
                                                                                                                                                                                                                          "SynCAM, a Synaptic Adhesion Molecule That Drives Synapse Assembly."; Science 297:1525-1531(2002).
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MEDLINE=22226620; PubMed=12242005; DOI=10.1016/S0378-1119(02)00835-1;
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MGD; MGI:1889972; Igsfan.
GO; GO:0045202; C:integral to membrane; TAS.
GO; GO:0045202; C:synapse; IDA.
GO; GO:0008021; C:synaptic vesicle; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:001555; P:cell adhesion; IDA.
GO; GO:0007155; P:cell adhesion; IDA.
Interbro; IPR003189; Ig.-C2.
Interbro; IPR003589; Ig.-C2.
Interbro; IPR003589; Neurexin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Fujita E., Aikawa K., Momoi T.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AFS39424; AANO1614.1; -.
EMBL; AB183399; BAD30018.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEam; PF00047; ig; 2.
SWART; SW00294; 4.lm; 1.
SWART; SW00409; IGC2; 1.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;
   01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Synaptic cell adhesion molecule 1 (RA175 isoform c)
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                                                 Name=Igsf4a; Synonyms=RA175;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.9%,
Best Local Similarity 100.0%
Matches 150, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                               STRAIN=C57BL
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Q8R4L1
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                                                                                 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
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                                  Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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A FUJITA E. Aikawa K., Momoi T.;

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

E RMBL; AB183400 BAD20019-1;

R GO; GO:0016021; C:synapse; IDA.

R GO; GO:000821; C:synapse; IDA.

R GO; GO:0005215; F:protein binding; IPI.

R GO; GO:000515; F:protein binding; IPI.

R GO; GO:000715; P:call adhesion; IDA.

R GO; GO:000716; P:synaptogenesis; IDA.

R GO; GO:00716; P:synaptogenesis; IDA.

R InterPro; IPR007310; Ig-like.

R InterPro; IPR007359; Ig-like.
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33.9%; Score 150; DB 2; Length 417; 100.0%; Pred. No. 1.3e-131; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00409; IG; 3.
SMART; SM00408; IGC2; 3.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 428 AA; 46903 MW; B10DFF1A2B893573 CRC64;
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                                                                                                                                                                                                                                                                                                                                           Created)
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01-OCT-2002 (TrEMBLrel. 22, Created)
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                               Matches 150; Conservative
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Matches 150; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                      RA175 isoform b.
                                                                                                                                                                                                                                                                                                                                                                                                         Name=RA175;
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 Query Match
Best Local S
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Q8K3T6
ID Q8K3'
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Query Match 33.9%
Best Local Similarity 100.0
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IR EMBL; AB064265; BAB3510.2; -.

IR MGD; MGI:1889272; Igsf4a.

BR GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0006515; C:synaptic vesicle, IDA.

BR GO; GO:0006515; F:protein binding; IPI.

BR GO; GO:0007155; P:call adhesion; IDA.

BR GO; GO:0007155; P:call adhesion; IDA.

BR GO; GO:0007165; P:scall adhesion; IDA.

BR GO; GO:0007165; P:scall adhesion; IDA.

BR HILEPPRO; IPR007110; IG-like.

BR InterPro; IPR003585; Neurexin-like.

BR Ffam; PF00047; ig; 2.
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Fukami T., Satoh H., Fujita E., Maruyama T., Fukuhara H., Kutamochi M., Takamoto S., Momoi T., Murakami Y.; "Identification of the Talc1 gene, a mouse orthologue of the human tumor suppressor TSLC1 gene.";
                                                                                                                                                                | Gene 295;7-12(2002).
| R MGD; MGI:1889272; Jg9f4a.
| R MGD; MGI:1889272; Jg9f4a.
| Go; GO:0016021; C:integral to membrane; TAS.
| GO; GO:0008021; C:integral to weaicle; IDA.
| R GO; GO:0008021; C:synapse; IDA.
| R GO; GO:0008021; F:protein binding; IPI.
| R GO; GO:000715; F:protein binding; IPI.
| R GO; GO:000715; P:cell adhesion; IDA.
| R GO; GO:000716; P:cell adhesion; IDA.
| R GO; GO:000716; P:synaptogenesis; IDA.
| R GO; GO:000716; P:synaptogenesis; IDA.
| R InterPro; IPR003189; Ig-1ke.
| R InterPro; IPR003589; Neurexin-like.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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SMART; SM00408; 1GC2; 1.
PROSITE; PS50835; IG LIKE; 3.
SEOUENCE 445 AA; 48664 MW; C5DSA070DAF70E55 CRC64;
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Last sequence update)
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                  34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                            Length 456;
                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Director MGC Project;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC078966, AAH789966.1;
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003598; Ig.
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SMART; SM00409; IG; 3.
SMART; SM00409; IGc2; 3.
PROSITE; PS0835; IGC_LIKE; 3.
Hypothetical protein.
SEQUENCE 476 AA; 51853 MW; 486A43D37082C8FE CRC64;
SMART; SM00294; 4.1m; 1.
SMART; SM0408; IG-2; IG-2;
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 456 AA; 49787 MW; 3226E866AABCIC7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                       33.9%; Score 150; DB 2; Lo
100.0%; Pred. No. 1.4e-131;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 DTAVEGEBIEVNCTAMASKPATTIRWFKGN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HID
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 MEDLINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8; Pujita E., Soyama A., Momoi T.; Paralla E., Soyama D.; Paralla E., P
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNIMIDIQK 153
 244
 245 VHIOMTYPLQGLTREGDALELTCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLN 304
 98 VHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVKVDDEMPQHAVLSGPNLFINNLN 157
 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 37 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 96
 38 ELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQ 97
 185 ELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQ
 Gaps
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 .;
0
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 33.9%; Score 150; DB 2; Length 476; 100.0%; Pred. No. 1.5e-131; ive 0; Mismatches 0; Indels
 Length 278;
 0; Indels
 Allocary,
Pfam, PP00047; ig; 1.
SWART; SM00294; 4.1m; 1.
SWART; SW00408; IGC2; 1.
PROSITE; PS50835; IG LIKE; 2.
SROUENCE 278 AA; 30636 MW; A295F4DEA2724B04 CRC64;
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 Score 127; DB 2; Le
Pred. No. 3.4e-110;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
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 28.7%; Score 127; DE 100.0%; Pred. No. 3.4
 Created)
 PRT;
 InterPro, IPR003585; Neurexin-like.
 Adhesion protein RA175N.
Name=1gsf4a; Synonyms=ra175n;
Mus musculus (Mouse).
 01-MAY-2000 (TrEMBLrel. 13,
 Conservative
 al Similarity 100.
150; Conservative
 PRELIMINARY;
 KTDNGTY 311
 KTDNGTY 164
 127; Conserv
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Query Match
Best Local S
Matches 150
 97
 157
 158
 94
 154
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 Query Match
Best Local
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 RESULT 12
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244
 Pujita E., Soyama A., Momoi T.;

"RA175, which is the mouse ortholog of TSLC1, a tumor suppressor gene
in human lung cancer, is a cell adhesion molecule.";

Exp. Cell Res. 287:57-6(2003).

R MGD; MCI:189272; Igsfau.

R GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:001551; P:protein binding; PPI.

R GO; GO:000715; P:protein binding; IPA.

GO; GO:000715; P:protein binding; IPA.

R GO; GO:000715; P:protein binding; IPA.

InterPro; IPR001598; Ig-c2.

R InterPro; IPR001598; Neurexin-like.

R Pfam; PF00047; Ig; 1.

SWART; SM00294; 4.1m; 1.

SWART; SM00408; IG-z; 1.

R RPROSITE; SS00835; IG LIKE; 2.

SEQUENCE 289 AA; 31811 MW; 8D1B836D0565AEA4 CRC64;
 245 VHIQMTYPLQGLTREGDALBLTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLN 304
 98 VHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLN 157
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SEQUENCE FROM N.A.
MEDLINE=22663149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8;
Pujita E., Soyama A., Momoi T.;
Fujita E., Soyama A., Momoi T.;
"RA175, which is the mouse ortholog of TSLC1, a tumor suppressor gene
 185 ELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQ
 MEDLINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8;
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ö
 28.7%; Score 127; DB 2; Length 289; 100.0%; Pred. No. 3.5e-110; ive 0; Mismatches 0; Indels
 OL-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adhesion protein RAI75B.
Name=Igsf4a; Synonyms=ra175b;
Mus musculus (Mouse)
 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 295 AA.
 PRT;
 Adhesion protein RA175A.
Name=Igsf4a; Synonyms=ra175a;
Mus musculus (Mouse).
 Best Local Similarity 100.0
Matches 127; Conservative
 PRELIMINARY;
PRELIMINARY;
 KTDNGTY 311
 KTDNGTY 164
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 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
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264 ELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAH 323
 98 VHIQMTYPLQGLTREGDALELTCEAIGKPQPVWVTWVRVDDEMPQHAVLSGPNLFINNLN 157
 117 ELTCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAH 176
 245 VHIQMTYPLOGLTREGDALELTCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLN 304
 38 ELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQ 97
 185 ELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQ
 Gaps
 0; Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 A Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
Lsubmitted (APR 1998) to the EMBL/GenBank/DDBJ databases.
Lsubmitted (APR 1998) to the EMBL/GenBank/DDBJ databases.
EMBL, APO61260; AAO67243.1; -.
R GO; GO:0016621; C:integral; on embrane; TAS.
R GO; GO:0016221; C:integral to membrane; TAS.
R GO; GO:0016221; C:integral DA.
R GO; GO:0005515; P:protein binding; IPI.
R GO; GO:000515; P:protein binding; IPI.
R GO; GO:000715; P:protein binding; IPI.
R GO; GO:000715; P:coll adhesion; IDA.
R GO; GO:000715; P:synaptogenesis; IDA.
R InterPro; IPR00710; ITI-1ke.
R InterPro; IPR003585; Neurexin-like.
R Pfam; PR00047; ig; 2.
R SWART; SW00404; ig; 2.
R RRART; SW00408; IGC2; 1.
R SRANT; SW00408; IGC2; 1.
 ;
0
 Length 295;
 Length 306;
 Query Match 23.5%; Score 104; DB 2; Length 29 Best Local Similarity 100.0%; Pred. No. 1.3e-88; Matches 104; Conservative 0; Mismatches 0; Indels
 0; Indels
306 AA; 33522 MW; A4CE37B0F23554D5 CRC64;
 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nactin-like protein 2.
Name=198f4a: Synonyms-Necl2;
Mus musculus (Mouse)
 Query Match 28.7%; Score 127; DB 2; Le Best Local Similarity 100.0%; Pred. No. 3.7e-110; Matches 127; Conservative 0; Mismatches 0;
 GGMZK6 PRELIMINARY; PRT; 84 AA.
QGMZK6;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 PRT;
 PRELIMINARY;
 305 KTDNGTY 311
 158 KTDNGTY 164
SEQUENCE
 RESULT 16
 RESULT 17
 Q6MZK6
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 EQUINCE FROM N.A.

MEDLINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8; MEDLINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8; Puljita E., Soyama A., Momoi T.;

Puljita E., Soyama A., Momoi T.;

Puljita E., Soyama A., Momoi T.;

In human lung cancer, is a cell adhesion molecule.";

Exp. Cell Res. 297:57-66(2003).

Exp. Cell Res. 297:57-66(2003).

MOJ. MGI:1889272; Igsf4a.

MOJ. MGI:1889272; Igsf4a.

MOJ. MGI:1889272; Igsfanges: IDA.

GO; GO:0016212; C:Gynapse: IDA.

GO; GO:0004202; C:Gynapse: IDA.

GO; GO:00015338; P:call adhesion; IDA.

GO; GO:0007155; P:call adhesion; IDA.

GO; GO:0007155; P:call adhesion; IDA.

RO; GO:0007155; P:call adhesion; IDA.

RO; GO:0007155; P:call adhesion; IDA.

RICEPPO: IPRO03585; Neurexin-like.

RICEPPO: IPRO03585; Neurexin-like.

PERM: PRO0407; IGS.

ROSSMAT; SM00049; IGS.

ROSSMAT; SM00408; IGS.

ROSSMAT; SM00408; IGS.

ROSSMAT; SM00408; IGS.

ROSSMAT; SM00408; IGS.

ROSSMAT; ROS
 185 ELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQ 244
 245 VHIQMIYPLQGLIREGDALELICEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLN 304
 38 ELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQ 97
 Gaps
 Exp. Cell Res. 287:57-66 (2003).

R MGD; MGI:1889-275-57 (1964).

R MGD; MGI:1889-275-57 (1964).

R GO; GO:0016021; C:integral to membrane; TAS.

R GO; GO:0016021; C:integral to membrane; TAS.

R GO; GO:0008021; C:synapte; IDA.

R GO; GO:0008021; C:synapte; IDA.

R GO; GO:0008021; F:protein binding; IPI.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:0007156; P:synaptogenesis; IDA.

R InterPro; IPR003598; Neurexin-like.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
 ö
 28.7%; Score 127; DB 2; Length 295; 100.0%; Pred. No. 3.6e-110; ive 0; Mismatches 0; Indels
 Pfam; PF00047; ig; i. SMART; SW00294; 4.1m; 1. SMART; SW00299; 1G-2; 1. SMART; SW00408; IGC-2; IG LIKE; 2. SEQUENCE 295 AA; 32347 MW; FDD9E8145C6B971B CRC64;
in human lung cancer, is a cell adhesion molecule.";
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adhesion protein RAI75C.
Name=158f4a; Synonyms=ral75C;
Mus musculus (Mouse)
 Query Match
Best Local Similarity 100.C
Matches 127; Conservative
 PRELIMINARY;
 KTDNGTY 311
 KTDNGTY 164
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061033;
01-ANG-1998 (TrEMBLrel. 07, Created)
01-ANG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein (Fragment).
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein (Fragment).
 98 AA.
 102 AA
 3.4%; Score 15; DB
100.0%; Pred. No. 1.2
tive 0; Mismatches
 PRT;
 PRT;
 339 PPTTTTTTTTT 353
 339 PPTTTTTTTTT 353
 71 PPTTTTTTTTT 85
 Best Local Similarity 100.0
Matches 15; Conservative
 Best Local Similarity 100.
Matches 15; Conservative
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 98
 Name=EMUCt-18;
 Name=EMUCe-11;
 Name=EMUCe-12;
 SEQUENCE
 SEQUENCE
 Query Match
 Query Match
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061058;
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 RESULT 21
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 RESULT 20
 061058
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 359 TDSRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAA 418
 1 TDSRAGEEGSIRAVDHAVIGGVVAVVVPAMLCLLIILGRYFARHKGTYFTHEAKGADDAA 60
 Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
 Gaps
 Di Noia J.M., D'Orso I., Aslund L., Sanchez D.Ö., Frasch A.C.;
"The Trypanosoma cruzi mucin family is transcribed from hundreds of
genes having hypervariable regions.";
J. Biol. Chem. 273:10843-10850(1998).
EMBL. ARO34411, AAC14222.1;
ELEMEN. PRO94411, Tryp_mucin.
Pfam; PPO1456; Mucin; I.
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
 TISSUE-Human retina;
The German Human cDNA Consortium;
The German Human cDNA Consortium;
Kochrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (ANG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX641042; CAE46024.1; -.
 MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
 ö
 19.0%; Score 84; DB 2; Length 84; 100.0%; Pred. No. 2.5e-70; tive 0; Mismatches 0; Indels
 Score 15; DB 2; Length 74;
Pred. No. 1.1e-05;
 0; Indels
 74 AA; 7743 MW; 734CC37663E21401 CRC64;
 84 AA; 8986 MW; D50A20AD25854087 CRC64;
 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein (Fragment).
 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 Created)
Last sequence update)
 Hypothetical protein DKF2p686F1789 (Fragment)
Name=DKF2p686F1789;
Homo sapiens (Human).
 3.4%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
 74 AA.
 419 DADTAIINAEGGONNSEEKKEYFI 442
 61 DADTAIINAEGGONNSEEKKEYFI 84
 01-AUG-1998 (TrEMBLrel. 07, Created)
 PRT;
 PRT;
 339 PPTTTTTTTTTT 353
 Q9TVF2;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
 73
 84; Conservative
 15; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Query Match
Best Local Similarity
 Local Similarity
 SEQUENCE FROM N.A.
 STRAIN=Cl-Brenner;
 SEQUENCE FROM N.A.
 Name=EMUCe-4;
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 Query Match
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 Q9TVF2
 061023
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Matches
 RESULT 18
061023
AC 06102
AC 06102
DT 01-AU
DT 0
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Trypanosoma cruzi.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5693;
 Trypanosoma cruzi.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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 STRAIN=C1-Brenner;
MEDLINE=9825151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
MEDLINE=9825151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
Di Noia J.M., D'Oreo I., Aslund L., Sanchez D.O., Frasch A.C.;
"The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions.";
J. Biol. Chem. 273:10843-10850(1998).
EMBL; AF036436; AAC14240.1;
InterPro; IPR000458; Tryp_mucin.
Pfam; PF01456; Mucin; 1.
 STRAIN=C1-Brenner;
MEDLINE=9825151; PubNed=9556557; DOI=10.1074/jbc.273.18.10843;
Di Noia J.W., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.;
Di Noia J.W. D'Orso I. Aslund L., Sanchez D.O., Frasch A.C.;
The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions.";
J. Biol., Chem. 273.10843-10850(1998).
EMBL, AP036465; AAC14259.1;
PINTEPPO; IPR000458; Tryp_mucin.
PFam, PF01456; Mucin. 1.
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 Length 86;
 3.4%; Score 15; DB 2; Length 98; 100.0%; Pred. No. 1.4e-05; ive 0; Mismatches 0; Indels
 0; Indels
 98 AA; 10158 MW; BE9146BAA3FD9520 CRC64;
 86 AA; 8963 MW; 7AD26B22604E36A9 CRC64;
 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein (Fragment).
 DB 2; Le
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Matches

RESULT 19

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Q9TVF2 ID Q9 AC Q9 DT 01

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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein (Fragment).
Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosoma:
 Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
 Trypanosoma cruzi.
Bukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5693;
 SEQUENCE FROM N.A. PubMed=14668015; DOI=10.1016/j.molbiopara.2003.09.006; Campo V., Di Noia J.M., Buscaglia C.A., Aguero F., Sanchez D.O., Frasch A.C.C.; "Differential accumulation of mutations localized in particular domains of the mucin genes expressed in the vertebrate host stage of
 SEQUENCE FROM N.A.
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MEDLINE-98225151; PubMed-9556557; DOI=10.1074/jbc.273.18.10843;
MEDLINE-98225151; PubMed-955657; DOI=10.1074/jbc.273.18.10843;
MEDLINE-98225151; PubMed-955657; DOI=10.1074/jbc.2773.18.10843;
Di Noia J.M., D'Orso I., Ashund L., Sanchez D.O., Frasch A.C.;
"The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariale regions.";
J. Biol. Chem. 273:10843-10850(1998).
EMBL, AF036450; AAC14247.1;
EMBL, AF036450; AAC14247.1;
Pfam: PP01456; Mucin.
Pfam: PP01466; Mucin; 1.
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100.0%; Pred. No. 1.6e-05;
tive 0; Mismatches 0; Indels
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Pfam, PF01456; Mucin; 1.
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01-MAR-2004 (TrEMBLrel. 07, Last sequence update)
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Mol. Biochem. Parasitol. 133:81-91(2004).
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MEDLINE=9825151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
Di Noia J.M., D'Oreso I., Aslund L., Sanchez D.O., Frasch A.C.;
Di Noia J.M., D'Oreso I., Aslund L., Sanchez D.O., Frasch A.C.;
J. The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions.";
J. Biol. Chem. 273.10843-10850(1998).
InterPro, IPRO36422; AAC14232.1;
InterPro, IPRO36422; ALUAIS2.1;
Pfam; PF01456; Mucin;
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 "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2018(1998).
 Score 15; DB 2; Length 102;
Pred. No. 1.4e-05;
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Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL AL032637; CAA21621.1; -
PIR; T26880; T26880.
 Wormbase, WBGene00012831, Y43FBC.9.
Wormbep, Y43FBC.9, CE1907.
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01-NOV-1999 (TrEMBLrel. 12, La
01-JUN-2003 (TrEMBLrel. 24, La
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ORFNames=Y43F8C.9.
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 Caenorhabditis elegans.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF398553; AAK94016.1; -.
InterPro; IPR000458; Tryp_mucin.
Pfam; PF01456; Mucin; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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 01-MAY-2000 (TrEMBLrel. 13,
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 01-AUG-1998 (TrEMBLrel. 07,
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 Preitas-Junior L.H., Briones M.R., Schenkman S.;
"Two distinct groups of mucin-like genes are differentially expressed in the developmental stages of Trypanosoma cruzi.";
Mol. Biochem. Parasitol. 93:101-114(1998).
EMBL: AR027872, ARC48350.1;
InterPro; IPR000458; Tryp_mucin.
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NCBI_TaxID=5693;
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Di Noia J.M., D'Oreso I., Aslund L., Sanchez D.O., Frasch A.C.;
Di Noia J.M., D'Oreso I., Aslund L., Sanchez D.O., Frasch A.C.;
Di Moia J.M., D'Oreso I., Aslund L., Sanchez D.O., Frasch A.C.;
Genes having hypervariable regions.";
J. Biol. Chem. 273:10843-10850(1998).

EMBL; AF036413; AAC14224-1; -..
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Di Noia J.M., Frasch A.C.C.;
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 339 PPTTTTTTTTT 353
 07,
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 3.48;
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01-MAR-2004 (TrEMBLrel. 2
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Name-EMUCe-9;
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Trypanosoma cruzi.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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 Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.;
"The Trypanosoma cruzi mucin family is transcribed from hundreds of
genes having hypervariable regions.";
J. Biol. Chem. 273:10843-10850(1998).
 MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843; D1 Noia J.W., D'Orso I., Aalund L., Sanchez D.O., Frasch A.C.; Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions.";
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STRAIN=C1-Brenner;
MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
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 Length 125;
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 D'Orso I., Di Noia J.M.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF036409; AAC14220.2; -.
InterPro; IPR00458; Tryp_mucin.
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SEQUENCE 126 AA; 13023 MW; F3858008D3C768A1 CRC64;
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Last annotation update)
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MEDLINE=97113006; PubMed=8943259; DOI=10.1074/jbc.271.50.32078;
Di Noia J.M., Pollevick G.D., Kavier M.T., Previato J.O.,
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"High diversity in mucin genes and mucin molecules in Trypanosoma cruzi.";
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Name=MUC.Y-1;
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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"Mol. Biochem. Parasitol. 133:81-91(2004).

EMBL; AY289908; AAQ74640.1;

InterPro; IPR000458; Tryp_mucin.
 J. Biol. Chem. 273:10843-10850(1998).
EMBL; AF036427; AAC14349.1; -.
InterProf. IPR000458; Tryp_mucin.
 genes having hypervariable regions.";
 Chem. 271:32078-32083 (1996).
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NCBI_TaxID=5693;
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Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.;
"The Trypanosoma cruzi mucin family is transcribed from hundreds of
 STRAIN=CL Brener;
MEDLINE=97113006; PubMed=8943259; DOI=10.1074/jbc.271.50.32078;
Di Noia J.M., Pollevick G.D., Xavier M.T., Previato J.O.,
Mendoca-Previato L., Sanchez D.O., Frasch A.C.;
"High diversity in mucin genes and mucin molecules in Trypanosoma cruzi.";
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 3.4%; Score 15; DB 2; Length 128; 100.0%; Pred. No. 1.7e-05; Live 0; Mismatches 0; Indels
 D'Orso I., Di Noia J.M.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AF036463; AAC14257.2; -.
Interbro; IRR004458; Tryp_mucin.
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SEQUENCE 126 AA; 13049 MW; F399EC78D3C768AI CRC64;
 J. Biol. Chem. 271:32078-32083 (1996).

EMBL; U62550; AAC47402.1; -.

InterPro; IPRO00458; Tryp_mucin.

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148 AA

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Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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MEDLINE-98324409; PubMed-9662032; DOI=10.1016/S0166-6851(98)00025-5;
Freitas-Junior L.H., Briones M.R., Schenkman S.;
"Two distinct groups of mucin-like genes are differentially expressed in the developmental stages of Trypanosoma cruzi.";
MOI. Biochem. Parasitol. 93:101-114(1998).
EMBL; AF027874; AAC48352.1;
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PubMed=14668015; DOI=10.1016/j.molbiopara.2003.09.006;
Campo V., Di Noia J.M., Buscaglia C.A., Aguero F., Sanchez D.O.,
Frasch A.C.C.;
"Differential accumulation of mutations localized in particular
domains of the mucin genes expressed in the vertebrate host stage of
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5693;
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 Length 148;
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 Mol. Biochem. Parasitol. 133:81-91(2004).

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J. Biol. Chem. 273:10843-10850(1998).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Mus musculus (Mouse). 12 days embryo head cDNA, RIKEN full-length enriched library, clone:3000008H23 product:hypothetical Acyl-COA dehydrogenase/Glutamic acid-rich region containing protein, full
 MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Giligo K., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
 Surface antigen P2 (Fragment).
Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
 Gaps
 Murray P.J., Spithill T.W.; "Variants of a Leishmania surface antigen derived from a multigenic
 ö
 ch 3.4%; Score 15; DB 2; Length 327; 1 Similarity 100.0%; Pred. No. 3.8e-05; 15; Conservative 0; Mismatches 0; Indels
 STRAIN-AX4;
Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC116986; AA051856.1; -.
DictyBase; DDB0168226; JC2V2_0_00892.
InterPro; IRR008654; IWSI_C.
InterPro; IRR008654; IWSI_C.
Hypothatical protein.
SEQUENCE 648 AA; 73372 MW; 2879FE40FCD76D3E CRC64;
 NON TER 1 1 2
SEQUENCE 327 AA; 34229 MW; 2571B35B6577E715 CRC64;
 ingert sequence.
Dictyostellum discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
NCBI_TaxID=44689;
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 327 AA.
 648 AA.
 family.";
J. Biol. Chem. 266:24477-24484 (1991).
EMBL, 7315; CRA40414.1;
PIR; S20074; S20074.
InterPro; IPR009030; Grow_fac_recept.
InterPro; IPR001611; IEGF.
InterPro; IPR001611; IERR.
InterPro; IPR007090; IERR.
InterPro; IRR07090; IERR.
SMART; SM00181; EGF; 1.
 PRT;
 PRT;
 STRAIN=V121;
MEDLINE=92105105; PubMed=1761547;
 339 PPTTTTTTTTTT 353
 PRELIMINARY;
PRELIMINARY;
 Nature 418:79-85(2002).
 Local Similarity
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 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 STRAIN=AX4;
 183
 Query Match
 Q86A81
 RESULT 39
086481
086481
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3.4%; Score 15; DB 2; Length 648;

Query Match

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 STRAIN=AX4, MBDLNBRA220522; PubMed=12097910; DOI=10.1038/nature00847; MBDLNBR2200522; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Bichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
 SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
Xu C.S., Chang C.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
Xu C.S., Chang C.F., Han H.P., Wang L., Wang S.F., Xing X.K., Shen G.M.,
Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
Submitted (ISEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY387047; AAQ91017.1;
EMBL, AY387047; AAQ91017.1;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 Gaps
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 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostelium discoideum (Slime mold). Histidine kinase
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0
 Match 3.4%; Score 15; DB 2; Length 1015; Local Similarity 100.0%; Pred. No. 0.0001; les 15; Conservative 0; Mismatches 0; Indels
 Query Match 3.2%; Score 14; DB 2; Length 58; Best Local Similarity 100.0%; Pred. No. 7.6e-05; Matches 14; Conservative 0; Mismatches 0; Indels
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 1015 AA; 116816 MW; 58CF6693543381A8 CRC64;
 Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 Dictyostelium discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 ö
 58 AA.
 1015 AA.
Mismatches
 EMBL; AC115594; AAO51537.1; -.
GO; GO:0016301; F:kinase activity; IEA
 PRT;
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0
 338 PPPTTTTTTTTT 352
 552 PPPTTTTTTTTT 566
 130 peptitititititi 144
15; Conservative
 338 PPPTTTTTTTTTTT
 PRELIMINARY;
 PRELIMINARY;
 Rattus norvegicus (Rat)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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 STRAIN=AX4;
 SEQUENCE
 Query Match
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304 AA

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STANDARD;
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 ORFNames=CG31439;
 NCBI_TaxID=6239;
 CG31439-PA.
 SEQUENCE
 Query Match
 QBIMS9;
 QBIMS9
 RESULT 45
 Q8IMS9
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 Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
NCBI_TaxID=5693;
 MEDLINE-STATING TO THE TATAL THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL Gaps
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 ö
 3.2%; Score 14; DB 2; Length 107; 100.0%; Pred. No. 0.00013; ive 0; Mismatches 0; Indels
 3.2%; Score 14; DB 2; Length 216; 100.0%; Pred. No. 0.00023;
 0; Indels
 STEALNI-GL-Brenner;

SIGNI-GL-Brenner;

Di Noia J.M., Frasch A.C.C.;

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AR398511; AAK94014.1; -.

InterPro; IPR000458; Tryp_mucin.

Pfan; PP01456; Mucin; 1.

SEQUENCE 216 AA; 21815 MW; 01C85738541BB6C6 CRC64;
 0362W6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein MUC-loc2.
 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 107 AA
 100.0%; Prec. ...
 Created)
 PRT;
 PRT;
 Mucin-like protein (Fragment).
 01-AUG-1998 (TrEMBLrel. 07,
 339 PPTTTTTTTTT 352
 340 PTTTTTTTTTT 353
 341 TTTTTTTTTTT 354
 34 TTTTTTTTTTT 47
 53 PPTTTTTTTT 66
 14; Conservative
 14; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Query Match
Best Local Similarity
 Local Similarity
 Trypanosoma cruzi.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Name=EMUCt-9;
 Query Match
 061050
 Q962W6
 RESULT 44
YOOB_CAEEL
 RESULT 42
061050
DD 06105
AC 06105
DD 01-AU
DD 01-AU
DD 01-AU
DD 01-AU
DD Namein
GN Trypa
OC BUKAT
OX REBLI
RN SERUE
RR
 RESULT 43
C962W
AC 0962W
AC 0962W
DT 01-DE
DT 01-DE
DE MUCIN
DE MUCIN
OX NCBI
RN III
RP SEQUE
RR STRAII
RP SIDN
RA DI NO
RL SUBMI;
DR EMBL;
DR EMBL;
SQ SEQUE;
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 MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; MEDLINE=20196006; PubMed=10731132, DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman U.R., Yandell M.D., Zhang Q., Chen L.X. Brandon R.C., Rogers Y.H., Blazei R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 Gaps
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
 ö
 Drosophila melanogaster (Fruit fly).
Bukaryota, metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neopiera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 "Genome sequence of the nematode C. elegans: a platform for investigating biology."; Science 282:2012-2018(1998).
-!- SIMILARITY: Some, to C.elegans R13F6.2 and R13F6.8.
 Hypothetical protein EEED8.11.
Poly-Thr.
; 60C223B88F534151 CRC64;
 3.2%; Score 14; DB 1; Length 304;
100.0%; Pred. No. 0.00031;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hypothetical protein EEED8.11 in chromosome II precursor.
 0; Indels
 Last sequence update)
Last annotation update)
 341 AA.
 100.0%; Prec. ...
 Potential
 STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
The C. elegans sequencing consortium;
 Created)
 WormBase; Wagene00017139; EEEDB.11.
WormPep; EEEDB.11; CE01884.
InterPro; IPR001304; Lectin_C.
SWART; SW00034; CLECT; 1.
Hypothetical protein; Signal.
SIGNAL
 PRT;
 64 92 Po
304 AA; 32982 MW;
 EMBL; U23484; AAC46771.1; -.
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
 340 PTTTTTTTTTT 353
 67 prirrirririr 80
 Best Local Similarity 100.0
Matches 14; Conservative
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A Ballew R.M., Agadyan A., An H.J., Andrews-Frankoon C., Baldew R.M., Basen A., Baxendale J., Bayraktaroglu L., Beaaley E.M., Beeson K.Y., Benos P.V., Barmen B.P., Bhandari D., Bolshakov S., Ra Bautris K.C., Busam D.A., Bucher H., Cadieu E., Center A., Chandra I., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Bordson K., Downes M., Dagan-Rocha S., Dunkov B.C., Dunn P., A Dodson K., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Posler C., Gabrielian A.E., Garg N.S., Gablart W.M., Glasser K., Randon K.J., Harvey D., Helman T.J., Hernandez J.R., Houck J., Ra Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Ra Harris N.L., Harvey D., Helman T.J., Wernandez J.R., Houck J., Rasko P., Lei Y., Levitsky A.A., Li J., Lai Z., Liang Y., Lin X., Rasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Rasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Rasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Rasko P., Mushy B., Mushy D.M., Neberon D., Lai Z., Liang Y., Lin X., Martei B. McIntosh T.C., McLeod M.P., McPherson D.L., R. Mallein N.V., Mobarry C., Morris J., Woshrefi A., Randers R.D., Scheeler F., Shen H., Rasher E., Spradling A.C., Stapleton M., Strong R., Sun E., Strader E., Spradling A.C., Stapleton M., Strong R., Sun E., Sylang E., Spradling A.C., Stapleton M., Strong R., Sun E., Strong F.N., Wooner S.W., Weissenbach J., Wassarman D.A., Weinstock G.W., Weissenbach J., Wassarman D.A., Weinstock G.W., Weissenbach J., Ray Y., Hoghen R., Shong F.N., Shang Y., Shang X.H., Schong F.N., Shan M., Zhong Y., Zhao G., MEDLINE=22426065, PubMed=12537568;
MEDLINE=22426065, PubMed=12537568;
MEDLINE=22426065, PubMed=12537568;
MEDLINE=22426065, PubMed=12537568;
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J.,
Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstrock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.",
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 Kaminker J.S., Bergman C.M., Kronniller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
 MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 Baldwin D.,
 "Annotation of the Drosophila melanogaster euchromatic genome: a
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C.,
 to the EMBL/GenBank/DDBJ databases.
 a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 Senome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
 MEDLINE=22426070; PubMed=12537573;
 Science 287:2185-2195(2000).
 FlyBase;
Submitted (SEP-2002)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A. FlyBase;
 review.
 SEQUENCE FROM N. A.
 systematic
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Gaps
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Name=agCGS2059; ORFNames=ENSANGG00000015451;
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Bukaryota; Metazoa; Arthopoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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NCBI_TaxID=180454;
 Anopheles Genome Sequencing Consortium;
Submittend (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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 Query Match 3.2%; Score 14; DB 2; Length 341; Best Local Similarity 100.0%; Pred. No. 0.00034; Matches 14; Conservative 0; Mismatches 0; Indels
 Score 14; DB 2; Length 350;
Pred. No. 0.00035;
 EMBL, AE003751, AAN14054.1; -
EMBL, AE003751, AAN14054.1; -
ENBL, AE003751, AAN14054.1; -
E1yBase; FBGN005576; Ciextracellular; IEA.
GO; GO:0008061; F:chitin hinding; IEA.
GO; GO:0008061; F:chitin metabolism; IEA.
InterPro; IPR002557; Chitin bind PerA.
InterPro; IPR002125; dCMP/Cyt_deam.
FAm; PF01607; CBM 14; 1.
SNART; SM00494; ChEBD2; 1.
PROSITE; PS09940; CHIT BIND II; 1.
PROSITE; PS09940; CHIT BIND II; 1.
PROSITE; PS09940; CHIT BIND II; 1.
SEQUENCE 341 AA; 38627 Mv; A935A06377885A15 CRC64;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
 350 AA; 37565 MW; F4765CEF710FA9A0 CRC64;
 01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
 Last sequence update)
Last annotation update)
 350 AA.
 100.0%; Pred. No.
 EMBL; AAAB01008980; EAA14126.1; -.
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR002000; Lamp.
PRINTE; PR00336; LYSASGOCTOMP.
PROSITE; PS00310; LAMP_1; UNKNOWN_1.
 01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last anno
 PRT;
 PRT;
 340 PTTTTTTTTTT 353
 170 Příříříříříříříříříří 183
 340 PTTTTTTTTTT 353
 79 PTTTTTTTTT 92
 Best Local Similarity 100.
Matches 14; Conservative
 PRELIMINARY;
 PRELIMINARY;
 preliminary data.
 SEQUENCE FROM N.A.
 STRAIN=PEST
 SEQUENCE
 Query Match
 Q7Q1R0
 Q7PZ21
 RESULT 46
Q7Q1R0
 RESULT 47
 Q7PZ21
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STRAIN=PEST;
 STRAIN=AX4;
 SEQUENCE
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 Q869R5
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 RESULT 49
 RESULT 50
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 GTRAIN=ORYAN,

Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

Jaffe D., FitzHugh W., Man J. J., Smirnov S., Purcell S., Rehman B.,

Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

Qui D., Janakiev P., Pedersen D., Nelson M., Washburne M.,

Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,

Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,

Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

Kamal M., Kamvysselis M., Maucell E., Bielke C., Rudd S., Frishman D.,

Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,

A Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,

DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,

A Yarden O., Plamann M., Seller S., Dunlap J., Radford A., Aramayo R.,

A Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

The Genome Sequence of the Filamentous Fungus Neurospora crassa.",

Nature Ol.O. (2003).
 Gaps
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 Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL; AAAB01008986; EAA00798.1; -.
 -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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 Neurospora crassa.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
 Query Match 3.2%; Score 14; DB 2; Length 356; Best Local Similarity 100.0%; Pred. No. 0.00036; Matches 14; Conservative 0; Mismatches 0; Indels
 Length 364;
 0; Indels
 356 356
356 AA; 39404 MW; C51B095A700DEC22 CRC64;
 .l protein.
364 AA; 40946 MW; ECIDF588FE543738 CRC64;
 Last sequence update)
Last annotation update)
 Score 14; DB 2; Le
Pred. No. 0.00036;
 3.2%; Scor.
100.0%; Pred. No. ...
 Created)
 PRT;
 EMBL; AABX01000420; EAA29686.1; -.
InterPro; IPR008547; DUF829.
Pfam; PF05705; DUF829; 1.
 01-MAR 2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein. Name=NCU09343.1;
 316 Priritiririri 329
 340 PITITITITIT 353
 340 PITITITITIT 353
 PTTTTTTTTTT 51
 Conservative
 PRELIMINARY;
 preliminary data.
 Query Match
Best Local Similarity
Matches 14; Conserva
 SEQUENCE FROM N.A.
NCBI_TaxID=180454;
 SEQUENCE FROM N.A.
 NCBI_TaxID=5141;
 Hypothetical
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SEQUENCE
 38
 SEQUENCE
 07S2P4
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MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85 (2002).
 Gaps
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 which is
 ö
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Q869R5;
Ol-UUN-2003 (TrEMBLrel. 24, Created)
Ol-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostelium discoideum (Slime mold). Histidine
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 Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry wh prellminary data.

EMBL; AAABO1008905; EAA09700.1; -.
 Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 365 AA; 39409 MW; 132DEB0383959196 CRC64;
 GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:000508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR001294; Peptidase SI.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR009003; Peptidase SIA.
 Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
 01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
 365 AA
 445 AA.
 Name=agCG50324; ORFNames=ENSANGG00000010153;
 100.0%; Prec. no.
 EMBL; AC116957; AAO52509.1; -. GO; GO:0016301; F:kinase activity; IEA.
 Dictyostelium discoideum (Slime mold)
PRT;
 PRT;
 PRINTS; PR00722; CHYMOTRYPSIN
 340 PTTTTTTTTT 353
 Prirritini 279
 Anopheles gambiae str. PEST
 Query Match
Best Local Similarity 100.0
Matches 14; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Pfam; PF00089; Trypsin;
 AgCP4397 (Fragment)
 SEQUENCE FROM N.A.
 NCBI_TaxID=180454;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 HSSP; P08709; 1JBU
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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 ure various Transcription factor. Interacts specifically with the W PUNCTION: Transcription factor. Interacts specifically with the W box (5'-(T)TGAC(C/T)-3'), a frequently occurring elicitor-responsive cis-acting element (By similarity).
SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: Belongs to the WRKY group I family.
SIMILARITY: Contains 2 WRKY domains.
 MEDLINE-20083487; PubMed=10617197; DOI=10.1038/45471; MEDLINE-20083487; PubMed=10617197; DOI=10.1038/45471; Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronini L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 Gapa
 10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 44, Last annotation update)
10-0CT-2003 (Rel. 44, Last annotation update)
10-0CT-2003 (Rel. 44, Last annotation 33).
Name-WRKY33; OrderedLocusNames=At2g38470; ORFNames=T19C21.4;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 DNA-binding, Nuclear protein, Repeat, Transcription regulation.
DOMAIN 123 135 Thr-rich.
 ö
 3.2%; Score 14; DB 2; Length 445; 100.0%; Pred. No. 0.00043; ive 0; Mismatches 0; Indels
 "Arabidopsis thaliana transcription factor WRKY33.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 445 AA; 48897 MW; 48A34474F5414364 CRC64;
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
Hydrolase; Protease; Serine protease.
 or send an email to license@isb-sib.ch).
 SEQUENCE FROM N.A.
STRAIN-cv. Columbia, TISSUE=Flower;
Lippok B., Somssich I.E.;
 PRT;
 EMBL; AF509499; AAM34736.1; -. EMBL; AC004683; AAM14994.1; -.
 340 PTTTTTTTTTT 353
 Prirrrrrrrrr 138
 InterPro; IPR003657; WRKY.
Pfam; PF03106; WRKY; 2.
 PROSITE, PS50811; WRKY; 2
 Best Local Similarity 100.
Matches 14; Conservative
 STANDARD;
 Nature 402:761-768(1999)
 PIR; T02498; T02498.
 SEQUENCE FROM N.A.
 Venter J.C.;
 thaliana.";
 WR33 ARATH
 NON TER
SEQUENCE
 Query Match
 RESULT 51
WR33_ARATH
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 Gaps
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 1-carboxylate + methylthicadenosine.
-!- COFACTOR: Pyridoxal phosphate.
-!- PATHMAY: Ethylene biosynthesis; first (rate-limiting) step.
-!- SUBUNIT: Homodimer.
-!- SIMILARITY: Belongs to the class-I pyridoxal-phosphate-dependent aminotransferase family.
 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
1-aminocyclopropanel carboxylate synthase (EC 4.4.1.14) (ACC synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
Name=ACS2; Synonyms=CARACC;
Name=ACS2; Synonyms=CARACC;
Dianthus caryophylus (Carnation) (Clove pink).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllaceae; Dianthus.
 Pyridoxal phosphate (By similarity)
 PROSITE; PS00105; AA TRANSFER CLASS 1; 1.
Ethylene biosynthesis; Fruit Tipening; Lyase; Multigene family;
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 3.2%; Score 14; DB 1; Length 517;
100.0%; Pred. No. 0.00049;
 DB 1; Length 512; 0.00049;
 Indels
 Indels
 171 235 WRKY 1.
349 414 WRKY 2.
461 481 Asn-rich.
512 AA; 56457 MW; 8F19CBE41BC18662 CRC64;
 Poly-Thr.
C31BA10732E940AE CRC64;
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 517 AA
 0; Mismatches
 0; Mismatches
 Score 14;
Pred. No.
 WRKY 1.
 MEDLINE=92119258; PubMed=1731995;
 517 AA; 58057 MW;
 3.2%; 2
 100.08;
 EMBL; M66619; AAA33275.1; -.
 Pfam; PF00155; Aminotran 1 2
PRINTS; PR00753; ACCSYNTHASE
 122 PITTITITITI 135
 340 PTTTTTTTTT 353
 Query Match
Best Local Similarity 100.
Matches 14; Conservative
 Local Similarity 100.
Les 14; Conservative
 STANDARD;
 PIR; S19252; S19252.
 Pyridoxal phosphate.
BINDING 277 2
 SEQUENCE FROM N.A.
 NCBI_TaxID=3570;
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DNA_BIND
DOMAIN
 SEQUENCE
 Query Match
 SEQUENCE
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ID 1A1C_DIA

AC P274\overline{8}6;
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Matches
 RESULT 52
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RESULT 53

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Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.
 SEQUENCE FROM N.A.
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams N.D., Cenliker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl .
GO; GO:000595; P:carbohydrate metabolism; IEA.
GO; GO:000152; P:metabohism; IEA.
Pfam; PF00553; CBM 2; 1.
Pfam; PF00704; Glyco hydro_18; 1.
SMART; SM00637; CBD_II; 1.
COMplete proteome.
SEQUENCE 717 AA; 78635 MW; FBCB55B9C850E38B CRC64;
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 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidaa; Drosophilidae; Drosophila.
 STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
HSSP; Q13231; 1LG2.
 Length 717;
 Length 667;
 3.2%; Score 14; DB 2; Length 71; 100.0%; Pred. No. 0.00065; ive 0; Mismatches 0; Indels
 Indels
667 AA; 73337 MW; 92F583112C839992 CRC64;
 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 Last sequence update)
Last annotation update)
 DB 2; Le
 717 AA
 746 AA.
 Query Match 3.2%; Score 14; DB Best Local Similarity . 100.0%; Pred. No. 0.0 Matches 14; Conservative 0; Mismatches
 Created)
 PRT;
 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-MAR-2004 (TrEMBLrel. 26, Putative chitinase.
 340 PITITITITITI 353
 541 PTTTTTTTTT 554
 235 PTTTTTTTTTT 248
 TTTTTTTTT 353
 OrderedLocusNames=PF1233;
 Local Similarity 100.
1es 14; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Pyrococcus furiosus
 SEQUENCE FROM N.A.
 ORFNames=CG8181;
 NCBI_TaxID=2261;
 340 PT
 CG8181-PA.
 SEQUENCE
 Query. Match
 Q8U1H5
 Q9V515
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Matches
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 GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA. GO:0016829; F:1yase activity; IEA. GO:0008483; F:transaminase activity; IEA. GO:0009058; P:biosynthesis; IEA.
 Gaps
 Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M., Vogel C., Teichmann S.A., Ivens A., Dear P.H.; "Integrated mapping, chromosomal sequencing and sequence analysis of
 01-00-1996 (TEMBLrel. 01, Created)
01-00-2003 (TEMBLrel. 01, Last sequence update)
1-aminocyclopropane 1-carboxylate synthase (EC 4.4.1.14).
Dianthus caryophyllus (Carnation) (Clove pink).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatcophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllaceae; Dianthus.
 ö
 3.2%; Score 14; DB 2; Length 518;
100.0%; Pred. No. 0.00049;
tive 0; Mismatches 0; Indels
 Michael M.Z.;
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; 218952; CAA79477.1; -.
PIR; S31442; S31442.
 Eukaryota, Alveolata, Apicomplexa, Coccidia, Bimeriida,
Cryptosporidiidae, Cryptosporidium.
NCBI_TaxID=5807;
 SEQUENCE 518 AA; 58003 MW; EF8B8BC8F03A493E CRC64;
 Created)
Last sequence update)
Last annotation update)
 518 AA
 667 AA
 PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
 PRT;
 PRT;
 EMBL, BX538353, CAD98350.1; -.
InterPro., IRRO00458; Tryp_mucin.
Pfam; PF01456, Mucin.
Hypothetical protein.
 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, Hypotheical protein. OFFNames=1MB.826;
 341 TTTTTTTTTT 354
 458 TTTTTTTTTTT 471
 341 TTTTTTTTTTT 354
 TTTTTTTTTTT 472
 Cryptosporidium parvum.";
 Local Similari,
nes 14; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Cryptosporidium parvum.
 Genome Res. 0:0-0(2003
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 TISSUE=Petal;
 Query Match
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Q7YYY0 Q7YYY0;

RESULT 54 Q7YYY0

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Matches

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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases

FlyBase

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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Ballew R.M., Basua A., Baxendale J., Bayraktaroglu C., Baldwin D.,
Ballew R.M., Basua A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Bennos P.V., Bernan B.P., Bandari D., Bolshakov S.,
RA Beeson K.Y., Bennos P.V., Bernan B.P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley C., Davier C., Ferraz C., Ferraz S., Pleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Alalai M., Kalush F., Karpen G.H., Ke Z., Kemnison J.A.,
Alalai M., Kalush F., Karpen G.H., Ke Z., Kemison J.A.,
Alalai M., Kalush F., Karpen G.H., Re Z., Kemison J.A.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Pacyler D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Pacyler D.,
RA Blazzol M., Fittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Rahling D.R., Siden-Kianok J., Simpson M., Skupski M.P., Smith T.,
Shie B.C., Siden-Kianok J., Simpson M., Skupski M.P., Smith T.,
Ry Harskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Ry Mang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Ry Khen S.M., Moy W., Rubin G.M., Venter J.C.,
Rheng X.H., Zhang F.N., Zhan M., Zhou S., Zhu X., Smith H.O.,
Rheng X.H., Zhong F.N., Zhong W., Zhou C.,
Ry Chence 287:2185-2195(2000).
 SEQUENCE FROM N.A.

MEDLINE=22446065; PubMed=12537568;

MEDLINE=22446065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

Pairskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.;

"Finishing a whole-genome shotgun: Release 3 of the Drosophila
 Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
 MEDLINE=22426069; PubMed=12537572; Matthews B.B., Campbell K.S., Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 'Annotation of the Drosophila melanogaster euchromatic genome: a
 melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 MEDLINE=22426070; PubMed=12537573;
 SEQUENCE FROM N.A.
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to the EMBL/GenBank/DDBJ databases

Submitted (SEP-2002)

FlyBase

SEQUENCE FROM N.A.

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 SEQUENCE FROM N.A.
MEDLINE=91140317; PubMed=8986798; DOI=10.1073/pnas.93.26.15260;
Shaulsky G., Escalante R., Loomis W.F.;
"Developmental signal transduction pathways uncovered by genetic
 DictyBase; DDB019119; mkcA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:00046713; F:protein serine(hreonine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR0011009; Kinase like.

InterPro; IPR002290; Ser thr pkinase.

InterPro; IPR002291; Ser thr pkinase.

InterPro; IPR001245; Tyr pkinase.

Pfam; PF00069; Pkinase; 1.
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 3.2%; Score 14; DB 2; Length 860;
100.0%; Pred. No. 0.00076;
 Length 746;
 0; Indels
 PRINTS; PRODOSO TYRKINASE.
PRODOM; PRODOSOUS; TYRKINASE.
PRODOM; PRODOSOUS; PROC. Kinase; 1.
SMART; SMOUZO; 2 TKC; 1.
PROSITE; PS500107; PROTEIN KINASE APP; UNKNOWN 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
ATP-binding; Hypothetical protein; Kinase; Transferase.
SEQUENCE 860 AA; 97812 MW; 20AEDBC81826DC21 CRC64;
 EMBL, AE003835, AAF59007.1; -.
Flybase, FBgn0033361, CG8181.
SEQUENCE 746 AA; 78593 MW; FB6F9F8DA3027334 CRC64;
 Dictyostelium discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein mkcA.
 Last sequence update)
Last annotation update)
 Proc. Natl. Acad. Sci. U.S.A. 93:15260-15265(1996).
 DB 2; Le
 860 AA.
 872 AA.
 3.2%; Score 14; DB
100.0%; Pred. No. 0.0
ive 0; Mismatches
 100.0%; Prec. ... 0; Mismatches
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 PRT;
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 EMBL; U60169; AAB03507.1; -. HSSP; Q13153; 1F3M.
 01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
01-MAR-2004 (TrEMBLrel. 26,
 01-NOV-1996 (TrEMBLrel. 01,
 340 PITITITITIT 353
 435 Priririririri 448
 339 PPTTTTTTTTT 352
 268 PPTTTTTTTTT 281
 Query Match
Best Local Similarity 100.0
Matches 14, Conservative
 Best_Local Similarity 100.
Matches 14; Conservative
 PRELIMINARY;
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 340 PITITITITIT 353
 250 Prirrirriri 263
 340 PTTTTTTTTT 353
 Query Match 3.29
Best Local Similarity 100.0
Matches 14; Conservative
 Query Match
Best Local Similarity 100.
Matches 14; Conservative
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 SEQUENCE FROM N.A.
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 Rep protein.
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 STRAIN=DG61;
MEDLINE=99189343; PubMed=10087212; DOI=10.1006/plas.1998.1385;
GONZAILES C.M., Spencer T.D., Pendley S.S., Welker D.L.;
"Dgpl and Dfpl are closely related plasmids in the Dictyostelium Ddp2 plasmid family.";
Plasmid 41:89-96(1999).
 STRAIN=DG61;
MEDLINE=92390516;
Yin Y., Welker D.L.;
"Dictyostelium giganteum plasmid Dgp1 is a member of the Ddp2 plasmid
 Gonzales C.M., Spencer T.D., Pendley S.S., Welker D.L.;
"Dgpl and Dfpl are closely related plasmids in the Dictyostellum Ddp2
plasmid family.",
Plasmid 41:89-96(1999).

EMBL, AF076279; AAC33156.1;
InterPro; IPR007778; Dict_REP.
Pfam; PF05086; Dicty_REP.
Plasmid.
 STRAIN=DG61;
MEDINE=98133494; PubMed=9472083;
Shammat I.M., Gonzales C., Welker D.L.;
"Dictyostelium discoideum nuclear plasmid Ddp6 is a new member of the
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 STRAIN=CR II 2B;
MEDLINE=99189343; PubMed=10087212; DOI=10.1006/plas.1998.1385;
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Plasmid Dgpl.
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=5787;
 Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
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Last sequence update)
Last annotation update)
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InterPro; IPR007778; Dict_REP.
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 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2004 (TrEMBLrel. 26,
 Curr. Genet. 33:77-82(1998)
 340 PITITITITITI 353
 259 Pritititititit 272
 Dictyostelium firmibasis.
Plasmid Dfp1.
 PRELIMINARY;
 family.";
Plasmid 28:37-45(1992)
 Ddp2 plasmid family
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 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Rep protein.
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 SEOUENCE
 Query Match
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 STRAIN=WS380B;
MEDLINE=91172902; PubWed=2077544;
Slade WnB., Chang A.C.M., Williams K.L.;
The sequence and organisation of Ddp2, a high copy number plasmid of Dictyostellum discoideum.";
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 Leiting B., Lindner I.J., Noegle A.A.; "The extrachromosomal replication of Dictyostelium plasmid Ddp2 requires a cis-acting element and a plasmid-encoded trans-acting
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 STRAIN=WSS80B;
MEDLINE=91172093; PubMed=2077545;
MEDLINE=91172093; PubMed=2077545;
Chang A.C.M., Slade M.B., Williams K.L.;
Identification of the origin of replication of the eukaryote Dicryostelium discoideum nuclear plasmid Ddp2.";
Plasmid 24:208-217(1990).
EMBL; X51478; CAA35843.1;
DicryBase; DDB0001933; Ddp2-rep.
InterPro; IPR007778; Dict_REP.
Pfam; PR05086; Dicty REP; 1.
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Eukaryosta: Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
 01-NOV-1996 (TrEMBLrel. 01, Created)
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pred. No. 0.00077;
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v 100.0%; Pred. No. v...
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 Mol. Cell. Biol. 10:3727-3736(1990).
EMBL; M55298; AAA33191.1; -.
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SUBQUINCE FROM N.A.

STRAIN=W8380B;

MEDLINE=90287164; PubMed=2192261;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R.A. Sutton G.G., Wortman J.R., Yandall M.D., Zhang Q., Chen L.X.,
Amark.H., Doyle C., Baxer B.G., Helt G., Nelson C.R., Gabor G.L.,
R.A. Abril J.F., Agbayani A., An H.J., Andrews-Ffannkoch C., Baldwin D.,
R.A. Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Bloadari D., Botchan B.A.,
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R. Bortis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
R. Bortis S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Posller C., Gabrielian A.E., Garg C., Ferriaz S., Fleischmann W.,
R. Glodek A., Gong F., Gorrell J.H., Gu Z., Gluan P., Harris M.,
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A Jalali M., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
R.A. Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
 Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
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tive 0; Mismatches 0; Indels
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 Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 937 AA; 106088 MW; 0AFD6F0123CE2967 CRC64;
 01-MAR-2003 (TrEMBLrel. 23, Created)
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ATP-binding; Hypothetical protein.
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 Nature 418:79-85(2002).
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 STRAIN=AX4;
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 MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostellum discoideum.";
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01-JUN-2003 (TrEMBLrel. 26, Last annotation update)
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FREM; PF04677; CWfJ C_1; I.
Pfam; PF04677; CWfJ C_1; I.
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InterPro; IPR007778; Dict_REP.
Pfam; PF05086; Dicty_REP; 1.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyostelium.
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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 Nature 418:79-85(2002)
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Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Muzny D.M., Nelson D.L.,
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Shue B.C., Siden-Kiamos I., Simpson M., Schoeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Suith T.,
Nang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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Cheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.,
The genome sequence of Drosophila melanogaster.",
 MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
 MEDLINE-22426065; PubMed=12537568;
MEDLINE-22426065; PubMed=12537568;
MEDLINE-22426065; PubMed=12537568;
MEDLINE-22426065; PubMed=12537568;
MEDLINE-S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Mizny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Weinstock G., Scherer S.E., Wyers E.W., Gibbs R.A., Rubin G.M.; Prinishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
 SEQUENCE FROM N.A.
MEDLINE-2246069; PubMed=12537572;
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Miller S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huany Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 Annotation of the Drosophila melanogaster euchromatic genome:
 Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
 Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003642; AAN10874.1; -.
EMBL; BT010014; AAQ22483.1; -.
 to the EMBL/GenBank/DDBJ databases
 a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002)
 FlyBase, FBgn0028905; CG32972.
GO; GO:0007155; P:cell adhesion; IEA.
 Submitted (SEP-2002)
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 systematic review
 IntAct; Q8IP52;
 Celniker S.
 Lewis S.
 FlyBase
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 Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85 (2002).
 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostelium discoideum (Slime mold). Nucleotide exchange
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Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
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Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
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100.0%; Pred. No. 0.00098;
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REGUENCE FROM N.A.

MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adamaentides P.G., Scherer S.E., in P.W., Hoskins R.A., Galle R.F., Adamaentides P.G., Scherer S.E., in P.W., Hoskins R.A., Galle R.F., Adamaentides P.G., Scherer S.E., in P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Brutonn G.G., Wortman J.R., Yandell M.W., Zhang Q., Chen L.K., Brandon R.C., Rogers Y.H., Zhang E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Barraktaroglu L., Beasley E.M., Barlew R.M., Basu M.R., Bouck J., Berokstein P., Brottier P., Borson K.Y., Berman M.R., Bouck J., Berokstein P., Brottier P., Borson K.Y., Dowly D.E., Dowley D., Brownsport L.B., Davises P., Acheriy J.M., Cawley S., Dalnkov S., Burkis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Borkova D., Bolcher A., Domg Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Dowl L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Brangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Burbin K.J., Brangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Harvey D., Haiman T.J., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Adalush F., Karpen G.H., Ke Z., Kenlison J.R., Kathen G.B., Karlush F., Karpen G.H., Ke Z., Kenlison J.R., Mattei B.E., Kodira C.D., Kraft K.J., Morriy D.M., Nebleon D.L., Nelson D.K., Musty D.M., Moharty D.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Rabine B.C., Siden-Kiamos I., Sampson M., Skupski M.P., Smith T., Shue B., Nelson K., John W., Wainsenbach J., Wainsenb
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 Gaps
 MEDLINE=99066935; PubMed=9851610; DOI=10.1016/S0166-6851(98)00119-4;
 Barnes D.A., Bonnin A., Huang J.X., Gousset L., Wu J., Gut J., Doyle P., Dubremetz J.F., Ward H., Petersen C.; "A novel multi-domain mucin-like glycoprotein of Cryptosporidium
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 Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 3.2%; Score 14; DB 2; Length 1832;
llarity 100.0%; Pred. No. 0.0014;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 PRT; 1853 AA.
 Mol. Biochem. Parasitol. 96.93-110(1998).
EMBL; AF068065; AAC98153.1; -.
PIR; T31113; T31113.
 Drosophila melanogaster (Fruit fly)
Cryptosporididae, Cryptosporidium
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 373
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MEDLINE=22426065; PubMed=12537568;

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Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

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 Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
 Gaps
 MEDLINE=22426069; PubMed=12537572;
MiSEA S., Campbell K.S.,
MiSEA S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
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Bettenourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.C., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 Annotation of the Drosophila melanogaster euchromatic genome: a
 ;
0
 Length 1853;
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 150213; FAS1; 2.
1853 AA; 201677 MW; 518684872828D53F CRC64;
 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
 Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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 3.2%; Score 14; DB 2; Les 100.0%; Pred. No. 0.0015; ive 0; Mismatches 0;
 a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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 Submittea (ran-2007)
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CSTRAIN-Berkeley;

A Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,

B Butenhoff C., Champe M., Cravez C., Chew M., Cisejolka L., Doyle C.M.,

A Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,

RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,

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RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,

RA Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,

RA Zieran L.L., Rubin G.M.;

RA Sethi H., Souly SAR44859.1;

BRIBL; Ag003409; AAR44859.1;

BRIBL; Ag003409; AAR44859.1;

CG; GG:0007155; Preell adhesion; IEA.

DR RIPEPPO; IPR01009; Kinssellike.

InterPro; IPR01009; Kinssellike.
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 MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Elchinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.P., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
 MEDLINE-99403001; PubMed=10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Hartis N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.
Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of
Genetics 153:179-219(1999).
 Gaps
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 3.2%; Score 14; DB 2; Length 1893; llarity 100.0%; Pred. No. 0.0015; Conservative 0; Mismatches 0; Indels
 1893 AA; 206483 MW; 2C3152610B858A4D CRC64;
 Dictyostelium discoideum (Slime mold).

Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hyportical protein.
 PRT; 2208 AA
 Pfam; PF02469; Fasciclin; 2.
SMART; SM00554; FAS1; 2.
PROSITE; PS50213; FAS1; 2.
 340 PTTTTTTTTTT 353
 447 Prirrirrirrir 460
 PRELIMINARY;
 Hypothetical protein.
 Local Similarity
nes 14; Conserv
 SEQUENCE FROM N.A.
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 SEQUENCE FROM N.A.
STRAIN=AX4;
Baumgart C.;
 STRAIN=AX4;
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2086HN4
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 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
 Gaps
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-1- SIMILIARITY: BAGLONGS to the ubiquitin-conjugating enzyme family.
EMBL; ACL16957; AAG52538.1; -.
HSSP; PS1966; 1C42.
 A GO; GO: 0004840; F: Ubiquitin conjugating enzyme activity; IEA.

R GO; GO: 0006512; P: Ubiquitin cycle; IEA.

R InterPro; IPR0005974; Traf_like.

R InterPro; IPR0006974; Traf_like.

R InterPro; IPR000608; UBQ_conjugat.

R Pfam; PF00179; UQ_con; 1.

R Pfam; PF00179; UQ_con; 1.

R Prodom; P0000461; UBQ_conjugat; 1.

R SWART; SW00212; UBCc; 1.

R SWART; SW00212; UBCc; 1.

R PROSITE; PS50144; MATH; 4.

R PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.

Hypothetical protein.
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 Couwenhoven R.I., Chuang S.;
"The Gene Encoding Mouse Muc19: cDNA, Genomic Organization and
Relationship to SMGC.";
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 STRAIN=BN/SsNHsdMCW;
Culp D.J., Latchney L.R., Fallon M.A., Denny P.A., Denny P.C.,
 3.2%; Score 14; DB 2; Length 2208; 100.0%; Pred. No. 0.0017;
 3.2%; Score 14; DB 2; Length 3295;
100.0%; Pred. No. 0.0024;
iive 0; Mismatches 0; Indels
 0; Indels
 3295 AA; 317336 MW; 322D0CF90BF9F292 CRC64;
 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 PRT; 3295 AA.
 100.0%; Pred. ...
 Physiol. Genomics (Online) 0:0-0(2004)
EMBL, BK005556, DAA05396.1, -.
InterPro; IPR005207; Cys knot.
InterPro; IPR009041; PMP_SGCI.
InterPro; IPR001007; VWF_C.
SMART; SM00041; CT; 1.
SWART; SM00214; VWC; 2.
 PROSITE; PS01185; CTCK 1; UNKNOWN 1. PROSITE; PS01225; CTCK 2; 1. PROSITE; PS01208; VWFC 1; UNKNOWN 1. PROSITE; PS50184; VWFC 2; 1.
 1681 PPTTTTTTTTT 1694
 1184 TTTTTTTTTTI 1197
 339 PPTTTTTTTTT 352
 341 TTTTTTTTTTT 354
 Mucin apoprotein (Fragment)
 Local Similarity 100.
 Best Local Similarity 100.
Matches 14; Conservative
 PRELIMINARY;
 SEQUENCE FROM N.A.
 NCBI TaxID=10116;
 Name=Muc19;
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RESULT 71 Q66GT4

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MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A. Sequence and analyais of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
 STRAIN=V333;
Hoffmann E.H., Silveira L.A., Tonhosolo R., Pereira F.J.,
Ribeiro W.L., Tonon A.P., Marrelli M.T., Kawamoto F., Ferreira M.U.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY008396; AAG30717.1; -.
 Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
 2.9%; Score 13; DB 2; Length 67;
100.0%; Pred. No. 0.00074;
tive 0; Mismatches 0; Indels
 2.9%; Score 13; DB 2; Length 56; 100.0%; Pred. No. 0.00064; tive 0; Mismatches 0; Indels
 Distriction.,
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC116551; AAO52164.1; -.
Hypothetical protein.
SEQUENCE 56 AA; 6096 MW; 5D1F0B92FE6D17C7 CRC64;
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67 67
67 AA, 5732 MW; 6B2B3F43575DB7C7 CRC64;
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Dictyostellum discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Merozoite surface protein 2 (Fragment).
 67 AA.
 56 AA
 PRT;
 341 TITITITITI 353
 341 TTTTTTTTT 353
 55 rrrrrrrrrrr 67
 1 TTTTTTTTTT 13
 24 rrrrrrrrrrr 36
 13; Conservative
 Local Similarity 100.
les 13; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Best Local Similarity
 SEQUENCE FROM N.A.
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 NCBI_TaxID=44689;
 STRAIN=AX4;
 Merozoite.
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 095UY4;
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 Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
 SEQUENCE FROM N.A.
STRAIN=prototype form 1;
STRAIN=prototype form 1;
MEDLINE=95107908; PubMed=7808998;
MEDLINE=95107908; PubMed=7808998;
Minian A.G., Stringer J.R., Walzer P.D.;
"Characterization of multiple unique cDNAs encoding the major surface glycoprotein of rat-derived Pneumocystis carinii.";
Parasitol. Res. 80:478-486(1994).
EMBL: U07057; AAA74069.1;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
 Gaps
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STRAIN=BN/SaNHsdMCW;
Cubb D.J. Latchney L.R., Fallon M.A., Denny P.C.,
Culb D.J., Latchney L.R., Fallon M.A., Denny P.C.,
A Couwenhoven R.I., Chuang S.;
"The Gene Encoding Mouse Muc19: cDNA, Genomic Organization and
T. Relationship to SWGC.";
T. Physiol. Genomics (Online) 0:0-0(2004).

EMBL; BKO05555; DAA05595.1; -.
IN InterPro; IPR002019; Cysrich TIL.
InterPro; IPR002019; Cysrich TIL.
InterPro; IPR0041; PWD_SGGT.
INTERPRO; IPR00146; VWF_D.
Reim; PP010182; TILL; 1.
Ffam; PP01084; VWD; 3.
SWART; SM00216; VWD; 3.
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 / Match 3.2%; Score 14; DB 2; Length 3550; Local Similarity 100.0%; Pred. No. 0.0025; No. 14; Conservative 0; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOCT-2002 (TrEMBLrel. 22, Last annotation update)
Major surface glycoprotein (Fragment).
 Created)
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Last annotation update)
 56 AA.
PRT; 3550 AA
 Potential.
 Mucin apoprotein precursor (Fragment)
Name=Muc19;
 PRT;
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25-OCT-2004 (TrEMBLrel. 28,
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 341 TTTTTTTTTTT 354
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PRELIMINARY;
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 Rattus norvegicus (Rat)
 Pneumocystis carinii
 Pneumocystis.
NCBI_TaxID=4754;
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RESULT 72

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 SEQUENCE FROM N.A.
STRAIN=VS7;
Hoffmann E.H., Silveira L.A., Tonhosolo R., Pereira F.J.,
Ribeiro W.L., Tonon A.P., Marrelli M.T., Kawamoto F., Ferreira M.U.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AY008394; AAG30715.1; -.
Merozoite. 1 1
NON TER 67 67
SEQÜENCE 67 AA; S706 MW; 6CSE8980203990C4 CRC64;
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O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Mercozoite surface protein 2 (Fragment).
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NOB1_TAXID=5833;
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 341 TITITITITI 353
 55 TTTTTTTTT 67
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Copyright (c) 1993 - 2005 Compugen Ltd.
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The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAB86066-A80623 encode the 12 secreted protein sequences given in AAB8556-B25993. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant; anti-inflammatory; antiarthritic; antizheumatic; dermatchlogical; antiproliferative; and antifungal activity. The proteins, polypeptides, agonists and antifungal activity. The proteins, polypeptides, agonists and antigual activity. The proteins, polypeptides, agonists and conditions examples of which include: immune disease, disorders and conditions examples of which include: immune disease, addison's disease and nephritis; dermatitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory bowel disease, crohn's disease and nephritis; hyperproliferative disorders e.g. coronary arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The proteins and polymucleotide sequences may also be used in wound healing proteins and polymucleotide sequences may also be used in wound healing and protein sequences are represented in sequences AAAB0616 and AAB2566 Sequences AAAB0677-AB0682 represent genes related to the
 Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, ameliaration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases.
 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
 TISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSBLKVSLTNVSISDEG 120
 coronary arteriosclerosis; myocarditis; cancer;
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 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
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 Moore PA,
 DB 3; Length 442;
 Indels
 Kenny JJ,
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
 Disclosure; Page 182-183; 803pp; English.
 melanoma; lymphoma; wound healing; human
 PE,
 Ruben SM, Olsen HS, Young
 99WO-US025031.
 (HUMA-) HUMAN GENOME SCI INC
 cardiovascular disorder;
 secreted protein gene#11
 WPI; 2000-387742/33.
 Local Similarity
les 442; Conserv
 Sequence 442 AA;
 WO200029435-A1
 27-OCT-1999;
 Homo sapiens.
 28-OCT-1998;
 25-MAY-2000
 Greene JM;
 61
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 181
 241
 121
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 Secreted protein, immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory disorder; crohn's disease; crohn's disease; crohn's disease;
 Human
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 Abu93935
Abu99788
Abr66458
Abr90876
Abu94303
Abu79185
 Abu 79490 | Abu 92881 | Abu 95840 |
 Abu91060
Abu90153
Abu90153
Abu90158
Abu90368
Abu91370
Abu84584
Abu893320
Abu93320
Abu93320
Abu93320
Abu93320
Abu93320
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Abu93320
Abu93320
Abu93320
 Abc08348 1
Abc08348 1
 Abm07903
Abo40383
 Abu94608
Abo04535
 Abul1312
Abu67131
Abu95535
 Abo05555
Abr73944
Abr95536
Abr80833
Abr81138
Abm00834
Abr8436
 Abu86819
 Abu86514
 Abu96744
 Protein encoded by human secreted protein gene #11.
 ALIGNMENTS
 ABO31486
ABM07903
ABO40383
 AAB25619 standard; protein; 442 AA
AAB25619;
 RESULT 1
 AAB25619
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 98US-00191280.
98US-00206647.
99US-0123404P.
 99WO-US026742
 (INCY-) INCYTE PHARM INC
 442; Conservative
 Tang YT, Corley NC, Gu
Hillman JL, Bandman O,
 WPI; 2000-376546/32.
N-PSDB; AAA27051.
 Local Similarity
 Sequence 442 AA;
 WO200028032-A2
 12-NOV-1999;
 07-DEC-1998;
08-MAR-1999;
 12-NOV-1998;
 18-MAY-2000
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 Query Match
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 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 SRAGEEGSIRAVDHAVIGGVVAVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
 31,31
 Human, HCSRP, cytostatic; antiarthritic; antirheumatic; antiasthmatic; immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic; neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma; rheumatoid arthritis; asthma; atherosclerosis; akathesia; Alzheimer's diseases; multiple sclerosis; epilepsy.
 NNLNKTDNGTYRCEASNI VGKAHSDYMLYVYDPPTTI PPPTTTTTTTTTTTTLTI LTI LTI TTD
 note= "potential phosphorylation site"
 'note= "potential phosphorylation site"
 'note= "potential phosphorylation site"
 note= "potential phosphorylation site"
 'note= "potential phosphorylation site"
 'note= "potential phosphorylation site"
 'note= "potential phosphorylation site"
 'note= "potential glycosylation site"
 'note= "potential glycosylation site"
 /note= "potential glycosylation site"
310
 'note= "potential glycosylation site"
 'note= "potential glycosylation site"
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 'note= "potential phosphorylation
 glycosylation
 Tabel= Immunoglobulin_domain
 label= Immunoglobulin domain
 label= Immunoglobulin_domain
 Human cell surface receptor protein #8.
 1. .44
/label= Signal_peptide
 DTAIINAEGGONNSEEKKEYFI 442
 Location/Qualifiers
 Ź
 'note= "potential
 AAY94341 standard; protein; 442
 'label= HCSRP-8
 '(first entry)
 315
 Homo sapiens
 22-AUG-2000
 AAY94341;
 301
 301
 361
 361
 421
 421
 Peptide
 Protein
 Region
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antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into contact with cells or tissues expressing HCSRP and for diagnosis of HCSRP-related disorder HCSRP and its catalytic or immunogenic fragments are useful for drug screening using libraries of
 TISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
 RYFCQLYIDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
 (HCSRP) designated HCSRP-8. The nucleotide sequence was identified in Incyte Clone 312256 from the CDNA library LUNGNTO2, which was made from RNA isolated from lung tissue. A number of Incyte Clones were used to assemble the consensus sequence. BLAST analysis showed that the sequence is homologous to immuno-superfamily protein B12 g3779242. HCSRP and its antagonist are useful for preventing or treating disorders associated with decreased or increased expression or activity of HCSRP. Such disorders include cancers such as leukaemia and melanoma, immune disorders uch as rheumatoid arthritis, asthma and atherosclerosis, bacterial and parasitic infections and neuronal disorders such as akathesia. Alzheimer's disease, multiple sclerosis and epilepsy. Polynucleotides encoding HSCRPs may be used as hybridisation probes to diagnose these conditions. Anti-HCSRP antibodies may be used as
 9
 9
 MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
 New human cell surface receptor protein and polynucleotide useful for diagnosis, prevention and treatment of cancer, immune disorders, infection and neuronal disorders.
 1 MASVVLPSGSQCAAAAAAAAAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
 Gaps
 present sequence is a novel human cell surface receptor protein
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 ä
 DB 3; Length 442;
 Lal
 Indels
 site"
'note= "potential phosphorylation site"
 Yue H, Baughn MR, Au-Young J;
 /note= "potential glycosylation site"
 /note= "potential phosphorylation
 /note= "potential phosphorylation
375. .394
/label= Transmembrane_domain
 ö
 100.0%; Score 442; I
 Mismatches
 Guegler KJ, Yu
), Azimzai Y,
 Claim 1; Page 81-82; 97pp; English
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(first entry)
 cell function.
 18-JUN-2002
 121
 181
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 301
 301
 361
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 AAE19887;
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 Query Match
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 B7-L1; T cell proliferation; natural killer cell; NK; tumour cell; blological activity; quality control reagent; treatment; inflammation; immune system disorder; autoimmune; viral infection; infectious disease; organ transplant rejection; home marrow; modulator; immune response.
 Jymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA
 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI
 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTT
 Human lymphoid derived dendritic cell adhesion molecule.
 /label= Mature_human_LDCAM_polypeptide 67. .69
 "N-Glycosylation site"
 101. .103
/note= "N-Glycosylation gite"
 note= "N-Glycosylation site"
 note= "N-Glycosylation site"
 308. .310
/note= "N-Glycosylation site"
 1. 374
/label= Extracellular domain
 label= Transmembrane domain
 396. .442
/label= Cytoplasmic_domain
 /note= "N-Glycosylation 304. .306
 1. .38
/label= Leader_peptide
 442
 DTAIINAEGGNNSEEKKEYFI 442
 Location/Qualifiers
 Ź
 DTAIINAEGGONNSEEKKEYFI
 AAY45092 standard; protein; 442
 98US-0095672P
 (first entry)
 .395
 165. .167
 .442
 note=
 Baum PR, Fanslow WC;
 (IMMV) IMMUNEX CORP
 WO200008158-A2
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 31-MAY-2000
 Homo sapiens
 37-AUG-1998;
 17-FEB-2000
 241
 AAY45092;
 301
 301
 361
 121
 421
 181
 361
 Peptide
 Protein
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The present amino acid sequence is the human lymphoid derived dendritic cell adhesion molecule, iDCAM. It is found on lymphoid derived dendritic cells and displays homology to adhesion molecules, B7-1 and cytoplasmic region of B7-Li. Human LDCAM is expressed in breast, retina, foetal carcinoma. LDCAM polypeptides interacts with T cell surface molecules to carcinoma. LDCAM polypeptides interacts with T cell surface molecules to carcinoma. LDCAM binding protein and increases natural killer (NK) cell populations. IT may be used to measure the biological activity and as quality control reagents of LDCAM binding proteins. LDCAM may be used for treating disorders associated with malfunctioning of immune system, cinflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for companient or reducing the effect of organ and bone marrow transplant crejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or cells bearing B7L-1
 ö
 360
 300
 360
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 180
 240
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 61 TISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
 Novel molecules designated LDCAM are capable of altering or modulating T
 9
 241 YKPQVHIQMTYPLQGLTREGDALBLTCEAIGKPQPVMVTWVKVDDEMPQHAVLSGPNLFI
 1 MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF
 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
 ö
 DB 3; Length 442;
 Indels
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0
 100.0%; Score 442; I
 0; Mismatches
 442
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 Claim 7; Page 42-43; 44pp; English
 AAE19887 standard; protein; 442
 DTAIINAEGGONNSEEKKEYFI
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Matches 442; Conservative
 2000-205712/18
WPI; 2000-205712,
N-PSDB; AAZ50882
 Sequence 442 AA;
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The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABQ93288-ABQ9332). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).

(I) is useful for gene therapy of diseases and (III) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's Parkinson's, Huntington's and amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent din not form part of the printed specification, but was obtained fit wipo.int/pub/published_pot_sequences
SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIIIGRYFARHKGTYFTHEAKGADDAADA 420
 Human; vulnerary; dermatological; neuroprotective; nootropic; cancer; antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antipabetic; antiallergic; gene therapy; wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
 New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA
 5
 DB 5; Length 442;
 Claim 20; SEQ ID NO 262; 284pp + Sequence Listing; English.
 Zhang J,
 Ren F, Zhar
Wehrman T;
 100.0%; Score 442; I
100.0%; Pred. No. 0;
 Asundi V, Zhou P, Xue AJ,
Wang D, Liu C, Drmanac RT,
 DTAIINAEGGONNSEEKKEYFI 442
 ABP62825 standard; protein; 442 AA.
 DTAIINAEGGONNSEEKKEYFI
 Human polypeptide SEQ ID NO 262.
 31-AUG-2001; 2001WO-US027093.
 01-SEP-2000; 2000US-00654935.
 14-OCT-2002 (first entry)
 WPI; 2002-583321/62.
 Query Match
Best Local Similarity
 (HYSE-) HYSEQ INC.
 N-PSDB; ABQ93304
 Sequence 442 AA;
 WO200218424-A2
 Homo sapiens
 Tang YT,
Zhao QA,
 361
 361
 421
 421
 ABP62825;
 ABP62825
 RESULT
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 The invention relates to a method for detecting cell proliferative disorder associated with tumour suppressor lung cancer 1 (TSLC1) in a subject. The method comprising contacting a cell component of a proliferating cell with a reagent that detects level of the cell component in the proliferating cell and determining modification in the component in proliferating cell as compared with a healthy cell, where modification indicates disorder associated with TSLC1. The method is useful for detecting a cell proliferative disorder cencer lung or pancreatic cancer) associated with tumour suppressor lung cancer 1 (TSLC1) in a subject. The invention is useful in gene therapy and for treating a cell proliferative disorder sund as lung cancer (human non-small cell lung cancer), liver cancer (heptocellular carcinoma) or pancreatic cancer associated with modification of TSLC1 production, where a reagent which modulates (preferably, increases) TSLC1 level in the cells, is employed. The present sequence is human TSLC1
 ö
 180
 240
 240
 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
 301 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTT 360
 Detecting cell proliferative disorder associated with tumor suppressor lung cancer (TSLC) 1 in subject, comprises contacting proliferating cell of subject with reagent detecting TSLC1 and detecting modification in
 9
 Human, hepatocellular carcinoma, tumour suppressor lung cancer 1, TSLC1,
liver, lung; pancreatic cancer, cell proliferative disorder, cytostatic;
 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG
 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF
 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
 1 MASVVLPSGSQCAAAAAAAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF
 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI
 ö
 DB 5; Length 442;
 Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
 0; Indels
 100.0%; Score 442; D
100.0%; Pred. No. 0;
ive 0; Mismatches
 (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 Disclosure; Page 49-50; 59pp; English.
 15-AUG-2001; 2001WO-US025690.
 15-AUG-2000; 2000US-0225264P.
 Conservative
 Reeves RH, Yoshinori M;
 WPI; 2002-241913/29.
 Local Similarity
 Sequence 442 AA;
 WO200214557-A1.
 gene therapy
 Matches 442;
 21-FEB-2002
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 Query Match
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 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
 360
 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 61 TISCQVNKSDDSVIQLIAPNRQTIYFRDFRPIKDSRPQLIAFSSSELKVSLTNVSISDEG 120
 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
 121 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEBIBVNCTAMASKPATTIRWF 180
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 9
 9
 MASVVLPSGSOCAAAAAAAAAPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTT
 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
 Gaps
 cytostatic; antiinflammatory; immunomodulator; neuroprotective; hemostatic; gene therapy; cancer; inflammation; immune disorder; neurological disorder; blood clotting disorder; food additive; preservative; human; secreted protein.
 ö
 0; Indels
 Human novel secreted protein from gene 11 #3.
 0; Mismatches
 DTAIINAEGGONNSEEKKEYFI 442
 DTAIINAEGGONNSEEKKEYFI 442
 Z
 ADA27144 standard; protein; 442
 28-OCT-1998; 98US-0105971P.
27-OCT-1999; 99WO-US025031.
19-APR-2000; 2000US-019407P.
30-OCT-2000; 2000US-023732P.
18-APR-2001; 2001US-00836353.
 29-OCT-2001; 2001US-00984130.
 (first entry)
442; Conservative
 YOUNG P E. YOUNG P E. CLSENY J J. CLSENY B S. MOORE P A. WEI Y. GREENE J.M. LIU D.
 JS2003055231-A1.
 Homo sapiens
 20-NOV-2003
 20-MAR-2003.
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 ADA27144;
 61
 181
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 301
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 361
 361
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(KENN/)
(OLSE/)
(MOOR/)
(WEIY/)
(GREE/)
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The invention relates to an isolated nucleic molecule that is at least CC 594 identical to 18 human cDNA sequences representing 12 novel genes encoding secreted proteins or a polymuclectide fragment of the CDNA.

CC defined in the specification, its species homologue, a variant or allelic variant of the polymuclectide having a longuage capable of the CDNA.

CC defined in the specification, its species homologue, a variant or allelic variant of the polymuclectide having a longuage under stringent conditions to a undele cade molecule of the polymuclectide sequence of only A or T residues. Also included are recombinant vectors, host cells (for producing the polymeptide), the secreted polypeptide fragment, domain, epitope, full-length protein, variant, allelic variant or species homologue), antibodies that protein, variant, allelic variant or species homologue), antibodies that protein, variant, allelic variant or species homologue), antibodies that protein, variant, allelic variant or species homologue), preventing or ameliorating a medical condition by administering the polymentide corresponding to the cDNA sequence and activity in a biological assay (by expressing the CDNA sequence in a cell, isolating the supernatant, and detecting an activity in a biological assay (by expressing the CDNA sequence in a cell, isolating the supernatant, and detecting an activity in a biological assay (by expressing the CDNA sequence in a cell, isolating the supernatant, and detecting an activity in a biological assay (by expressing the CCC dentifying an activity, in a biological and antibodies are used to a susceptibility to a pathological condition, such as cancer, inflammation and other immune disorders, neurological and blood clotting disorders (many examples are estriction mapping). The polypeptides and antibodies are also are also useful for thromosome identification, radiation hybrid mapping or long-range restriction mapping) The polypeptides are longued as a foot additive or or preventing invariant or negonist may also be
 New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
 Greene JM;
 Wei Y,
 Moore PA,
 Olsen HS,
 Disclosure; Page 72; 454pp; English.
 Crocker PR;
 Kenny JJ,
 WPI; 2003-567103/53
 Young PE,
M, Liu D,
(CROC/) CROCKER P
 Sequence 442 AA;
 disorders.
 Ruben SM,
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Gaps ö 6; Length 442; Indels .. 0 BB 100.0%; Score 442; C 100.0%; Pred. No. 0; cive 0; Mismatches Best Local Similarity luu. Matches 442; Conservative Local Similarity Query Match

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240 240 241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300 61 TISCOVNKSDDSVIOLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120 120 180 180 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300 9 9 181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ MASVVLPSGSQCAAAAAAAPPGLRLRLILLLFSAAALIPTGDGQNLFTKDVTVIEGEVA TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 1 MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQ 61 121 121 241 181 ઠે g ò g à d ਨੇ ద à

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Sequence 442 AA;
 JS2003129685-A1
 29-JAN-2004
 Homo sapiens
 28-OCT-1998;
27-OCT-1999;
 19-APR-2000;
 10-JUL-2003
 IN (/CCIN)
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 121
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 421
 ADE86685;
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 human;
neural
 ADE86685
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 The invention discloses a composition comprising two or more isolated rate or human polymucleotides or a polymucleotide which represents a fragment, or human polymucleotides or allelic variation of the mucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a compound that regulates the activity of one or more of the polypeptides given in the contivity in an animal of one or more of the polypeptides given in the contivity in an animal of one or more of the polypeptides given in the contivity in an animal of one or more of the polypeptides given in the contivity in a method for identifying a compound useful in treating and a pecification, a method for identifying a compound useful in treating and a pecification and animal or more of the polypeptides given in the continual and animal or more of the polypeptides given in the continual and animal continual and animal commonities of the polypeptides given in the continual and animal continual and animal commonities and animal continual animal animal c
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating
 NNLNKTDNGTYRCBASNIVGKAHSDYMLYVYDPPTTIPPPFTTTTTTTTTTTTLTILTI
 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
 Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 Costigan M;
 Human Protein NP_055148, SEQ ID NO 41
 DTAIINAEGGONNSEEKKEYFI 442
 Z
 ADE54238 standard; protein; 442
 Claim 1; Page; 1017pp; English.
 Befort K,
 14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
 14-AUG-2002; 2002WO-US025765.
 (first entry)
 (GEHO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
 WPI; 2003-268312/26.
 Woolf C, D'urso D,
 GENBANK; NP 055148.
 WO2003016475-A2.
 Homo sapiens
 29-JAN-2004
 27-FEB-2003
 361
 ADE54238;
 301
 301
 361
 421
 421
 ADE54238
 RESULT
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240
 180
 240
 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVKVDDEMPQHAVLSGPNLFI 300
 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPPTTTTTTTTTTTTTTTTTTT 360
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIIIGRYFARHKGTYFTHEAKGADDAADA 420
 120
 TISCQVNKSDDSVIQLLNPNRQTIYFRDPRPLKDSRPQLLNFSSSELKVSLTNVSISDEG 120
 RYPCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTT 360
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CGI) and spared nerve injury (SII) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 9
 9
 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
 MASVVLPSGSQCAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
 TISCOVNKSDDSVIOLLNPNROTIYFRDFRPLKDSRFOLLNFSSSELKVSLTNVSISDEG
 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF
 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPV1 CQVEHPAVTGNLQTQRYLEVQ
 MASVVILPSGSQCAAAAAAAAAPPGLRIRLILLIFSAAALIPTGDGQNLFTKDVTVIEGEVA
 Gaps
 ö
 DB 7; Length 442;
 cancer; liver disorder; hepatitis;
 Indels
 Novel human secreted protein #11 associated protein #1
 ö
 ; Score 442; DB
; Pred. No. 0;
0; Mismatches
 secreted protein; cancer; live disorder; Alzheimer's disease.
 ADE86685 standard; protein; 442 AA.
 DTAIINAEGGONNSEEKKEYFI
 100.0%;
 98US-0105971P.
99WO-US025031.
2000US-0198407P.
 18-APR-2001; 2001US-00836353
 (first entry)
 Query Match
Best Local Similarity 100.
Matches 442; Conservative
```

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Human, PRO protein; tumour necrosis factor family, TNF, cytokine; secreted protein, transmembrane protein; inflammation disorder.
 Nucleic acids encoding PRO secreted and transmembrane proteins
 Human PRO355 protein sequence.
 (GETH) GENENTECH INC
 Goddard A,
 WPI; 1999-371118/31
 N-PSDB; AAX80055
 Homo sapiens
 WO9928462-A2
 01-DEC-1998;
 12-AUG-1999
 1997
 05-JAN-1998
 16-DEC-1997
16-DEC-1997
 16-DEC-1997
 DEC-1997
 17-DEC-1997
18-DEC-1997
 09-FEB-1998
25-FEB-1998
 10-JUN-1999
 12-DEC-1997
 Wood WI,
 56
 98
 84
 Query Match
 11-DEC-
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 allelic variant, a fragment of the CDNA sequence, or its fragment, domain, epitope or species homologue. The nucleic acid is useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, liver disorders such as habitainer's disease. The present sequence represents the amino acid sequence of a novel human secreted protein associated
 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
 TISCQVNKSDDSVIQLINPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTT 360
 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTT 360
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 1 MASVVLPSGSQCAAAAAAAAPGLRIRILILIFSAAALIPTGDGQNLFTKDVTVIEGEVA 60
 1 MASVVLPSGSQCAAAAAAAAAPPGLRLLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF
 New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g. cancer, liver disorders or neural disorders.
 Greene JM;
 Gaps
 The invention relates to an isolated nucleic acid sequence, or its
 ö
 DB 8; Length 442;
 Wei Y,
 0; Indels
 Moore PA,
 100.0%; Score 442; D
100.0%; Pred. No. 0;
tive 0; Mismatches
 Disclosure; SEQ ID NO 136; 380pp; English
 Olsen HS,
 DTAIINAEGGONNSEEKKEYFI 442
 Young PE, Kenny JJ,
 Conservative
 (KENN/) KENNY J J.
(OLSE/) OLSEN H S.
(MOOR/) MOORE P A.
(WEIY/) WEI Y.
(RREE/) GREENE J M.
(RUBE/) RUBEN S M.
 WPI; 2004-020335/02
YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
 al Similarity
442; Conserv
 Seguence 442 AA;
 Ruben SM:
 61
 121
 181
 241
 Query Match
 61
 181
 301
 301
 361
 361
 421
 421
 Local
 (YOUN)
 Best Loca
Matches
 RESULT 9
AAY17830
ID AAY1
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AC AAY1
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Chen J;

Baker KP,

Yuan J,

Gurney AL,

970S-0069278P. 970S-0069334P. 970S-0069425P. 970S-0069694P. 970S-006960P. 970S-0069870P. 970S-0069873P. 970S-0069873P. 970S-0069873P. 970S-0069873P. 970S-0069873P.

98WO-US025108

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ö
 transmembrane proteins used therapeutically. The PRO proteins have evytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polymuclectides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
 145
 205
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL 265
 143
 203
 85
 83
 24 LRILILIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIX
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRNFKGNTELKGKSEVEEWSDMYTVTSQL
 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 Gaps
 present invention describes nucleic acids encoding PRO secreted
 ..
0
 94.3%; Score 417; DB 2; Length 440;
 Indels
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 100.0%; Pred. ...
Claim 12; Fig 27; 123pp; English.
 Matches 417; Conservative
 Local Similarity
 Sequence 440 AA;
 206
 204
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AAY17830 standard, protein; 440

AAY17830,

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98WO-USO25108.
98US-0112850P.
98US-0113296P.
 99WO-US028301
 (GETH) GENENTECH INC.
 WPI; 2000-412324/35
 N-PSDB; AAA49563
 Sequence 440 AA;
 01-DEC-1998;
16-DEC-1998;
22-DEC-1998;
 01-DEC-1999;
 08-JUN-2000
 56
 98
 84
 206
 266
 264
 326
 324
 386
 384
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TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 324 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 383
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTT38RAGEEGSIRAVDHAVIGGVVAVVV 385
 PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO71; PRO327; PRO243; PRO71; PRO345; PRO341; PRO355; PRO355; PRO355; PRO355; PRO355; PRO355; Lransmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human.
 442
 FAMI.CLLI ILGRYFARHKGTYFTHEAKGADDAADADTAI INAEGGONNSEEKKEYFI
 111...15
//note= "N-glycosylation site"
//note= "N-glycosylation site"
//note= "N-glycosylation site"
//note= "N-myristoylation site"
//note= "N-myristoylation site"
//note= "Tyrosine kinase phosphorylation site"
 /note= "N-myristoylation site"
319. .328
/note= "Tyrosine kinase phosphorylation site"
365. .371
 376. .382
/note= "N-myristoylation site"
 102. .408
'note= "N-myristoylation site"
 /note= "N-myristoylation site"
430. .434
 "N-myristoylation site"
 'note= "N-myristoylation site"
 302. .306/
/note= "N-glycosylation site"
 note= "N-glycosylation site"
 'note= "N-glycosylation site"
 372. .393
/label= Transmembrane domain
 411. .417 /note= "N-myristoylation
 'note= "N-myristoylation
 306. .310
/note= "N-glycosylation
 "N-glycosylation
 1. .36
/label= Signal peptide
 Location/Qualifiers
 AAB01321 standard; protein; 440 AA
 (first entry)
 .433
 .432
 . .313
 Human PRO355 polypeptide.
 .103
 65. .69
/note= "1
 9. .15
/note=
 WO200032776-A2
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Homo sapiens
 25-SEP-2000
 AAB01321;
 264
 326
 386
 384
 Peptide
 Domain
 AABBU1311
AABB01321
AABB012
AABB01321
AABB0132
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New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptors/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources
 FRDFRPLKDSRFOLLNESSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 205
 265
 203
 263
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTT3385
 New human nucleic acids encoding secreted and transmembrane polypeptides,
designated as PRO polypeptides, useful as pharmaceutical and diagnostic
 82
 83
 440
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 Gaps
 PAMLCLIIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 ö
 DB 3; Length 440;
 Indels
 ;
0
 Query Match 94.3%; Score 417; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
 AAU29040 standard; protein; 440 AA.
 Claim 12; Fig 24; 187pp; English.
 AAU29040;
 RESULT 11
AAU29040
ID AAU290
XX
AC AAU290
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detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNP) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation of differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also breast, prostate, rectal, cervical, or liver tumours, and also breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
 325
 145
 143
 203
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 264 TCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 82
 83
 440
polypeptides and their associated nucleic acids can be used to
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 144 NLMIDIQKDTAVEGEBIEVNCTAMASKPATTIRNFKGNTELKGKSEVEEWSDMYTVTSQL
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIX
 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
 Human, PRO, cytostatic; tumour, cancer; breast; lung; stomach; liver;
dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
antibody-dependent enzyme mediated prodrug therapy.
 Gaps
 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
 ;
0
 Query Match
94.3%; Score 417; DB 4; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0; Indels
 ABU58416 standard; protein; 440
 21-JUN-2002; 2002US-00176492
 15-APR-2003 (first entry)
 Human PRO polypeptide #17.
 Sequence 440 AA;
 US2003027272-A1
 Homo sapiens
 06-FEB-2003
 98
 84
 146
 206
 326
 386
 ABU58416;
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 PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and screen for modulators of the compounds.
 Godowski PJ, Gurney AL;
ng Z;
 , Goddard A, Go
Wood WI, Zhang
 Human PRO polypeptide sequence #17.
 Desnoyers L,
Watanabe CK, W
 Claim 11; Fig 34; 774pp; English
 2000US-0191007P.
2000US-0191048P.
2000US-0191314P.
 2000US-0192655P
2000US-0193032P
2000US-0194449P
2000US-0194647P
2000US-0194647P
2000US-0194647P
2000US-0196600P
2000US-0196690P
2000US-0196690P
2000US-0196820P
2000US-0196820P
2000US-0196820P
2000US-019882P
2000US-019882P
 2000US-0199654P.
2000US-0201516P.
2000WO-US013705.
 2000WO-US005841.
2000US-0187202P.
2000US-0186968P.
 2000US-0189328P.
2000WO-US006884.
2000US-0190828P.
 2000WO-US014042.
2000WO-US014941.
 2000US-0189320P.
 2000US-0199550P.
 2000US-0209832P
 2000US-00644848
 2000WO-US032678
 28-FEB-2001; 2001WO-US006520
 (first entry)
 (GETH) GENENTECH INC.
 2001-602746/68.
 Chen J,
 Smith V,
 WPI; 2001-602746/
N-PSDB; AAS45941
 WO200168848-A2
 14-MAR-2000; 2
14-MAR-2000; 2
21-MAR-2000; 2
21-MAR-2000; 2
21-MAR-2000; 2
21-MAR-2000; 2
29-MAR-2000; 2
29-MAR-2000; 2
39-MAR-2000; 2
 04-APR-2000; 2
11-APR-2000; 2
11-APR-2000; 2
11-APR-2000; 2
11-APR-2000; 2
11-APR-2000; 2
 18-APR-2000; 2
18-APR-2000; 2
25-APR-2000; 2
25-APR-2000; 2
 22-MAY-2000; 2
30-MAY-2000; 2
02-JUN-2000; 2
05-JUN-2000; 2
 25-APR-2000;
03-MAY-2000;
 17-MAY-2000;
 08-NOV-2000;
 Homo sapiens
 18-DEC-2001
 Baker KP,
 Pan J,
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CXSX LLLX CY X LLX CY X LX 
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| 98US-0088738P.<br>98US-0088740P.<br>98US-0088811P.<br>98US-0088825P.<br>98US-0088861P.<br>98US-0088861P.<br>98US-0088861P.<br>98US-0089876P.<br>98US-008910EP.<br>98US-0089512P.<br>98US-0089514P.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 9805-0089552F<br>9805-0089952P<br>9805-0090246P<br>9805-0090242P<br>9805-0090423P<br>9805-0090443P<br>9805-0090444P<br>9805-0090444P<br>9805-009068B<br>9805-009068B<br>9805-009068B<br>9805-009068B<br>9805-009068B<br>9805-009068B<br>9805-009068B                         | 98US-00105413.<br>98US-0090862P<br>98US-0091010P<br>98US-009153P<br>98US-0091547AP<br>98US-0091628P<br>98US-0091628P<br>98US-0091628P<br>98US-0091628P<br>98US-0091628P<br>98US-0091628P<br>98US-0095282P<br>98US-0095282P<br>98US-0095082P<br>98US-0096012P<br>98US-0096012P                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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980S-0099602P- 980S-0099602P- 980S-0099602P- 980S-0099602P- 980S-0099602P-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               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| 10-UW-1998;<br>10-UW-1998;<br>10-UW-1998;<br>10-UW-1998;<br>10-UW-1998;<br>11-UW-1998;<br>11-UW-1998;<br>12-UW-1998;<br>12-UW-1998;<br>16-UW-1998;<br>16-UW-1998;<br>16-UW-1998;<br>17-UW-1998;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 14-70N-1298;<br>19-70N-1298;<br>22-70N-1298;<br>22-70N-1298;<br>24-70N-1298;<br>24-70N-1298;<br>24-70N-1298;<br>24-70N-1298;<br>24-70N-1298;<br>25-70N-1298;<br>25-70N-1298;<br>25-70N-1298;<br>25-70N-1298;<br>25-70N-1298;<br>25-70N-1298;<br>25-70N-1298;<br>25-70N-1298; | - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 - 300 | 17-AUG-1998   18-AUG-1998   18-AUG-1998   18-AUG-1998   26-AUG-1998   26 |
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| SEP-1997  SEP-1997  OCT-1997                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | NOV-15<br>NOV-15<br>DEC-19<br>DEC-19<br>DEC-19<br>DEC-19<br>MAR-19<br>MAR-19<br>MAR-19<br>MAR-19<br>APR-19                                                                                                                                                                   | APR-1998 APR-1998 APR-1998 APR-1998 APR-1998 APR-1998 APR-1998 APR-1998 APR-1999 APR-1999 APR-1999 APR-1999 APR-1999 APR-1999 APR-1999 APR-1999 APR-1999                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 15-MAY-1998;<br>18-MAY-1998;<br>22-MAY-1998;<br>22-MAY-1998;<br>28-MAY-1998;<br>28-MAY-1998;<br>20-JUN-1998;<br>03-JUN-1998;<br>04-JUN-1998;<br>04-JUN-1998;<br>04-JUN-1998;<br>04-JUN-1998;<br>05-JUN-1998;<br>05-JUN-1998;<br>05-JUN-1998;<br>05-JUN-1998;<br>05-JUN-1998;<br>05-JUN-1998;<br>06-JUN-1998; 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 07-OCT-1998
 84
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Human; secreted and transmembrane protein: PRO; gene therapy; tumour necrosis factor-alpha release; TNF-alpha release; chondrocyte proliferation; chondrocyte differentiation; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
 Novel human secreted and transmembrane protein PRO355
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980S-0080313P.
 2002US-00183012
(first entry)
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PR 18-AUG-1998 9 98US-0096949P.
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83

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146

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203

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tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
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 Human; secreted and transmembrane protein; PRO; TNP-alpha;
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
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9705-0063121P-
9705-0063131P-
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9705-0083
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18 - SEP - 1997;

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02-JUN-1998;
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 27-FEB-2003
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324 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVV 383
 New isolated PRO polypeptide and encoding nucleic acid, useful for the diagnosis and treatment of disorders associated with the PRO polypeptide, such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.
 The invention relates to an isolated PRO polypeptide (a secreted or transmembrane protein) comprising: (a) at least 80% sequence identity or positives when compared to any of 15 sequences, fully defined in the specification, lacking or with its associated signal peptide, or least 80% sequence identity to a sequence encoded by the full-length coding sequence of a DNA deposited in the American Type Culture Collection (ATCC). Also included are: (1) an isolated nucleic acid comprising: (a) at least 80% sequence identity to a nucleotide sequence that encodes a PRO protein; (b) at least 80% sequence identity to a
 442
 440
 FAMICLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI
 FAMLCLI I I LGRY PARHKGTYFTHEAKCADDAADADTA I INAEGGONNSEEKKEYF I
 Human; PRO; secreted protein; transmembrane protein; anti-HIV; cytostatic; antiatateriosclerotic; antiatidiabetic; cardiant; AIDS; acquired immunodeficiency syndrome; cancer; atherosclerosis; inflammatory disease; diabetic complication;
 A, Godowski PJ, Grimaldi JC, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
 Ferrara N, Filvaroff E;
 Human secreted/transmembrane protein PRO355
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 Claim 12; Fig 24; 178pp; English.
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 98WO-US019330.
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99WO-US012252.
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 2000WO-US020710.
2000WO-US032678.
2001WO-US006520.
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99WO-US028313
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 31-AUG-2001; 2001US-00944654
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 2000WO-US014042
 26-MAR-2003 (first entry)
 Gerritsen ME, Goddard A
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 (GETH) GENENTECH INC.
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 01-DEC-1999;
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 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
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 Gaps
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RESULT 20 ABU89843 ID ABU89843 standard; protein; 440 AA. XX

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 (first entry)
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 Homo sapiens.
 21-JUN-2002;
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24-0CT-1997;
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larity 100.0%; Pred. No. (
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02-JUL-1998

10-JUL-1998

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|                                              |            |        |        |                  |          |                  |            |                  |        |       |                  |          |       |            |       |                  |       |                  |        |        |                  |        |            |        |                  |                  |       |                |          |        |        |        |                  |       |                  |        |        |        |          |                  |        |       |
|                                              |            |        |        |                  |          |                  |            |                  |        |       |                  |          |       |            |       |                  |       |                  |        |        |                  |        |            |        |                  |                  |       |                |          |        |        |        |                  |       |                  |        |        |        |          |                  |        |       |
|                                              |            |        |        |                  |          |                  |            |                  |        |       |                  |          |       |            |       |                  |       | ٠٠.              |        |        |                  |        |            |        |                  |                  |       |                |          |        |        |        |                  |       |                  |        |        |        |          |                  |        |       |
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| 1998;<br>1998;<br>1998;                      | 1998;      | 1998;  | 1998;  | 1998;<br>1998;   | 1998;    | 1998;            | 1998;      | 1998;            | 1998;  | 1998; | 1998;<br>1998;   | 1998;    | 1998; | 1998;      | 1998; | 1998;<br>1998;   | 1998; | 1998;            | 1998;  | 1998;  | 1998;            | 1998;  | 1998;      | 1998;  | 1998;            | 1998;            | 1998; | 1998;          | 1998;    | 1998;  | 1998;  | 1998;  | 1998;            | 1998; | 1998;            | 1998;  | 1998;  | 1998;  | 1998;    | 1998;            | 1998;  | 1998; |
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|                                              |            |        |        |                  |          |                  |            |                  |        |       |                  |          |       |            |       |                  |       |                  |        |        |                  |        |            |        |                  |                  |       |                |          |        |        |        |                  |       |                  |        |        |        |          |                  |        |       |
| # # #                                        | <b>4</b> 8 | Ж.     | ኛ ጜ    | <b>E</b> E       | <b>K</b> | ¥ K              | <b>K</b> 5 | F. F.            | R 6    | PR    | R 8              | <b>胚</b> | R     | K 6        | R.    | <u> </u>         | R     | 7. Y             | K 8    | 7 H    | PR<br>PR         | E E    | ጸ <b>ଟ</b> | Ж<br>К | <b>.</b> K       | R R              | R 1   | ¥ K            | ۲.<br>۲. | 7. K   | R 8    | 전      | K K              | PR    | R R              | R 6    | ¥      | K K    | <b>K</b> | 7. K             | R 6    | PR:   |

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 82
 83
 440
 Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
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 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
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 FAMLCLIIIGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI
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 6; Length 440;
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 Human secreted polypeptide PRO355, SEQ ID NO:34.
 B
 94.3%; Score 417; DE llarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
 ABR94621 standard; protein; 440 AA
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97US-0059266P.
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264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNINKTDNGTYRCEASNIVGKAHSD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 383
cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are also useful in biotechnological and medical research and in various industrial applications. Sequences ABU60230-ABU60245 represent human PRO polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
                                                                                                                                                                                                                                                                                                                                                                                                                                        FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDBGRYFCQLYTDPPQESYTTITVLVPPR
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                                                                                                                                                                                                                                                                                                          26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
                                                                                                                                                                                                                                                                                                                                  LELLELE PSAAALI PTGDGQNLFTKDVTVI EGEVATISCOVNKSDDSVI QLINPNRQTIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCEA1GKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAMLCLIIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, PRO, secreted polypeptide; transmembrane polypeptide;
tumour necrosis factor alpha; TNF-alpha; chondrocyte cell; tumour;
                                                                                                                                                                                               94.3%; Score 417; DB 6; Length 440; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU85594 standard; protein; 440 AA
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98US-0020264.
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                                                                                                                                                 Sequence 440 AA;
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07-DEC-1998;
03-MAR-1999;
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07-OCT-1998;
06-NOV-1998;
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16-SEP-1998
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             industry; cytostatic; antiinflammatory; cardiant; antiinfertility; anti-HIV; antiarteriosclerotic; antidiabetic.
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, Godowski PJ, Grimaldi JC, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
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22-FEB-2000; 2000WO-US004414.
02-MAR-2000; 2000WO-US005641.
22-MAY-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
28-JUL-2000; 2000WO-US014042.
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97US-0069334P
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99WO-US030095.
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28-FEB-2001; 2001WO-US006520.
25-MAY-2001; 2001US-00866028.
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ME, Goddard A,
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16-DEC-1997;
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Baker KP,

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TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO bolypeptide and a method for detecting the presence of tumour in a mammal. The polypeptides and polymucleotides are useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. Sequences ABUBSSPR-ABUBSBRS represent human PRO polypeptides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy;
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100.0%; Pred. No. 0;
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Matches 417; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acids encoding PRO polypeptides, useful a medicament for diagnosing or treating tumor.
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Zhang Z;
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Watanabe CK,
99WG-US012252.
99US-00380137.
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10-JUN-1998; 10-JUN-1998; 11-JUN-1998; 11-JUN-1998; 11-JUN-1998; 12-JUN-1998; 12-JUN-1998; 16-JUN-1998; 16-JUN-1998; 17-JUN-1998; 17-JUN-1998;	2 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 -	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	18-AUG-1998; 26-AUG-1998; 26-AUG-1998; 26-AUG-1998; 26-AUG-1998; 26-AUG-1998; 01-SEP-1998; 01-SEP-1998; 02-SEP-1998; 02-SEP-1998; 03-SEP-1998; 10-SEP-1998; 10-SEP-1998; 11-SEP-1998; 11-SEP-1998; 11-SEP-1998; 11-SEP-1998; 11-SEP-1998; 11-SEP-1998; 11-SEP-1998; 11-SEP-1998; 11-SEP-1998; 11-SEP-1998; 11-SEP-1998; 11-SEP-1998; 11-SEP-1998;
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cervical tumour; liver tumour; chromosome identification.
                                                                                     97US-0059263P.
97US-0059263P.
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24-0CT-1997;
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31-0CT-1997;
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llarity 100.0%; Pr
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98US-0100919P.
98US-0100849P.
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02-JUN-1998;
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     Human; gene therapy; chromosome identification; tissue typing.
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                                                                                                           ABU91675 standard; protein; 440 AA
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970S-0059266P.
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970S-0069870P.
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                     144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
                                                                                 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
                                                                    MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
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97US-0053266P.
97US-0063212P.
97US-0063121P.
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ses 417; Conservative
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25-UW-1998; 25-UW-1998; 25-UW-1998; 25-UW-1998; 25-UW-1998; 25-UW-1998; 26-UW-1998; 26-UW-1998; 26-UW-1998; 26-UW-1998; 01-UU-1998; 01-UU-1998; 02-UU-1998; 02-UU-1998; 02-UU-1998;	22-JUL-1998; 24-JUL-1998; 10-AUG-1998; 10-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 18-AUG-1998; 18-AUG-1998; 26-AUG-1998;	02-5EP-1998, 02-5EP-1998, 02-5EP-1998, 10-5EP-1998, 10-5EP-1998, 10-5EP-1998, 10-5EP-1998, 10-5EP-1998, 16-5EP-1998, 16-5EP-1998, 16-5EP-1998, 17-5EP-1998, 17-5EP-1998, 17-5EP-1998, 17-5EP-1998, 17-5EP-1998, 17-5EP-1998, 18-5EP-1998, 18-5EP-1998, 23-5EP-1998, 23-5EP-1998, 23-5EP-1998, 23-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 24-5EP-1998, 25-5EP-1998, 26-5EP-1998, 26-5EP-1998, 27-5EP-1998, 28-5EP-1998, 28-5EP-1998, 28-5EP-1998, 28-5EP-1998, 28-5EP-1998, 28-5EP-1998, 28-5EP-1998, 28-5EP-1998,
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14-MAY-1999;
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22-MAY-2000;
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28-AUG-2001;
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Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL; Pan J, Smith V, Watanabe CK, Wood WI, Zhang \mathbf{Z}_i

WPI; 2003-332034/31. N-PSDB; ACA73401. Three hundred and five nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, and for detecting the presence of tumor in a mammal.

Claim 11; Fig 34; 707pp; English.

The invention relates to three hundred and five nucleic acids encoding PRO polypeptides (secreted and transmembrane), sequences 80% identical to them, or encoding a PRO polypeptide lacking its associated signal peptide or an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide. Also included are the encoded PRO proteins, PRO expression vectors, host cells transformed with the vector (used to

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necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
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         tumour necrosi
tissue typing.
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28-AUG-2001;
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         produce PRO proteins), a chimaeric molecule comprising the PRO
polypeptide fused to a heterologous amino acid sequence, an anti-PRO
artibody, a method for stimulating the ralease of tumor necrosais factor
alpha (TNR-alpha) from human blood (by contacting the blood with PRO1079,
PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or
PRO4331), a method for stimulating the proliferation or differentiation
of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
a method for detecting the presence of tumour in a mammal and an
oligomucleotide probe darived from any of the nucleotide sequences cited
above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
medicament for treating a condition that is responsive to the PRO
polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
complements of the presence of a transgenic animals or knockout
antisense RNA and DNA. PRO nucleic acids are also useful in preparing procypeptides, in assays to identify other proteins or molecules involved
animals, which in turn are useful in the development and screening of
therapeutically useful reagence from numeric acid molecules are also
useful for detecting the presence of a tumour in a mammal, simulating
proliferation or differentiation of chondrocyte cells, stimulating
curlease of tumour necrosis factor-alpha from human blood, in gene
purposes. The anti-PRO antibodies may be used in diagnostic assays for
PRO, or for the affinity purification of PRO from recombinant cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | FAMLCLLIIGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEEKKEYFI 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.3%; Score 417; DB 6; Length 440; 100.0%; Pred. No. 0; Nismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted and transmembrane protein; PRO; TNF-alpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 440 AA;
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12-JUL-2002; 2002US-00194423
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RESULT 36

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25-MAY-2001;
01-JUN-2001;
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25-AUG-1
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                                                                                                                                                                                                                                                                                                                                                               liver;
                                     ABU80450
                                                                                                                                BEREE BEREER BETER BEREER BETER B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ransmembrane (PRO) polypeptides. Also disclosed is a antibody that specifically binds to the PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TWF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the PRO nucleotide sequences. The nucleotide sequences are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight maxkers for protein electrophoresis purposes, for for stimulating the release of TWR-alpha from human blood, for stimulating the presence of a tumour. The PRO polypeptides and cetecting the presence of a tumour. The PRO polypeptides and cetecting the presence of a tumour. The PRO polypeptides and cetecting the presence of a tumour. The PRO polypeptides and cetection acids may also be used diagnostically for tissue typing. The sequences presented in ABU67406-ABU67710 are the PRO polypeptides of the invention
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                                                                                                                                                                                                                                                                                                                                                                                   New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YMLYVYDPPTTIPPPTTTTTTTTTTTTTLTTTDSRAGEEGSIRAVDHAVIGGVVAVVV 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAMLCLIIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEEKKEYFI 440
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                                                                                                                                                                                                Gurney AL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention discloses human nucleic acids encoding secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.3%; Score 417; DB 6; Length 440;
100.0%; Pred. No. 0;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                             Godowski PJ,
                                                                                                                                                                                                , Goddard A, Godov
Wood WI, Zhang Z;
                                                                                                                                                                                                KP, Chen J, Desnoyers L,
Smith V, Watanabe CK, V
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29-AUG-2001; 2001WO-US027099.
04-SEP-2001; 2001US-00946374.
15-JAN-2002; 2002US-00052586.
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Matches 417; Conservative
                                                                                                                                (GETH ) GENENTECH INC.
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N-PSDB; ACA05716.
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tumour; adrenal; lung; colon; breast; prostate; rectal; cervical; PRO; gene therapy.
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ABU80450 standard; protein; 440
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99US-00380137.
99US-00380138.
99US-00380142.
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2001US-00854208.
2001US-00854280.
2001US-00866028.
2001US-US017800.
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98WO-US025108.
98US-00202054.
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2000US-00664610
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                                                      (first entry)
                                                                                   Human PRO protein #17.
                                                                                                                                                                                       US2003036137-A1.
                                                                                                                                                            Homo sapiens.
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01-SEP-1999;
15-SEP-1999;
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                                                        23-JUN-2003
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Homo sapiens.
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28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
31-OCT-1997;
31-OCT-1997;
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29-APR-1998;
29-APR-1998;
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21-NOV-1997;
24-NOV-1997;
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20-MAR-1998;
27-MAR-1998;
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11-MAR-1998;
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12-DEC-1997
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31-MAR-1998
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08-APR-1998
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                                                                   ABR99368;
                          RESULT 37
                                     ABR99368
                                                         | FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPDQESYTTITVLVPPR 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTT3385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Three hundred and five nucleic acids encoding secreted and transmembrane RNO polypeptides, useful for the diagnosis, prevention and/or treatment of tumors, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumors.
                                                                                                                                                                                                                                                                                                                      The invention relates to three hundred and five nucleic acids encoding PRO polypeptides (secreted and transmembrane). Methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of tumours, such as defaulated, colon, breast, prostate, rectal, cervical or liver tumours. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human CDNA, genomic DNA or mRNA. The PRO genes are also be used in gene therapy, particularly for replacing a defective gene. The present sequence represents a human PRO polypeptide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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th V, Watanabe CK, Wood WI, Zhang Z;
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05-JUN-2001, 2001US-00874503.
20-JUN-2001, 2001WO-US019692.
29-JUN-2001, 2001WO-US021066.
09-JUL-2001, 2001US-00908827.
18-JUL-2001, 2001US-00924419.
13-AUG-2001, 2001US-00924419.
13-AUG-2001, 2001US-00924419.
16-AUG-2001, 2001US-0091836.
29-AUG-2001, 2001US-0091992.
29-AUG-2001, 2001US-0091992.
29-AUG-2001, 2001US-00941992.
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98US-0095282P.
98US-0095282P.
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98US-0096012P.
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   TCEAIGKPQPVMVTWVVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
                                                                                                                                                      YMLYUYDPPTIIPPPTTTTTTTTTTTTILTIITDSRAGEEGSIRAUDHAVIGGVVAVVV 385
                                                             263
                                                                                                                                                                      144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
                                                                                                                                                                                                                 extracellular domain; tumour necrosis factor alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; alon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
                             MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHI QMTYPLQGLTREGDALEL
                                               PRO; secreted protein; transmembrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted polypeptide PRO355, SEQ ID NO:34.
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97US-0053266P.
97US-0063120P.
97US-0063121P.
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 Human; secreted and transmembrane protein; PRO; TNF-alpha; tunour acrosis factor alpha; chondrocyte cell; tunour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; brostate tumour; rectal tumour; cervical tumour;
                                                             Human secreted/transmembrane protein (PRO) #17
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9705-0053264P

9705-0063121P

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                                    (first entry)
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05-MAY-1998

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15-MAY-1998

15-MAY-1998
                                                                                                                                                                                                                          25-JUN-2002;
                                                                                                                                                    Homo sapiens
                                   30-AUG-2003
                                                                                                                                                                                                  06-MAR-2003
            ABO18822;
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New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, or for preparing a medicament for treating a condition
                                                                                TCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
                      TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
                                                                YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT3388GEEGSIRAVDHAVIGGVVAVVV 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human PRO secreted/transmembrane polypeptides (ABR78227-ABR78531) and nucleic acids encoding them (ACF00100-00404). The invention also relates to sequences at least 80% identical to the PRO nucleic acid had polypeptide sequences of the invention, recombinant vectors and host cells comprising a PRO nucleic acid, a method for the recombinant production of a PRO polypeptide, antibodies against a PRO polypeptide, and fusion proteins comprising a PRO polypeptide. Nucleic acids encoding PRO polypeptides of the invention were initially identified via homology screening using consensus sequences based on the extracellular domain sequences from known secreted proteins. Human cDNA libraries containing sequences of interest were identified using oligonucleotides based on the consensus sequences, and cDNA clones were isolated and characterised. The PRO polypeptides are useful for
                                                                                                                              442
                                                                                                                                                                                                                                                                                                                                                                               extracellular domain, tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
                                                                                                                                                            440
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that is responsive to the PRO polypeptide or anti-PRO antibody.
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                                                                                                                                                                                                                                                                                                                                                                      PRO; secreted protein; transmembrane protein;
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tanabe CK, Wood WI, Zhang Z;
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02-JUN-1999; 99WO-US012252.
25-AUG-1999; 99US-00380137.
28-FEB-2001; 20UNO-US06520.
15-JAN-2002; 2002US-00052586.
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417; Conservative
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Matches 41
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the continuating release of tumour necrosis factor-alpha (TNF-alpha) from human blood and may thus be used in the treatment of conditions in which cannated TNF-alpha release would be beneficial. They are also useful for stimulating the proliferation or differentiation of chondrocytes and as conditional to the treatment of various bone and/or cartilage disorders such as arthritis and sports injuries. The RDO polypeptides may be used in the treatment of various bone and/or cartilage consend it method for detecting the presence of a tumour. Proseste tumour, rectal tumour, cervical tumour or liver tumour, proseste conforted tumour, cervical tumour or liver tumour, proseste in test and control samples, where a higher level of expression of PRO polypeptide in the test sample as compared to the control sample is inclicative of the presence of a tumour. The PRO polypeptides are additionally useful for in drug screening to identify agonists and antagonists of PRO polypeptides are useful as higher latengation probes (for isolation of cDNA molecules), in chromosome and controlisation probes (for isolation of cDNA molecules), in chromosome and controlisation probes (for isolation of cDNA molecules), in chromosome and controlisation probes (for isolation also be used for mapping genes encoding PRO polypeptides, for generation of antisense RNA and DNA and in gene therapy. The nucleic acids can also be used for mapping genes encoding PRO polypeptides, for generation of streams and screening of the rangelly useful compounds. Sequences ABRY8227-ABR78531 represent the human PRO secreted/transmembrane polypeptides of the invention. Note: The sequence data for this patent is also available in electronic format the form to prove the properties of the properties of the provence of the properties of the provence o
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                                                   324 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTDSRAGEEGSIRAVDHAVIGGVVAVVV 383
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                                                                                                                                            FAMLCLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 440
                                                                                                             FAMLCLLI ILGRYFARHKGTYFTHEAKGADDAADADTAI INAEGGQNNSEEKKEYFI
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Cornelia de Lange syndrome; gene therapy; immune disorder;
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inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; cardiac injury; AIDS; cancer; diabetic complication.
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970S-0069334P.
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970S-0069702P.
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transmembrane polypeptides and polynucleotides useful for chromosome identification, tissue typing, gene therapy, in chromosome and gene mapping, or as molecular weight markers. , Godowski PJ, Grimaldi JC, Gurney AL. Napier MA, Roy MA, Tumas D, Wood WI; Baker in, Gourne Gerritsen ME, Gourne KT, Kljavin IJ, WPI; 2003-311003/30. N-PSDB; ABX96814.

Filvaroff E;

Ferrara N,

Eaton DL,

Baker KP, Botstein D,

δ 원 à 요 Claim 12; Fig 24; 172pp; English.

The invention relates to an isolated nucleic acid encoding a secreted/ transmembrane polypeptide (designated as PRO proteins). 15 PRO polypeptides and their encoding polymucleotides are disclosed. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the vector, a process for producing a PRO polypeptide (by culturing the host cell under conditions for the expression of the PRO polypeptide, and recovering the PRO polypeptide from the cell culture, an isolated polypeptide having at least 80% amino acid sequence identity to the PRO polypeptides, a chimaeric molecule comprising PRO fused to a heterologous amino acid sequence and an antibody which specifically binds

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        in chromosome and gene mapping, in generating sense and antisense FNA or the development and screening of therapingally useful reagents, and in gene therapy. The polypetides may be used as molecular weight markers for protein electrophoresis purposes. The PRO polypeptides and nucleic acids may also be used for chromosome identification, and tissue typing. PRO24! (identified as Chordin) is a candidate gene for cornella de Lange syndrome. Other PRO proteins are variously implicated in immune disorders, inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, cardiac injury, ALDS, cancer and diabetic complications. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
                                                                                                                                                                                                                                                                                                                                                                                                                          YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTT3385
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy; chondrocyte stimulator; chromosome mapping; gene mapping; transgenic animal; knock-out animal; tumour.
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                                                                                                                                                            Query Match
Best Local Similarity 100.
                                                                                                                                                Sequence 440 AA;
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                                                                                                                          a PRO protein
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 Human; gene therapy; tumour necrosis factor alpha; TNF-alpha; chondrocyte stimulation; tumour; tissue typing.
         Novel human secreted and transmembrane protein PRO355
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Human; secreted and transmembrane protein; PRO; TNF-alpha; tumour secrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
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                                                              Human secreted/transmembrane protein (PRO) #17.
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28-0CT-1997;
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31-0CT-1997;
24-NOV-1997;
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08-APR-1998;
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11-DEC-1997;
12-DEC-1997;
17-DEC-1997;
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98US-0098014P

98US-0098014P

98US-0098821P

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98US-0099743P

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98US-010147P

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98US-01025A

98US-01025A

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26-AUG-1998

26-AUG-1998

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26-AUG-1998

01-SEP-1998

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02-SEP-1998

10-SEP-1998

10-SEP-1998

10-SEP-1998

11-SEP-1998

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30-SEP-1998
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02-0CT-1998
06-0CT-1998
06-0CT-1998
07-0CT-1998
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DB 6;
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9805-010231P-
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01-OCT-1998;
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Gaps .. 0

Length 440; 0; Indels

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06-MAY-1998;
07-MAY-1998;
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07-MAY-1998;
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28-MAY-1998;
02-JUN-1998;
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03-JUN-1998;
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24-JUN-1998;
24-JUN-1998;
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04-JUN-1998;
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17-JUN-1998;
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19-JUN-1998;
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15-MAY-1998
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   FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted and transmembrane protein; PRO; TNF-alpha; tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440
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97US-0069425P.
97US-0069425P.
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17-OCT-1997;
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24-OCT-1997;
28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
21-OCT-1997;
31-OCT-1997;
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98US-0102331P.
98US-0102487P.
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98US-0102684P.
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30-SEP-1998;
01-OCT-1998;
02-OCT-1998;
06-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
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                                                                                                                                                                                                                     FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
                                                                                                                                                                                                                                                                                                                             NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
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                                                                                                                                    LRLLLLLFSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLLNPNRQTI Y
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Length 440;
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Query Match 94.3%; Score 417; DE Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
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YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
                                                                                                                                                                              Human, gene therapy; chondrocyte stimulation; TNF-alpha release; chondrocyte proliferation; chondrocyte differentiation; tumour detection;
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                                                               MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
                                                                                                         TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated PRO polypeptide and encoding nucleic acids, useful for the diagnosis and treatment of disorders such as inflammatory disease, atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a novel isolated PRO polypeptide. The methods a compositions of the present invention are useful for the diagnosis and treatment of disorders such as inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications and mutations in general. This is the amino acid sequence of a novel human secreted PRO protein
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, Godowski PJ, Grimaldi JC, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
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100.0%; Pred. No. 0;
ive 0; Mismatches 0; Indels
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97US-0069425P.
97US-006969P.
97US-0069702P.
97US-0069870P.
97US-0069813P.
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98US-0070440P.
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98US-0112850P.
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99US-00254311.
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2000WO-US032678.
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Gerritsen ME, Goddard A,
Hillan KJ, Kljavin IJ, N
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417; Conservative
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N-PSDB; ABX78468.
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28-JUL-2000; 2
01-DEC-2000; 2
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22-FEB-2000;
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09-FEB-1998,
25-FEB-1998,
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25-JUN-1998; 25-JUN-1998; 25-JUN-1998; 26-JUN-1998; 26-JUN-1998;	JUL-1998	JUL-1998	JUL-1998	JUL-1998 -AUG-1998	10-AUG-1998; 10-AUG-1998;	-AUG-1998 -AUG-1998	-AUG-1998 -AUG-1998	98	96	96	86	86	8 6	01-SEP-1998; 02-SEP-1998;	98	86	98	8 8	86	86	0 0	8 8	86	98	86	0 6 6	9 6	860	86	98	96	96	96	30-SEP-1998; 30-SEP-1998;	01-OCT-1998; 01-OCT-1998;
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                                                                                                                                  FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
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                                                                  Gaps
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                                            DB.6; Length 440;
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100.0%; Pred. No. v.
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97US-0063120P.
97US-0063121P.
97US-0063540P.
97US-0063541P.
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98US-0103258P.
98US-0103449P.
98US-00168978.
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24-0CT-1997;
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28-0CT-1997;
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98US-0101475P.
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-JUN-1998; -JUN-1998; -JUN-1998; -JUN-1998;	-JUN-1998; -JUN-1998; -JUN-1998;		-JUN-1998;	-JUN-1998;	-JUN-1998;		-JUN-1998;	-JUN-1998;	2-JUN-1998;	4-JUN-1998;		4-JUN-1998;	4-JUN-1998; 4-JUN-1998;		-JUN-1998;	-JUN-1998;		-JUN-1998;	6-JUN-1998;	6-JUN-1998; 1-JUL-1998;	1-JUL-1998;	2-JUL-1998;	-JUL-1998; -JUL-1998;	2-JUL-1998;	4-JUL-1998; 4-AUG-1998;	-AUG-1998;		-AUG-1998; -AUG-1998;		-AUG-1998;	8-AUG-1998;	-AUG-1998; -AUG-1998;	6-AUG-1998;	6-AUG-1998;	6-AUG-1998; 1-SEP-1998;	1-SEP-1998;		2-SEP-1998; 9-SEP-1998;
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extracellular domain, tumour necrosis factor-alpha, TNF-alpha, chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury, cancer; tumour; diagnosis; adrenal tumour; lung; colon, breast; prostate; kidney; rectum; cervix; liver; drug screening; cransgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
                                                                              Human; PRO; secreted protein; transmembrane protein;
                                                           Human secreted polypeptide PRO355, SEQ ID NO:34.
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 ABR59201 standard; protein; 440
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970S-0059266P.
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12-DEC-1997;
17-DEC-1997;
18-DEC-1997;
10-MAR-1998;
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98US-0099741P.
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Matches 417; Conservative
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RESULT 52 ABR59201

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86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145

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26 LRILLLIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
24 LRILLLIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY

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Query Match 94.3%; Score 417; DB 6; Length 440; Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 146 NEMIDIOKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205

206 MLKVHKEDDGVPVICQVEHPAVTGNLGTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265

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05-MAX-1998;
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26-JUN-1998;
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 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
                                                                         204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
                                                                                                                                                                                                                                                                                                                                   Human; secreted and transmembrane protein; PRO; TNP-alpha; tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
                                                                                                                                               FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
                                                                                                                                                                                                                                                                                                           Human secreted/transmembrane protein (PRO) #17.
                                                                                                                                                                                                                          AB009263 standard; protein; 440 AA
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970S-0063250P.
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24-OCT-1997;
24-OCT-1997;
28-OCT-1997;
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21-OCT-1997;
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12-DEC-1997;
17-DEC-1997;
10-MAR-1998;
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31-MAR-1998;
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                                                                                                    FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
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                                        LRLLLLLFSAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted and transmembrane protein; PRO; chromosome mapping; gene mapping; transgenic animal; knockout animal; tissue typing; chromosome identification; tumour; humors, producoyte proliferation; chondrocyte differentiation; tumour necrosis factor-alpha release;
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98WO-US019330.
98WO-US021141.
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98UG-002054.
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99UG-002054.
99UG-00305028.
99WO-US010733.
99WO-US010733.
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   Best Local Similarity 100.
Matches 417; Conservative
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06-NOV-1998

06-NOV-1998

07-DEC-1998

07-DEC-1999

08-MAR-1999

14-MAY-1999

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Godowski PJ, Gurney AL;
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ood WI, Zhang Z;
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          18 - OCT - 1999; 9918-00403297.

18 - OCT - 1999; 9918-00403297.

10 - DEC - 1999; 9940-USC0283101.

20 - DEC - 1999; 9940-USC02851.

30 - DEC - 1999; 9940-USC02851.

18 - FEB - 2000; 2000WO-USC01341.

21 - FEB - 2000; 2000WO-USC01341.

22 - FEB - 2000; 2000WO-USC01341.

23 - FEB - 2000; 2000WO-USC01341.

24 - FEB - 2000; 2000WO-USC01341.

15 - MAR - 2000; 2000WO-USC01341.

16 - MAR - 2000; 2000WO-USC01341.

17 - MAY - 2000; 2000WO-USC01341.

18 - MAY - 2000; 2000WO-USC01341.

22 - MAY - 2000; 2000WO-USC014941.

23 - MAY - 2000; 2000WO-USC014941.

24 - MG - 2000; 2000WO-USC014941.

25 - MG - 2000; 2000WO-USC014941.

26 - JUL - 2000; 2000WO-USC013264.

27 - MG - 2000; 2000WO-USC013264.

28 - JUL - 2000; 2000WO-USC013264.

28 - JUL - 2000; 2000WO-USC013264.

29 - JUL - 2000; 2000WO-USC013264.

20 - JUL - 2000; 2000WO-USC01326.

20 - DEC - 2000; 2000WO-USC01326.

21 - BEC - 2000; 2000WO-USC01326.

21 - BEC - 2000; 2000WO-USC01326.
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10-MAY-2001; 2001US-00854280.

10-MAY-2001; 2001US-00854280.

25-MAY-2001; 2001US-00866028.

10-JUN-2001; 2001WO-08517800.

65-JUN-2001; 2001WO-US019692.
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09-JUL-2001; 2001WO-US02135.

18-JUL-2001; 2001US-00908827.

30-JUL-2001; 2001US-00918585.

13-AUG-2001; 2001US-00924419.

15-AUG-2001; 2001US-00929404.
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29-AUG-2001; 2001UG-US027099
04-SEP-2001; 2001US-00946374
15-JAN-2002; 2002US-00052586
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v secreted and transmembrane PRO polypeptides and nucleic acids, useful gene therapy, chromosome identification, tissue typing, for detecting presence of tumor in a mammal, or as hybridization probes in gene mapping the 5

Claim 11; Fig 34; 707pp; English

The invention describes a novel isolated PRO polypeptide. The PRO polypeptide or anti-PRO antibody is useful for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically

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useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful for detecting the presence of tumour in a mammal, stimulating proliferation or differentiation of chondrocyte cells, stimulating the release of tumour necrosis factor-alpha from human blood, in gene therapy, or as molecular weight markers for protein electrophoresis purposes. The anti-PRO purification of PRO from recombinant cell culture or for the affinity purification of PRO from recombinant cell culture or natural sources. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                               205
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100.0%; Pred. No. 0;
ive 0; Mismatches
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97US-0059266P.
97US-0062250P.
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Les 417; Conservative
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17-OCT-1997;
21-OCT-1997;
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10-JUN-1998; 10-JUN-1998; 11-JUN-1998; 11-JUN-1998;	11-JUN-1998; 12-JUN-1998;	12-JUN-1998; 16-JUN-1998;	17-JUN-1998;	17-JUN-1998;	18-JUN-1998; 19-JUN-1998;	22-JUN-1998; 22-JUN-1998;	22-JUN-1998;	24-JUN-1998;	24-JUN-1998; 24-JUN-1998;	24-JUN-1998;	25-JUN-1998;	25-JUN-1998; 25-JUN-1998;	25-JUN-1998;	25-JUN-1998; 25-JUN-1998;	25-JUN-1998;	26-JUN-1998;	26-JUN-1998;	26-JUN-1998;	01-JUL-1998;	02-JUL-1998;	02-JUL-1998;	02-JUL-1998; 02-JUL-1998;	24-JUL-1998;	04-AUG-1998; 10-AUG-1998;	10-AUG-1998;	17-AUG-1998; 17-AUG-1998;	17-AUG-1998; 17-AUG-1998;	17-AUG-1998;	18-AUG-1998; 18-AUG-1998;	18-AUG-1998;	26-AUG-1998;	26-AUG-1998;	26-AUG-1998;	26-AUG-1998;	01-SEP-1998;	02-SEP-1998; 02-SEP-1998;	02-SEP-1998;	09-SEP-1998; 10-SEP-1998;	10-SEP-1998;	10-SEP-1998;	15-SEP-1998; 16-SEP-1998;	16-SEP-1998; 16-SEP-1998;
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97US-0063120P. 97US-0063121P. 97US-0063540P. 97US-0063541P.	97US-0063544P. 97US-0063564P.	97US-0063734P. 97US-0063870P.	97US-0064103F. 97US-0065311P. 97US-0066120P	97US-0066466P.	97US-0069335P.	97US-0069425P. 97US-0069870P.	97US-0068017P.	98US-0077632P.	98US-0077649P. 98US-0078886P.	98US-0078939P.	98US-0079786P.	98US-008010/F.	98US-0080327P.	98US-008U333F.	98US-0081070P.	98US-0081195P.	98US-0082568P.	98US-0082569P.	98US-0082797P.	98US-0083322P.	98US-0083496P.	98US-0083499P. 98US-0083559P.	98US-0084366P.	98US-0084614F.	98US-0084640P.	98US-0085579P.	98US-0085580P. 98US-0085582P.	98US-0085700P.	98US-0086392P.	98US-0086486P.	98US-0087208P.	98US-0087609P.	98US-0087827P.	98US-0088025P.	98US-0088029P.	98US-0088033P. 98US-0088326P.	98US-0088167P.	98US-0088ZUZF. 98US-0088Z1ZP.	98US-0088217P.	98US-0088722P.	98US-0088738P. 98US-0088740P.	98US-0088811P. 98US-0088824P.
24-OCT-1997; 24-OCT-1997; 28-OCT-1997; 28-OCT-1997;	OCT-199 OCT-199	OCT - 199	10V-199	VOV - 199	DEC-199	DEC-199 DEC-199	DEC-199	MAR-199	4ar-199 4ar-199	MAR-199 Mar-199	MAR-199	AR-199 AR-199	APR-1998	4PK-1998 4PR-1998	APR-1998	APR-1998	APR-1998	APR-1998 APR-1998	APR-1998	APR-1998	APR-1998	APR-1998 APR-1998	4AY-1998	AX-1998 AX-1998	MAY-1998	AY-1998	(AY-1998 (AY-1998	(AY-1998	AY-1998	MY-1998	AX-1998	TUN-1998	TUN-1998	JUN-1998	JUN-1998	TUN-1998	TUN-1998	JUN-1998 JUN-1998	10N-1998	TUN-1998	7UN-1998 7UN-1998	199 10N-199
PR PR PR																																										

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Human; PRO; secreted protein; transmembrane protein; TNP-alpha; extracellular domain; tumour necrosis factor-alpha; reaching transments chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; advernal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
                                                                                                                                                                                                                                             9705-0059263P.
9705-0059264P.
9705-0063426P.
9705-0063121P.
9705-0063121P.
9705-0063544P.
9705-0063544P.
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9705-0063544P.
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9705-006374P.
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                                                                                                                           Homo sapiens
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28-0CT-1997;
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29-0CT-1997;
31-0CT-1997;
13-0CT-1997;
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11-MAR-1998;
20-MAR-1998;
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08-APR-1998;
09-APR-1998;
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05-MAY-1998;
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22-MAY-1998;
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Local Similarity 100.0%; Pred. No. 0; les 417; Conservative 0; Mismatches
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98WO-US019330.
98US-0100683P.
98US-01009319P.
98US-0100943P.
98US-010144P.
98US-0101472P.
98US-0101477P.
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98US-0101477P.
98US-0101473P.
98US-0101738P.
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98US-0101738P.
98US-0102240P.
98US-0102540P.
98US-0102570P.
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98US-010258P.
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16-SEP-1998,
17-SEP-1998,
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26-AUG-1998; 26-AUG-1998; 26-AUG-1998; 26-AUG-1998; 26-AUG-1998; 01-SEP-1998; 01-SEP-1998; 02-SEP-1998; 02-SEP-1998; 02-SEP-1998; 03-SEP-1998; 04-SEP-1998; 05-SEP-1998; 06-SEP-1998;	PR 10-SEE-1998 980S-0099754FP. PR 10-SEE-1998 980S-0099754FP. PR 10-SEP-1998 980S-0099754FP. PR 11-SEP-1998 980S-0099754FP. PR 15-SEP-1998 980S-0100564FP. PR 16-SEP-1998 980S-0100564FP. PR 16-SEP-1998 980S-0100564FP. PR 17-SEP-1998 980S-010054FP. PR 18-SEP-1998 980S-01014FP. PR 23-SEP-1998 980S-010147FP. PR 23-SEP-1998 980S-0101475FP. PR 23-SEP-1998 980S-0101477FP. PR 24-SEP-1998 980S-0101478FP. PR 24-SEP-1998 980S-0101477FP. PR 24-SEP-1998 980S-0101478FP. PR 24-SEP-1998 980S-0101477FP. PR 24-SE	24-SEP-1998; 98US-010.1431. 24-SEP-1998; 98US-010.11932P. 25-SEP-1998; 98US-010.1786P. 29-SEP-1998; 98US-010.2207P. 29-SEP-1998; 98US-010.231P. 29-SEP-1998; 98US-010.231P. 30-SEP-1998; 98US-010.231P. 30-SEP-1998; 98US-010.257P. 30-SEP-1998; 98US-010.257P.	Query Match Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 26 LRILLLESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 85 Db 24 LRILLLESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83	Qy 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145 Db 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143 Qy 146 NLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205 Db 144 NLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203	Oy 206 MIKVHKEDDGVPVICQVEHPATGNLQTQRYLEVQYKEQVHIQMTYPLGGLTREGDALEL 265
98US-0087098 98US-0087208 99US-0087759 98US-0087759 98US-008728 99US-008028 99US-0088028 99US-008803 99US-008803 99US-008803 99US-008803 99US-008803 99US-008803	9 9005-00882117. 9 9005-0088722P. 9 9005-0088722P. 9 9005-0088732P. 9 9005-0088811P. 9 9005-0088825P. 9 9005-0088826P. 9 9005-0088863P. 9 9005-0088863P. 9 9005-0088863P. 9 9005-0088712P. 9 9005-0089512P. 9 9005-008951P.	28. 98US-0090245 39. 98US-0090255 98. 98US-0090429 39. 98US-0090435 98US-0090446 39. 98US-0090461 39. 98US-0090546 39. 98US-0090546 39. 98US-0090546 39. 98US-0090546 39. 98US-0090546 39. 98US-0090546 39. 98US-0090548 39. 98US-0090548 39. 98US-0090548	3; 98US-0090694 3; 98US-0090695 3; 98US-0010696 3; 98US-0010541 3; 98US-0090862 3; 98US-0090863 3; 98US-0090863 4; 98US-00911010	3; 98US-0091545 98US-0091478 3; 98US-0091486 3; 98US-0091628 3; 98US-0091628 3; 98US-0091632 3; 98US-0091632 3; 98US-009183	98US-0095998 98 98US-0096712 98US-0096712 98US-0096867 98 98US-0096897 98US-0096897 98US-0096897 98US-0096897 98US-0096897 98US-0096897
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 324 YMLYVYDPPTTIPPPJTTTTTTTTTTTTTTTTTDSRAGEEGSIRAVDHAVIGGVVAVVV 383
                                                                                                                                            Human; secreted and transmembrane protein; PRO; TNF-alpha; tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
                FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
                         Human secreted/transmembrane protein (PRO) #17
                                                                          ABO15976 standard; protein; 440 AA
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970S-0059266P.
970S-0063212P.
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98US-0083322P.
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31-MAR-1998;
01-APR-1998;
01-APR-1998;
08-APR-1998;
09-APR-1998;
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84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
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                                                                                                                                                    264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted and transmembrane protein; PRO; TNF-alpha; tumour acrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
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                                                 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
                                       NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
                                                                                        MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
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24-0CT-1997;
28-0CT-1997;
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31-0CT-1997;
31-0CT-1997;
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24-NOV-1997;
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17-DEC-1997;
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21-OCT-1997;
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98US-0091632P

98US-0095282P

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98US-0096677P

98US-0096697P

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02-JUL-1998;
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10-AUG-1998;
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17-AUG-1998;
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18-AUG-1998;
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26-AUG-1998;
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01-SEP-1998

02-SEP-1998

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10-SEP-1998

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116-SEP-1998

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86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145

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01-DEC-1998;
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This invention relates to a nucleotide sequence encoding an isolated secreted and/or transmembrane protein. The nucleotide sequences of the invention may have antiinflammatory, antiarteriosclerotic, cardiant, anti-infertility, anti-HIV, cytostatic and antidiabetic activities and may be used in gene therapy. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          442
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Godowski PJ, Grimaldi JC, Gurney AL;
apier MA, Roy MA, Tumas D, Wood WI;
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2000WO-US014042.
2000WO-US020710.
2000WO-US032678.
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2000WO-US003565.
2000WO-US004414.
2000WO-US005841.
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25-MAY-2001; 2001US-00866028.
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Gerritsen ME, Goddard A,
Hillan KJ, Kljavin IJ, N
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Matches 417; Conservative
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  Human; PRO; secreted protein; transmembrane protein; cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; ecrical tumour; ecrical tumour; tiper tumour; tiper tumour; tiper tumour; tiper tumour; tiper tumour; chondrocyte cell; bone disorder; cartilage disorder; sports injury.
 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
                                                                                                                                                     Human secreted/transmembrane protein, SEQ ID 34.
                                                                   ABU65585 standard; protein; 440
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97US-0053266P-
97US-0063250P-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; PRO; secreted polypeptide; transmembrane polypeptide; cytostatic; tumour necrosis factor-alpha; TNF-alpha; blood; tumour; chondrocyte cell;
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                                                                                                                                                                       LRLILLIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY
                                                                                                                                                    LRILILILFSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLLNDNRQTI Y
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                                                                         Query Match 94.3%; Score 417; DE Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
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98US-00168978.
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145 205 265 143 203 263 325 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385 82 83 442 TCEAIGKPQPVWVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD extracellular domain, tumour necrosis factor alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; civer; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy. MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD MLKVHXEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL LRILLILLESAAALI PTGDGQNLFTKDVTVI EGEVATISCQVNKSDDSVIQLLNPNRQTIY NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL Gaps FAMLCLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI FAMLCLL I I LGRYFARHKGTYFTHEAKGADDAADDADTAI I NAEGGONNSEEKKEYFI ö Length 440; Indels Human; PRO; secreted protein; transmembrane protein; ö Human secreted polypeptide PRO355, SEQ ID NO:34 9 DB Score 417; DB; Pred. No. 0; 0; Mismatches 94.3%; Sco larity 100.0%; Pr Conservative 0; ABR67068 standard; protein; 440 98US-0101472P.
98US-0101477P.
98US-0101738P.
98US-0101739P.
98US-0101743P.
98US-0101922P.
98US-0101220P.
98US-0102240P.
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98US-0102571P. 98US-0102687P. 98US-0102965P. 98US-0103258P. 98US-0103449P. (first entry)

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98US - 0088326P

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The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides, with or without their associated signal corrections and sclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNR-alpha) from human blood by contacting the blood with a Cifferentiation of chondrocyte cells by contacting the blood with a RRO polypeptide, a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO polypeptide, a method for detecting the presence of a tumour in a mammal an onligonucleotide sequences are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoresis purposes, for chromosome identification, as chromosome markers, as therapeutic agents, for stimulating the presence of TNF-alpha from human blood, for stimulating the presence, prevention and/or treatment of a tumour, such as detecting the presence, prevention and/or treatment of a tumour, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumour. The PRO polypeptides and nucleic acids may also be used disapnostically contribution. Note: The sequence data for this patent can also be betained contribution.

"The PRO polypeptides and nucleic acids may also be obtained contribution of contribution of charactined in a PRO polypeptide."

"The PRO polypeptides and nucleic acids may also be used disapnostically contribution. Note: The sequence data for this patent can also be betained."

"The PRO polypeptides and nucleic acids may also be obtained contribution."
                                                                                                                                                                                   Human; secreted and transmembrane protein; PRO; TNF-alpha; tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Three hundred and five nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating tumor or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gurney AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for the manufacture of a medicament for diagnosing or treati
for measuring or detecting expression of an associated gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Desnoyers L, Goddard A, Godo
Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                       Human secreted/transmembrane protein (PRO) #17.
standard; protein; 440 AA
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28-FEB-2001; 2001WO-US006520.
15-JAN-2002; 2002US-00052586.
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                                                                                           (first entry)
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                                              AB015671;
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26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 85 LELLILLESAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLLNPNRQTI Y 24 셤 ઠે

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94.3%; Score 417; DB 6; Length 440; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 417; Conservative

Sequence 440 AA;

Query Match

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                                                                                                                                MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL 265
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                                                                                                                                                                                                                                                                    Human; secreted protein; transmembrane protein; PRO; antiarthritic; vulnerary; tumour necrosis factor-alpha; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour; bone disorder; cartilage disorder;
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protein electrophoresis, tumour necrosis factor-alpha, TNF-alpha, blood,
chondrocyte differentiation, chondrocyte proliferation, tumour.
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Best Local Similarity
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11JUN-1998; 12JUN-1998; 16JUN-1998; 16JUN-1998; 17JUN-1998; 17JUN-1998; 17JUN-1998; 18JUN-1998; 19JUN-1998; 19	-SEP-19 -SEP-19 -SEP-19 -SEP-19
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                                                                                                                                                                                                                                                                                                                                                                       Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy;
chromosome mapping; gene mapping; transgenic animal; knock-out animal;
tumour.
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  384 FAMLCLLIILGRYPARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
                                                                                                                  Human, PRO; secreted, transmembrane, cytostatic, TNF-alpha; blood,
tumour necrosis factor alpha release, chondrocyte cell; proliferation,
differentiation; tumour, gene therapy.
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                                                 ABU71128 standard; protein; 440
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05-MAY-1998;
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                                  RESULT 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, PRO, secreted polypeptide, transmembrane polypeptide, cytostatic, tumour necrosis factor-alpha, TNF-alpha, blood, tumour, chondrocyte cell, cancer, adrenal, lung, colon, breast, prostate, rectum, cervix, liver.
                                                                                                                                                                                                                                                                                                                                                       144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
                                                                                                                  TCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
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                                                                                              MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
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97US-0053266P.
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98US-0096012P-
98US-00960757P-
98US-0096891P-
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98US-0102965P.
98US-0103258P.
98US-0103449P.
98US-00168978.
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08-MAR-1999;
14-MAY-1999;
02-JUN-1999;
26-JUL-1999;
25-AUG-1999;
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New secreted and transmembrane PRO polypeptide useful in preparing medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody.
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Wood WI, Zhang Z;
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99WO-US030095
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99WO-US028551
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Smith V, W
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22-MAY-2000;
30-MAY-2000;
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06-JAN-2000;
11-FEB-2000;
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24-FEB-2000;
24-FEB-2000;
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30-NOV-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
20-DEC-1999;
30-DEC-1999;
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15-MAR-2000;
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Gurney AL;

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The invention relates to human PRO secreted/transmembrane polypeptides (ABR69963-ABR70267) and nucleic acids encoding them (ACC90994-ACC91298). The invention also relates to sequences at least 80% identical to the PRO nucleic acid and polypeptide sequences of the invention, recombinant recombinant recombinant recombinant production of a PRO polypeptide, and tubinant production of a PRO polypeptide, and fusion proteins comprising a PRO polypeptide. Nucleic acids encoding PRO polypeptides of the invention were initially acids encoding PRO polypeptides of the invention were initially acids encoding PRO polypeptides of the invention were initially libraries containing sequences from known secreted proteins. Human cDNA libraries containing sequences of interest were identified using consensus sequences based on the consensus sequences, and CDNA clones were isolated and characterised. The PRO polypeptides are useful for stimulating release of tumour necrosis factor-alpha (TNF-alpha) from chuman blood and may thus be used in the treatment of conditions in which channel the proliferation or differentiation of chondrocytes and as

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antiarthritic; vulnerary; gene therapy.
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                                                  Homo sapiens.
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01-APR-1998
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31-OCT-1997
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           cuch may be used in the treatment of various bone and/or cartilage
disorders such as arthritis and sports injuries. The PRO polypeptides may
be used in a method for detecting the presence of a tumour (e.g., an
adrenal tumour, lung tumour, colon tumour, breast tumour, prostate
tumour, rectal tumour, cervical tumour niver tumour) in a mammal. This
tumour involves comparing the level of expression of the PRO polypeptide
in test and control samples, where a higher level of expression of PRO
colypeptide in the test sample as compared to the control sample is
indicative of the presence of a tumour. The PRO polypeptides are
additionally useful for in drug screening to identify agonists and
antagonists of PRO polypeptides. PRO nucleic acids are useful as
thyridisation probes (for isolation of cDNA molecules), in chromosome and
con mapping, in the generation of antisense RNA and DNA and in gene
therapy. The nucleic acids can also be used for mapping genes encoding
con mapping, in the generation of antisense RNA and DNA and in gene
therapy. The nucleic acids can also be used for mapping senescic
disorders, and for genetic analysis of individuals with genetic
animals which are useful in the development and screening of
the rapecular ly useful compounds. Sequences ABR6963-ABR70267 represent
the human PRO secreted/transmembrane polypeptides of the invention. Note:
The sequence data for this patent is also available in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIKVHKEDDGVPVICQVEHPAVTGNIQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAMLCLIIILGRYFARHKGTYFTHEAKGADDAADADIAIINAEGGONNSEEKKEYFI 440
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94.3%; Score 417; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 440 AA;
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ABR69312
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9705-0063541P

9705-0063541P

9705-0063134P

9705-0063134P

9705-0063131P

9705-0066120P

9705-0066120P

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98US-0086486P.
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28-JUN-2002; 2002US-00184629
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FRDFRPLKDSRFOLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145

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YMLYVYDPPTTIPPPTTTTTTTTTTTTTLTILTIDSRAGEBGSIRAVDHAVIGGVVAVVV 385

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386

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	6; Length 440; 0; Indels
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	re 417; D ed. No. 0; Mismatches
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	ch 11 Si 417;
	Mat Loca es
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Query Match
Best Local Similarity
transmembrane protein; tumour necrosis factor alpha; TNF-alpha; adrenal; chondrocyte cell; colon; breast; prostate; rectum; cervix; liver.
                                                          Human; PRO; tumour; cytostatic; cancer; secreted protein; lung;
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               ABO01453 standard; protein; 440
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98US - 0079664P
98US - 0080107P
98US - 0080127P
98US - 0080127P
98US - 0081049P
98US - 0081049P
98US - 0081195P
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98US-0082569P-
98US-0082704P-
98US-008372P-
98US-0083496P-
98US-0083496P-
98US-0083499P-
98US-0083496P-
98US-0083496P-
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97US-0059266P.
97US-0063486P.
97US-0063121P.
97US-0063121P.
97US-0063540P.
97US-0063540P.
97US-0063544P.
97US-0063544P.
97US-006354P.
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97US-006646EP.
97US-006933SP.
97US-006942SP.
97US-0069870P.
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98US-0084639P.
98US-0084640P.
98WO-US019330.
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98US-0077632P.
98US-0077649P.
98US-0078886P.
                                    (first entry)
                                               Human PRO polypeptide #17
                                                                                           US2003008353-A1
                                                                                                                                                                                                      21-NOV-1997;
24-NOV-1997;
24-NOV-1997;
                                                                                Homo sapiens
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12-DEC-1997;
17-DEC-1997;
18-DEC-1997;
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20-MAR-1998;
27-MAR-1998;
27-MAR-1998;
                                    07-AUG-2003
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28-APR-1998;
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13-NOV-1997
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29-APR-1998
                                                                                                      09-JAN-2003
                          AB001453;
     RESULT 72
          ABO01453
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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody that specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human blood by contacting the blood with a PRO polypeptide and a method for stimulating the proliferation or endoacocyte cells by contacting the blood with a PRO polypeptide. The polypeptides and polynucleotides are useful for detecting the presence of a tumour, such as an adrenal, lung, colon, polypeptide. The polynucleotides are useful as hybridisation probes, in tumours and gene mapping and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. Sequences ABOO1741 represent human PRO polypeptides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Three hundred and five nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO, useful for detecting the presence of, or treating tumor, e.g. adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumor.
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Pan J, Smith V, Watanabe CK, Wood WI, Zhang
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98WO-US025108.
99WO-US005028.
99WO-US010733.
99WO-US01252.
99WO-US021111.
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2000WO-US006884
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2000WO-US023328
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2001WO-US021066
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N-PSDB; ACD06949.
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18-FEB-2000; 2
18-FEB-2000; 2
22-FEB-2000; 2
24-FEB-2000; 2
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02-MAR-2000;
15-MAR-2000;
30-MAR-2000;
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22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
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24-AUG-2000;
08-NOV-2000;
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20-DEC-2000;
28-FEB-2001;
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02-JUN-1999;
01-SEP-1999;
01-DEC-1999;
02-DEC-1999;
30-DEC-1999;
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94.3%; Score 417; DB 6; Length 440; 100.0%; Pred. No. 0;

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9805-0077452P-
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22-JUN-1998;
22-JUN-1998;
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06-MAY-1998;
07-MAY-1998;
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07-MAY-1998;
15-MAY-1998;
15-MAY-1998;
    MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL 265
                                                                                                                                                                                                                       385
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                                                                      Human, PRO; tumour necrosis factor-alpha; TNF-alpha; blood;
chondrocyte cell; tumour; adrenal; kidney; lung; colon; breast; prostate;
rectum; cervix; liver; cytostatic.
                      82
                                         83
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                                                                                                TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
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   Gaps
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   0; Indels
   Mismatches
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97US-0053266P.
97US-0063280P.
97US-0063121P.
97US-0063540P.
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97US-0063511P.
97US-0063734P.
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  Conservative
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18-SEP-1997;
21-OCT-1997;
24-OCT-1997;
24-OCT-1997;
28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
21-OCT-1997;
417;
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Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis feator-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
 Human secreted polypeptide PRO355, SEQ ID NO:34.
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98US-0085582P.
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                                                                                                   Homo sapiens.
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FOR THE OF UNANTION WOLECULES DESIGNATED LDCAM
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CURRENT APPLICATION NUMBER: US/09/778,187B
CURRENT FILING DATE: 1999-08-05
FRIOR APPLICATION NUMBER: PCT/US99/17905
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FRIOR FILING DATE: 1999-08-05
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PRIOR FILING DATE: 1999-08-07
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TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PF489P1
CURRENT APPLICATION NUMBER: US/09/836,353A
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR PILING DATE: 1999-10-27
PRIOR PILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver: 2.0
SSQ ID NO 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 442; Dest Local Similarity 100.0%; Pred. No. 0; Matches 442; Conservative 0; Mismatches
Best Local Similarity 100.0%; Pred. No. 0; Matches 442; Conservative 0; Mismatches
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; Publication No. US20030129685A1
; GENERAL INFORMATION:
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US-09-836-353A-136
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                                                                                                                                                             Length 442;
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TITLE OF INVENTION: 12 Human Secreted Proteins FILE REFERENCE: PP489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-40
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR PILING DATE: 1999-10-27
PRIOR PILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIN Ver. 2.0
; FER OF NO NOS: 149
                                                                                                                                                        100.0%; Score 442; D
100.0%; Pred. No. 0;
tive 0; Mismatches
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SOFTWARE: Patentin version 3.1 SEQ ID NO 2
                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 442; Conservative
                                                             ; TYPE: PRT
; ORGANISM: homo sapiens
US-09-778-187B-2
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QQ		qq	301 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTT 360
දු පු	181 KGNTELKGKSEVEEWSDMYTVTSQLALKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240 	රු සි	361 SRACEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
Š Š	241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMYTWYRVDDEWPQHAVLSGPNLFI 300 	ob ov	421 DTAIINAEGGONNSEEKKEYFI 442
oy Oy	301 NNLNKTDNGTVRCEASNIVGKAHSDYMLYVVDPPTTIPPPTTTTTTTTTTTTTTTTTT 360	RESULT 6 US-10-403-107-1	13-107-1
ò	SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCL1.II.LGRYFARHKGTYFTHEAKGADDAADA	; sequei ; Public ; GENER	ice 1, Application US/10403107 cat in No. US20030165974Al LINPORMATION:
qq		; APPL: ; APPL:	CANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE CANT: REEVES, Roger
දු දු	421 DTAIINAEGGNNSEEKKEYFI 442 	, APPL , TITL ; FILE	CANT: YOSHINORI, Muramaki OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS REFREENCE: JHU1770-1
RESULT 5 US-10-3C	RESULT 5 - Semience 20 annication HS/10202041	CURRI CURRI PRIOI	; CURRENT FILING DATE: 2003-03-28; FRIOR APPLICATION NUMBER: US/09/930,803; PRIOR APPLICATION NUMBER: US/09/930,803; PRIOR FILING DATE: 2001-08-15; PRIOR PIOR FILING DATE: 2001-08-15; PRIOR FILING DATE: 2001-08-15
Public GENERA	cation No. US20030144478A1 LINCOMMATION:	SOFTI SEQ II	ARE: Patentin Version 3.0
TITLE	TCALL: Data Note of the Control of t	TYPI	LENGTH: 44Z TYPE: PRT ORGANISM: Homo sapiens
CORRE CURRE PRIOR	CURRENT AFFILIATION WOMBER: US/10/02,041 CURRENT FILING DATE: 2002-11-21 PRIOR APPLICATION NUMBER: US/09/778,510 PRIOR FILING DATE: 2001-02-07	SO .	100.0%; Score 442; DB 14; Length 442; 100.0%; Pred. No. 0;
; PRIO	R AFFLICATION NUMBER: PCI/US99/17906 R FILING DATE: 1999-08-05	Matche	s 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PRIOF	R APPLICATION NUMBER: 60/095,663 R FILING DATE: 1998-08-07 SR OF SED ID NOS: 22	& 43	1 MASVVLPSGSQCAAAAAAAPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA 60
SEQ ID	FIWARE: PACENCIN VEY: 2.0 ID NO 20.	ζ,	TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG
; TYPE ; ORGA: US-10-30	TYPE: PRT ORGANISM: Homo sapien 10-3102-041-20	සි දි	61 TISCQVNKSDDSVIQLLANPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120 121 RVECCIVTNDDDGSVTTTTVIXDDDRIMIDIOKDTAVEGERIEVNCTAMASKDATTIRWF 180
)	Match 100.0%; Score 442; DB 14; Length 442;	3 8	RYFCOLYTDPPOESYTTITUL/PPRILMIDIOKOTAVEGEEIEVNCTAMASKPATIIRWF
Best Lo Matches	cal Similarity 100.0%; Pred. No. 0; 442; Conservative 0; Mismatches 0; Indels	λo	KGNTELKGKSBVEBWSDMYTVTSOLMLKVHKEDDGVPVICQVBHPAVTCNLQTQRYLEVQ
ò	1 MASVVLPSGSQCAAAAAAAAPPGLRLELLLLFSAAALIPTGDGQNLFTKOVTVIEGEVA 60	ପ୍ର	181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
අ <u>ද</u>	1 MASVVLPSGSĞÇAAAAAAAPPGLRLRLILLLESAAALIPTGDĞQNLFTKDVTVIEGEVA 60 61 TISCOVNKSDDSVIOLINDNPOFTVERDERPEDIKDSBF011.NFSSSSEIKVSTFNVSTSNFG 120	& £	241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLF1 300 241 YKPQVHIQMTVPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLF1 300 241 YKPQVHIQMTVPLQGLTBPGDALELTCEAIGKPDPVMVTWVDVDFMPDHAVLSGPNLF1 300
g qa	TISCOVNKSDDSVIQLINPRRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLINVSISDEG 12	8 8	NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
& £	121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOXDTAVEGEEIEVNCTAMASKPATTIRWF 180 121 BYFCOLYTDPDPDFSYTTITVLVPDPNIMIDIOXDTAVEGEEIEVNCTAMASKPATTIRWF 180	g &	301 NNINKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTT 360
8 8	24	3 8	SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARKGTYFTHEAKGADDAADA 42
qq	181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240	λō	421 DTAIINAEGGQNNSEEKKEYFI 442
ر م	241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300 [qa	421 DTAIINAEGGONNSEEKKEYFI 442
} &	NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTT 36	RESULT 7 US-10-015-11	5-115-111

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SRAGEECSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 442;
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR PELING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
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, Publication No. US20040204568A1
, GENERAL INFORMATION:
 APPLICANT: Baum, Peter R.
 TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
 FILE REPERENCE: 2873-US
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                                                421 DTAIINAEGGONNSEEKKEYFI
                                                                             421 DTAIINAEGGONNSEEKKEYFI
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Best Local Similarity 100.0
Matches 442; Conservative
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ORGANISM: Homo sapiens
US-10-363-616-262
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US-10-622-237-2
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Application US/10015115
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Padigaru, Muralidhara
                                             APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Paturajan, Meera
APPLICANT: Rekutajan, Meera
                                                                                                                                                        Gangolli, Esha A
Shimkets, Richard A
Taupier, Raymond J
                 US20030207800A1
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ORGANISM: Homo sapiens
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Best Local Similarity
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1 MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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                         DB 17;
            Score 442; DF
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Patent No. US20020058309A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botetein, David
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 442; Conservative 0;
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Filvaroff, Ellen
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Goddard, Audrey
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Roy, Margaret
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US-09-866-028-61
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APPLICANT: GALIBERT, Laurent J.
APPLICANT: YAN, Wei
TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
FILE REFERENCE: 3467-A
CURRENT APPLICATION NUMBER: US/10/898,408
CURRENT FILING DATE: 2004-07-23
PRIOR FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 2.
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CURRENT APPLICATION NUMBER: US/10/622,237
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: US/09/778,187B
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: US 60/095,672
PRIOR APPLICATION NUMBER: US 60/095,672
NUMBER: OF SEQ ID NOS: 10
SEQ ID NO S: SEQ ID NOS: 10
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US-10-898-408-2
; Sequence 2, Application US/10898408
; Publication No. US20050058642A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: homo sapiens
US-10-622-237-2
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; ORGANISM: homo sapiens
US-10-898-408-2
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Best Local Similarity
Matches 442; Conserv
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PICI CURRENT APPLICATION NUMBER: US/09/866,028 CURRENT FILING DATE: 2001-05-25
                                                                                                                                                   Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
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RICHERNT PILING DATE: 2001-09-26
RICHERNT PILING DATE: 2001-05-26
RICHERNOR APPLICATION NUMBER: 60/067,411
RICHER APPLICATION NUMBER: 60/067,411
RICHER APPLICATION NUMBER: 60/063,334
RICHER RILING DATE: December 11, 1997
RICHER APPLICATION NUMBER: 60/069335
RICHER APPLICATION NUMBER: 60/06935
RICHER APPLICATION NUMBER: 60/06936
RICHER APPLICATION NUMBER: 60/06936
RICHER APPLICATION NUMBER: 60/06936
RICHER APPLICATION NUMBER: 60/069378
RICHER APPLICATION NUMBER: 60/069378
RICHER APPLICATION NUMBER: 60/069425
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100.0%; Pred. No. 0;
tive 0; Mismatches
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APPLICATION NUMBER: 60/069,696
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APPLICATION NUMBER: 60/069,694
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Patent No. US20020102647A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Best Local Similarity 100.
Matches 417; Conservative
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Goddard, Audrey
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Hillan, Kenneth
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Tumas, Daniel
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94.3%; Scc. 100.0%; Pred. No. v, ... 0; Mismatches
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Best Local Similarity 100.0
Matches 417; Conservative
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FILING DATE: December 17,
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LENGTH: 440
TYPE: PRT
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                                                                                              FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
                                                                                                                                                                                                                  NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
                                                                                                                                                                                                                                                                                                                                            MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Patent No. US20020110859A1
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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Napier, Mary
Roy, Margaret
Tumas, Daniel
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COR APPLICATION NUMBER: 09/216,021
COR FILING DATE: December 16, 1998
COR FILING DATE: December 22, 1998
COR FILING DATE: December 22, 1998
COR PELLING DATE: December 22, 1998
COR FILING DATE: March 3, 1999
COR FILING DATE: March 3, 1999
COR APPLICATION NUMBER: PCT/US99/1252
COR FILING DATE: September 15, 1999
COR FILING DATE: PCT/US99/2840
COR FILING DATE: PCT/US99/28313
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APPLICATION UNBER: PT/1US99/28301
FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
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94.3%; Score 417; DE
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches
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PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/05841
PRIOR PLING DATE: March 2, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR PELING DATE: May 22, 2000
PRIOR PELING DATE: May 22, 2000
PRIOR PELING DATE: DATE: PCT/USO0/14042
PRIOR PLING DATE: July 28, 2000
PRIOR PELING DATE: DECEMBER: PCT/USO1/06520
PRIOR PLING DATE: DECEMBER 1, 2000
PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR PLING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US98/25108
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FILING DATE: February 11, 2000
                                                                                                                                                                                                                                                                                                                                       R FILING DATE: February 25, 1998
RR APPLICATION NUMBER: 60/112,850
RFILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
RFILING DATE: December 22, 1998
R APPLICATION NUMBER: 60/146,222
FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/066,017
FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 60/074,086
                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/074,092
                                                                                                                                                                                                                                                                           FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/075,945
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFRERENCE: P2248P1C1:
CURRENT APPLICATION NUMBER: US/09/944,862
CURRENT PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-05-25
PRIOR PLING DATE: December 3, 1997
PRIOR FILING DATE: December 1, 1997
PRIOR PLING DATE: December 11, 1997
PRIOR PLING DATE: December 12, 1997
PRIOR PLING DATE: December 16, 1997
PRIOR PLING DATE: December 17, 1997
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                                                                  NLMIDIOKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
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Patent No. US20020115145A1
GENERAL INFORMATION:
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Filvaroff, Ellen
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Botstein,David
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Godowski, Paul
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Wood, William
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PRICK APPLICATION NUMBER: 09/216, 021
PRICK FILING DATE: December 16, 1998
PRICK FILING DATE: December 22, 1998
PRICK FILING DATE: December 22, 1998
PRICK FILING DATE: March 3, 1999
PRICK FILING DATE: March 3, 1999
PRICK FILING DATE: JUNE 22, 1999
PRICK FILING DATE: Warch 22, 1999
PRICK FILING DATE: September 15, 1999
PRICK FILING DATE: September 15, 1999
PRICK APPLICATION NUMBER: PCT/US99/28409
PRICK FILING DATE: No. US20020115145A1ember 30, 1999
PRICK FILING DATE: No. US20020115145A1ember 30, 1999
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PRIOR FILING DATE: March 2, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: DECEMBER: PCT/USO0/32678
PRIOR FILING DATE: DECEMBER: PCT/USO1/06520
PRIOR FILING DATE: PEDRUARY 28, 2001
PRIOR FILING DATE: PEDRUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
USGANISM: Homo Sapien
US-09-944-862-61
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
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FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US98/25108
FILING DATE: December 1, 1998
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PRIOR APPLICATION NUMBER: PCT/US00/04114
PRIOR FILING DATE: February 22, 2000
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FILING DATE: March 2, 2000
                                                            FILING DATE: January 5, 1998
APPLICATION WUMBER: 60/074,086
APPLICATION WUMBER: 60/074,095
APPLICATION NUMBER: 60/074,092
                                                                                                                                                                                             FILING DATE: February 9, 1998
APPLICATION WUMBER: 60/075, 1998
FILING DATE: February 25, 1998
APPLICATION WUMBER: 60/112,850
LING DATE: December 18, 1997
PLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
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Best Local Similarity 100.
Matches 417; Conservative
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206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
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OR APPLICATION NUMBER: PCI/US98/25108
OR APPLICATION NUMBER: PCI/US98/25108
OR APPLICATION NUMBER: PCI/US98/25108
OR APPLICATION NUMBER: 09/218, 517
OR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: 09/254, 311
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254, 311
OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: PCT/US99/21090
OR APPLICATION NUMBER: PCT/US99/21090
OR PILING DATE: September 15, 1999
OR APPLICATION NUMBER: PCT/US99/28409
OR APPLICATION NUMBER: PCT/US99/28409
OR APPLICATION NUMBER: PCT/US99/28313
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APPLICATION UNWBER: PCT/US99/28301
FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
                                                        PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 25, 1998
PRIOR FILING DATE: February 25, 1998
PRIOR FILING DATE: December 16, 1999
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PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: December 16, 1999
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PRIOR FILING DATE: PEDIACATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: PEDIACATION NUMBER: PCT/US99/0095
PRIOR FILING DATE: PEDIACATY 11, 2000
PRIOR FILING DATE: PEDIACATY 11, 2000
PRIOR FILING DATE: PEDIACATY 11, 2000
PRIOR FILING DATE: MARCH 2, 2000
PRIOR FILING DATE: MARCH 30, 2000
PRIOR FILING DATE: PEDIACATION NUMBER: PCT/US00/020710
PRIOR FILING DATE: PEDIACATY 22, 2000
PRIOR FILING DATE: PEDIACATY 22, 2000
PRIOR FILING DATE: PEDIACATY 22, 2000
PRIOR FILING DATE: PEDIACATION NUMBER: PCT/US00/020710
PRIOR FILING DATE: PEDIACATY 22, 2000
PRIOR FILING DATE: JULY 28, 2001
PRIOR FILING DATE: PEDIACATY 28, 2001
PRIOR FILING DATE: PEDIACATION NUMBER: PCT/US00/020710
PRIOR FILING DATE: JULY 20
PRIOR FILING DATE: PEDIACATY 20, 2000
PRIOR PRIOR FILING DATE: PEDIACATY 20, 2000
PRIOR PRIOR FILING DATE: PEDIACATY 2
          February 9, 1998
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       FILING DATE:
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/09/945,587
CURRENT FILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-05-25
PRIOR PLILING DATE: 2001-05-25
PRIOR PLILING DATE: 2001-05-25
PRIOR PLILING DATE: 2001-05-25
PRIOR PLILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PLILING DATE: December 11, 1997
PRIOR PLILING DATE: December 12, 1997
PRIOR PLILING DATE: December 16, 1997
PRIOR PLILING DATE: December 17, 1997
PRIOR PLILING DATE: DA
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TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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Patent No. US20020127643A1
GENERAL INFORMATION:
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Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
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APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Fartara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritaen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christog
APPLICANT: Girmaldi, Christog
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
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Tumas, Daniel
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US-09-945-587-61
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PRIOR APPLICATION NUMBER: 09/466,028

PRIOR FILING DATE: 2001-05-26

PRIOR FILING DATE: December 11, 1997

PRIOR PELING DATE: December 12, 1997

PRIOR FILING DATE: December 16, 1997

PRIOR FILING DATE: December 16, 1997

PRIOR PELING DATE: December 16, 1997

PRIOR PELING DATE: December 16, 1997

PRIOR PELING DATE: December 17, 1997

PRIOR PELING DATE: December 19, 1997

PRIOR PELING DATE: DECEMBER: 60/070, 410

PRIOR PELING DATE: DECEMBER 19, 1997

PRIOR PELING DATE: DECEMBER: 60/070, 410

PRIOR PELING DATE: DECEMBER: 60/070, 410
TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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                                                                                                                                                                                                                     YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTT388GEGSIRAVDHAVIGGVVAVVV 385
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FILING DATE: February 9, 1998
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Grimaldi, Christopher
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Wood, William
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                                                                                  PRIOR APPLICATION NUMBER: 60/113,296
PRIOR APPLICATION NUMBER: 60/1146,222
PRIOR PILING DATE: December 22, 1998
PRIOR FILING DATE: December 15, 1998
PRIOR PILING DATE: DECEMBER: 60/146,222
PRIOR PELING DATE: DECEMBER: 60/146,222
PRIOR PELING DATE: DECEMBER: FCT/US98/1930
PRIOR PILING DATE: DECEMBER: 10/1998
PRIOR PILING DATE: DECEMBER: 09/216,021
PRIOR PILING DATE: DECEMBER: 09/216,131
PRIOR PILING DATE: DECEMBER: 09/216,131
PRIOR PILING DATE: MATCH 3, 1999
PRIOR PILING DATE: MATCH 3, 1999
PRIOR PILING DATE: WWERE: PCT/US99/12050
PRIOR APPLICATION NUMBER: PCT/US99/1200
PRIOR PILING DATE: SEPTEMBER: PCT/US99/28301
PRIOR PILING DATE: SEPTEMBER: PCT/US99/28301
PRIOR PILING DATE: DECEMBER: 16, 1999
PRIOR PILING DATE: SEPTEMBER: PCT/US99/28301
PRIOR PILING DATE: DECEMBER: PCT/US00/04414
PRIOR PILING DATE: PEDTUATY 11, 2000
PRIOR PILING DATE: PEDTUATY 22, 2000
PRIOR PILING DATE: PEDTUATY 21, 2000
PRIOR PILING DATE: MATCH 3, 2000
PRIOR APPLICATION NUMBER: PCT/US00/0439
PRIOR PILING DATE: MATCH 3, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05201
PRIOR PILING DATE: DECEMBER: 1, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05201
PRIOR PILING DATE: PEDTUATY 28, 2001
PRIOR PILING DATE: PEDTUATY 28, 2001
PRIOR PILING DATE: PEDTUATY 28, 2001
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100.0%; Pred. No. 0;
iive 0; Mismatches 0
                                                                  FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
February
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Best Local Similarity 100.
Matches 417; Conservative
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ORGANISM: Homo Sapien
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CURRENT PELLICATION NUMBER: 00/066,088

PRIOR PELLICATION NUMBER: 00/066,188

PRIOR PELLING DATE: December 11, 1997

PRIOR PELLING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR PLING DATE: December 11, 1997

PRIOR PELLING DATE: December 16, 1997

PRIOR PELLING DATE: December 17, 1997

PRIOR PELLING DATE: Pechanary 5, 1998

PRIOR PELLING DATE: Pebruary 5, 1998

PRIOR PELLING DATE: Pebruary 5, 1998

PRIOR PELLING DATE: Pebruary 3, 1998

PRIOR PELLING DATE: Pebruary 9, 1998
264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
                                                                                         YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTT338
                                                                                                                          384 FAMLCLIIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 440
                                                                                                                                                                                                    386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
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US-09-944-396-61
Sequence 61, Application US/09944396
; Patent No. US20020132981A1
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Goddard, Audrey
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Tumas, Daniel
Wood, William
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PRIOR APPLICATION NUMBER: BU1440, 221
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: July 28, 1999
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR PELICATION NUMBER: 09/216,021
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR PLING DATE: December 22, 1998
PRIOR PLING DATE: December 15, 1999
PRIOR PLING DATE: December 15, 1999
PRIOR PLING DATE: DECEMBER: PCT/US99/21090
PRIOR PLING DATE: NUMBER: PCT/US99/22091
PRIOR PLING DATE: NUMBER: PCT/US99/23019
PRIOR PLING DATE: NU WHERE: PCT/US99/23019
PRIOR PLING DATE: NO US20020132981A1ember 30, 1999
PRIOR PLING DATE: DECEMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR PLING DATE: DECEMBER: PCT/US99/3095
PRIOR PLING DATE: DECEMBER: PCT/US99/3095
PRIOR PLING DATE: DECEMBER: PCT/US99/0849
PRIOR PLING DATE: DATE: DECEMBER: PCT/US99/08439
PRIOR PLING DATE: MUMBER: PCT/US90/08439
PRIOR PLING DATE: MAY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US90/20710
PRIOR PLING DATE: MAY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US90/20710
PRIOR PLING DATE: MAY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US90/20710
PRIOR PLING DATE: PED-LATY 28, 2001
PRIOR PLING DATE: PED-LATY 28, 20
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Best Local Similarity 100.
Matches 417; Conservative
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                                                                                              FAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
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CURRENT APPLICATION NUMBER: US/09/944,432
CURRENT PILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR PLILOXION NUMBER: 09/866,028
PRIOR PLILOXION NUMBER: 00/66,411
PRIOR PLILING DATE: December 11, 1997
PRIOR PLILING DATE: December 11, 1997
PRIOR PLILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,336
PRIOR PLILING DATE: December 11, 1997
PRIOR PLILING DATE: December 11, 1997
PRIOR PLILING DATE: December 11, 1997
PRIOR PRILING DATE: December 11, 1997
PRIOR PLILING DATE: December 11, 1997
PRIOR PRILING DATE: December 11, 1997
PRIOR PLILING DATE: December 16, 1997
PRIOR PLILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR APPLICATION NUMBER: 60/069, 973
PRIOR PLILING DATE: December 17, 1997
PRIOR PLILING DATE: PED'UATY 9, 1998
PRIOR PLILING DATE: PED'UATY 25, 1998
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APPLICATION NUMBER: PCT/US98/19330
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                                                                                                                                                                                                                                                                                                        Sequence 61, Application US/09944432
Patent No. US20020142419A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Godowski, Paul
Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                       Baker, Kevin
Botstein,David
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020142419Alember 30, 1999
PRIOR FILING DATE: No. US20020142419Alember 30, 1999
PRIOR FILING DATE: No. US20020142419Alember 30, 1999
PRIOR FILING DATE: December1, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: PCT/US99/30095
PRIOR FILING DATE: PCT/US99/30095
PRIOR PAPLICATION NUMBER: PCT/US09/03565
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PRIOR APPLICATION NUMBER: PC1/USOU/USSOS)
PRIOR FILING DATE: FEBRUARY 22, 2000
PRIOR PILING DATE: FEBRUARY 22, 2000
PRIOR PILING DATE: MATCH 2, 2000
PRIOR PELING DATE: MATCH 2, 2000
PRIOR APPLICATION NUMBER: PCT/USSOV/08439
PRIOR FILING DATE: MATCH 30, 2000
PRIOR PILING DATE: MAY 22, 2000
PRIOR PILING DATE: MAY 22, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR FILING DATE: DECEMBER: PCT/USSOU/3678
PRIOR FILING DATE: DECEMBER: PCT/USSOU/3678
PRIOR FILING DATE: PERUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
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                                                                                                                                                            FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
R FILING DATE: December 1, 1998
R APPLICATION NUMBER: 09/216,021
R FILING DATE: December 16, 1998
R PAPLICATION NUMBER: 09/218,517
R FILING DATE: December 22, 1998
R APPLICATION NUMBER: 09/254,311
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Best Local Similarity 100.
Matches 417; Conservative
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TYPE: PRT
ORGANISM: Homo Sapien
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TITLE OF INVENTION: SCREETED AND TRANSHEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACCESTED AND TRANSHEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACCESTED AND TEAMSHEMBRANE POLYPEPTIDES AND NUCLEIC CURRENT FILLING DATE: 1001-09-26 STRING PAPELICATION NUMBER: 109/966,028

RRIOR APPLICATION NUMBER: 60/66,1411

PRIOR APPLICATION NUMBER: 60/66,334

PRIOR RILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/69,336

PRIOR PRIOR APPLICATION NUMBER: 60/69,336

PRIOR FILLING DATE: December 11, 1997

PRIOR PAPELICATION NUMBER: 60/69,3278

PRIOR FILLING DATE: December 11, 1997

PRIOR PAPELICATION NUMBER: 60/69,3278

PRIOR FILLING DATE: December 11, 1997

PRIOR PAPELICATION NUMBER: 60/69,3278

PRIOR FILLING DATE: December 11, 1997

PRIOR PAPELICATION NUMBER: 60/69,370

PRIOR PAPELICATION NUMBER: 60/70,394

ILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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                                                                                                                                                                                    Sequence 61, Application US/09943762
Patent No. US200230142558A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
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Grimaldi, Christopher
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Filvaroff, Ellen
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Kljavin, Ivar
Napier, Mary
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Botstein, David
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Goddard, Audrey
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Wood, William
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                                                                           PRIOR FILLING DATE: December 14, 1230
PRIOR FILLING DATE: December 15, 1999
PRIOR FILLING DATE: March 3, 1999
PRIOR FILLING DATE: March 3, 1999
PRIOR FILLING DATE: March 3, 1999
PRIOR FILLING DATE: SEPTEMBER: PCT/US99/12030
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/3801
PRIOR APPLICATION NUMBER: PCT/US99/3809
PRIOR APPLICATION NUMBER: PCT/US09/0356
PRIOR APPLICATION NUMBER: PCT/US00/0356
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR APPLICATION NUMBER: PCT/US00/0841
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR APPLICATION NUMBER: PCT/US00/08630
PRIOR APPLICATION NUMBER: PCT/US00/08500
                         APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
   DATE: December 16, 1998
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266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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          OR FILING DATE: June 22, 1999

OR APPLICATION NUMBER: PCT/US99/21090

OR FILING DATE: September 15, 1999

OR FILING DATE: September 15, 1999

OR FILING DATE: No. US20020142959Alember 30, 1999

OR RILING DATE: No. US20020142959Alember 30, 1999

OR RILING DATE: No. US20020142959Alember 30, 1999

OR APPLICATION NUMBER: PCT/US99/28301

OR RILING DATE: December1, 1999

OR APPLICATION NUMBER: PCT/US99/30095

OR APPLICATION NUMBER: PCT/US99/30095

OR APPLICATION NUMBER: PCT/US90/03565

OR PRILING DATE: PECHUARY 11, 2000

OR PILING DATE: PCT/US90/04144
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PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: March 2, 2000
PRIOR FILING DATE: March 2, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: DECEMBER: PCT/US00/32678
PRIOR FILING DATE: DECEMBER: PCT/US00/32678
PRIOR FILING DATE: DECEMBER: PCT/US00/32678
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
TYPE: PRI
ION NUMBER: PCT/US99/12252
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Best Local Similarity 100.
Matches 417; Conservative
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US-09-944-654-61
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Patent No. US20020142959A1
GENERAL INFORMATION:
                                                                                                                                                                                    Godowski, Paul
Grimaldi, Christopher
                                                               APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
                                                                                                                                                  Gerritsen, Mary
Goddard, Audrey
                                                                                                                                                                                                                                     Hillan, Kenneth
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204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL 263
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                PRIOR FILING DATE: No. US20020150976Alember 30, 1999
PRIOR FILING DATE: No. US20020150976Alember 30, 1999
PRIOR PELING DATE: No. US20020150976Alember 30, 1999
PRIOR PELING DATE: No. US20020150976Alember 30, 1999
PRIOR PELING DATE: December 1, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR PELING DATE: PETVINSON/0414
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR PELING DATE: February 22, 2000
PRIOR PELING DATE: February 22, 2000
PRIOR PELING DATE: March 2, 2000
PRIOR PELING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR PELING DATE: March 30, 2000
PRIOR PELING DATE: March 30, 2000
PRIOR PELING DATE: December 1, 2000
PRIOR PELING DATE: December 1, 2000
PRIOR FILING DATE: PEDTUARY 28, 2001
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US-09-944-413-61
; Sequence 61, Application US/09944413
; Patent No. US20020156004A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
   September 15, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
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APPLICANT: WOOD MAILLAM
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CURRENT PATHOCHER NOBEL: US/09/04/4851A
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PRINCE PATHOCHER NUMBER: US/09/04/4851A
PRINCE APPLICATION NUMBER: US/09/05/334
PRINCE APPLICATION NUMBER: US/09/05/334
PRINCE APPLICATION NUMBER: US/09/05/344
PRINCE APPLICATION NUMBER: US/09/05/34/344
PRINCE APPLICA
                                                                                                                                                                                                                                               Godowski, Paul
Grimaldi, Christopher
                                                                                                                    Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
                      Baker, Kevin
Botstein, David
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                                                                                          Eaton, Dan
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86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
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FILING DATE: No. US20020156004Alember 30, 1999
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                                       PRIOR PILLING DATE: December1, 1999
PRIOR PILLING DATE: December1, 1999
PRIOR PILLING DATE: December1, 1999
PRIOR PILLING DATE: December16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/0365
PRIOR PILLING DATE: PEDRUARY 11, 2000
PRIOR PILLING DATE: PEDRUARY 22, 2000
PRIOR FILLING DATE: PEDRUARY 22, 2000
PRIOR PILLING DATE: PEDRUARY 22, 2000
PRIOR PILLING DATE: PEDRUARY 23, 2000
PRIOR PILLING DATE: March 30, 2000
PRIOR PILLING DATE: March 30, 2000
PRIOR PILLING DATE: March 30, 2000
PRIOR PILLING DATE: May 22, 2000
PRIOR PILLING DATE: May 22, 2000
PRIOR PILLING DATE: May 22, 2000
PRIOR PILLING DATE: December 1, 2000
PRIOR PILLING DATE: PEDRUARY 28, 2001
NUMBER OF SEQ ID NOS: 120

LENGTH: HOMO 51

LENGTH: HOMO Sapien
                         PLICATION NUMBER: PCT/US99/28301
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Patent No. US20020165143A1
GENERAL INPORMATION:
APPLICANT: Baker, Kevin
', APPLICANT: Baten, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
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PRICE PRICE ALTO APPLICATION WINNERS: 10,916-60-20  
PRICE PRICE PRICE ALTO APPLICATION WINNERS: 10,916-60-20  
PRICE PRILING DATE: 2001-09-25  
PRICE PRILING DATE: 2001-09-25  
PRICE PRILING DATE: 2001-09-25  
PRICE PRILING DATE: 1091-09-25  
PRICE PRILING DATE: 1091-09-25  
PRICE PRILING DATE: December 11, 1997  
PRICE PRILING DATE: December 12, 1997  
PRICE PRILING DATE: December 16, 1998  
PRICE PRILING DATE: December 17, 1998  
PRICE PRILING DATE: DECEMBER 107, 1999  
PRICE PRIL
                                                                                                                                        Grimaldi,Christopher
                                                     Gerritsen, Mary
Goddard, Audrey
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Roy, Margaret
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APPLICANT:
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144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
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                                                                                                                                                                                                                                                                                                       Length 440;
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      PRIOR PILLING DATE: February 11, 2000
PRIOR PLING DATE: February 12, 2000
PRIOR PILLING DATE: February 22, 2000
PRIOR PILLING DATE: February 22, 2000
PRIOR PILLING DATE: March 2, 2000
PRIOR PILLING DATE: March 30, 2000
PRIOR PILLING DATE: March 30, 2000
PRIOR PILLING DATE: May 22, 2000
PRIOR PILLING DATE: May 22, 2000
PRIOR PILLING DATE: July 28, 2000
PRIOR PILLING DATE: December 1, 2000
PRIOR PILLING DATE: December 1, 2000
PRIOR PILLING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
APPLICATION NUMBER: PCT/US00/03565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 61, Application US/09944896
Patent No. US20020168715A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
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Best Local Similarity 100.
Matches 417; Conservative
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APPLICANT: Botstein, David
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ORGANISM: Homo Sapien
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86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
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100.0%; Pred. No. 0;
iive 0; Mismatches 0
                   PRIOR APPLICATION NUMBER: PCT/USGO/08439
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/USGO/20710
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR PILING DATE: Pebruary 28, 2001
PRIOR FILING DATE: Pebruary 28, 2001
SEQ ID NO 61
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Patent No. US20020173463A1
GENERAL INFORMATION:
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
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Filvaroff, Ellen
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Best Local Similarity 100.0
Matches 417; Conservative
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APPLICANT: Botstein, David
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Goddard, Audrey
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US-09-944-896-61
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TYPE: PRT
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                   APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR FILING DATE: December 15, 1998
OR APPLICATION NUMBER: 09/218,517
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/218,131
OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: September 15, 1999
OR APPLICATION NUMBER: PCT/US99/28409
OR FILING DATE: September 15, 1999
OR FILING DATE: PCT/US99/28409
OR FILING DATE: PCT/US99/28413
OR APPLICATION NUMBER: PCT/US99/28313
OR FILING DATE: No. US20020168715Alember 30, 1999
OR FILING DATE: No. US20020168715Alember 30, 1999
OR FILING DATE: NO. US20020168715Alember 30, 1999
                                                                                                                                                                       FILING DATE: P2548PICI
CURRENT FILING DATE: 2001-08-11
PRIOR APPLICATION NUMBER: 05/06/034
PRIOR APPLICATION NUMBER: 06/06/334
PRIOR PILING DATE: 2001-08-11
PRIOR APPLICATION NUMBER: 06/06/334
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 16, 1997
PRIOR PILING DATE: December 17, 1997
PRIOR PILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,634
PRIOR APPLICATION NUMBER: 60/069,634
PRIOR APPLICATION NUMBER: 60/069,634
PRIOR PILING DATE: December 17, 1997
PRIOR PILING DATE: PED-THATY 5, 1998
PRIOR PILING DATE: PED-THATY 9, 1998
PRIOR PILING DATE: PED-THATY 9, 1998
PRIOR PILING DATE: DECEMBER: 60/014,086
PRIOR PILING DATE: DECEMBER: 60/0146,225
PRIOR PILING DATE: DECEMBER: 60/0146,229
PRIOR PILING DATE: DECEMBER: 61, 1998
PRIOR PILING DATE: DECEMBER: 61, 1999
PRIOR PILING DATE: PED-THATY 31, 299
PRIOR PILING DATE: PED-THATY 21, 299
PRIOR PILING DATE: POT/US99/128311
PRIOR PILING DATE: POT/US99/128311
PRIOR PILING DATE: POT/US99/13095
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PRIOR PILING DATE: POT/US99/13095
PRIOR PILING DATE: PED-THATY 11, 2000
PRIOR PILING DATE: PED-THATY 11, 2000
PRIOR PILING DATE: PED-THA
Kljavin, Ivar
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THILE DE INVESTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/09/44,944

CURRENT APPLICATION NUMBER: US/09/44,944

PRIOR FILING DATE: 2001-09-26

PRIOR PLING DATE: 2001-09-26

PRIOR PLING DATE: 2001-09-26

PRIOR PLING DATE: 2001-09-26

PRIOR PLING DATE: 09/866,028

PRIOR PLING DATE: 06/69,334

PRIOR PLING DATE: DECEMBER: US/09/86,239

PRIOR PLING DATE: DECEMBER: US/09/84,944

PRIOR PLING DATE: DECEMBER: US/09/84,944

PRIOR PLING DATE: DECEMBER: US/09/84,937

PRIOR PLING DATE: DECEMBER: US/09/86,425

PRIOR PLING DATE: DECEMBER: US/09/84,937

PRIOR PLING DATE: DECEMBER: US/09/84,938

PRIOR PLING DATE: DECEMBER: US/09/84,939

PRIOR PLING DATE: DECEMBER: US/09/84,939

PRIOR PLING DATE: DECEMBER: US/09/84,1930

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 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 205
 203
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTLIITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 324 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTSBSRAGEEGSIRAVDHAVIGGVVAVVV 383
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 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
 24 LRILLILFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY
 144 NLMIDIQKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PILL CURRENT APPLICATION NUMBER: US/09/944,929
CURRENT PILING DATE: 2001-08-31
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 Query Match 94.3%; Score 417; DB 9; Length 440; Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: DECEMBER: PCT/US00/32678
PRIOR PILING DATE: DECEMBER: PCT/US00/32678
PRIOR PILING DATE: PEDTUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
 Sequence 61, Application US/09944929
Publication No. US20020197612A1
GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
 Goddard, Audrey
 Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William
 Kljavin, Ivar
 US-09-944-944-61
 US-09-944-929-61
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 US-09-944-884-61
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 NEMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 265
 264 TCEAIGKPQPVMVTWTVDVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 82
 24 LKLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 FAMLCLIIIGRYFARHKGTYFTHEAKGADDAADAADTAIINAEGGQNNSEEKKEYFI 440
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P2548PIC1 CURRENT APPLICATION NUMBER: US/09/944,907 CURRENT FILING DATE: 2001-08-31 PRIOR APPLICATION NUMBER: 09/866,028 PRIOR FILING DATE: 2001-05-25 NUMBER OF SEQ ID NOS: 120
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
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 26 LRLLLLLLFSAAALIPTGDGONLFTKDVTVIEGEVATISCOVNKSDDSVIOLLNPNROTIY
 Gaps
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 DB 9; Length 440;
 0; Indels
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94.3%; Score 417; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
 ; Sequence 61, Application US/09944907
; Publication No. US20020198147A1
; GENERAL INFORMATION:
 Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
 Ferrara, Napoleone
Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gerritsen, Mary
Goddard, Audrey
 Godowski, Paul
 Tumas, Daniel
Wood, William
 Napier, Mary
Roy, Margaret
 TYPE: PRT
ORGANISM: Homo Sapien
 Eaton, Dan
 RESULT 27
US-09-944-907-61
 US-09-944-929-61
 LENGTH: 440
 86
 144
 204
 326
 146
 206
 266
 384
 APPLICANT:
APPLICANT:
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203
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 206 MLKVHKEDDGVPVICQVEHPAVTGNLGTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL 265
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 144 NLMIDIQKDTAVEGEBIEVNCTAMASKPATTIRWFKGNTELKGKSEVEBWSDMYTVTSQL
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P25491816 CURRENT APPLICATION NUMBER: US/09/944,884 CURRENT FILING DATE: 2001-08-31 PRIOR PEDICATION NUMBER: 09/866,028 PRIOR FILING DATE: 2001-08-25 NUMBER OF SEQ ID NOS: 120
 24 IRILILIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY
 26 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 94.3%; Score 417; DB 10; Length 440;
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 0; Indels
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94.3%; Score 417; DB 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0
 Sequence 61, Application US/09944884
Publication No. US20030077698A1
GENERAL INFORMATION:
 Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
 Ferrara, Napoleone
 Filvaroff, Ellen
 Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gerritsen, Mary
 Roy, Margaret
Tumas, Daniel
Wood, William
 ORGANISM: Homo Sapien
 Eaton, Dan
 Query Match
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPREMENTS: P2248PICI
CURRENT APPLICATION UNMERR: US/09/943,780
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR PAPLICATION NUMBER: 60/067,411
PRIOR PAPLICATION NUMBER: 60/069,334
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 12, 1997
PRIOR PILING DATE: December 16, 1997
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
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 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 384 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADAAIINAEGGONNSEEKKEYFI
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI
 PRIOR FILING DATE: December 16, 1997 PRIOR APPLICATION NUMBER: 60/069,870 PRIOR FILING DATE: December 17, 1997
 Sequence 61, Application US/09943780 Publication No. US20030096742A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin APPLICANT: Botstein, David
 Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerritsen, Mary
 Gurney, Austin
Hillan, Kenneth
 Godowski, Paul
 Wood, William
 Kljavin, Ivar
 Roy, Margaret
Tumas, Daniel
 Napier, Mary
 Eaton, Dan
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 APPLICANT:
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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
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 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTT338
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTBBBGBEGSIRAVDHAVIGGVVAVVV
 83
 442
 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
 APPLICANT: Napler, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tunas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
 LRLILLLESAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 FAMLCLL11LGRYFARHKGTYFTHEAKGADDAADADTA11NAEGGQNNSEEKKEYF1
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 Length 440;
 0; Indels
 0; Indels
 DB 10;
 Query Match
94.3%; Score 417; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches
100.0%; Pred. No. 0; tive 0; Mismatches
 FILE REFERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/944,852
CURRENT FILING DATE: 2001-08-31
 CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
 ; Sequence 61, Application US/09944852; Publication No. US20030083479A1; GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
 Best Local Similarity 100.
Matches 417; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Goddard, Audrey
 NUMBER OF SEQ ID NOS: 120
 Kljavin, Ivar
Napier, Mary
 TYPE: PRT
ORGANISM: Homo Sapien
 Eaton, Dan
 US-09-944-852-61
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 SEQ ID NO 61
 324
 98
 84
 146
 144
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 204
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 264
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 384
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203 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323 YMLYVYDPPTTIPPPTTTTTTTTTTTTTLTIITDSRAGEEGSIRAVDHAVIGGVVAVVV 385 442 PAMLCLIIIGRYFARHKGTYFTHEAKGADDAADAAINAEGGQNNSEEKKEYFI 440 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PILCT
CURRENT APPLICATION NUMBER: US/09/945,584
CURRENT FILING DATE: 2001-09-26 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: December 3, 1997
PRIOR PILING DATE: December 1, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069326 Sequence 61, Application US/09945584 Publication No. US20030211570A1 GENERAL INFORMATION: APPLICATION NUMBER: 60/069,69 APPLICATION NUMBER: 60/069,42 FILING DATE: December 16, 199 APPLICATION NUMBER: 60/069,69 Grimaldi,Christopher December APPLICATION NUMBER: 60 FILING DATE: December FILING DATE: December FILING DATE: December FILING DATE: December APPLICANT: Baker, Kevin APPLICANT: Botstein, David Gerritsen, Mary Goddard, Audrey Gurney, Austin Kljavin, Ivar Roy, Margaret Tumas, Daniel Napier, Mary Eaton, Dan FILING DATE: 326 386 384 APPLICANT: APPLICANT: APPLICANT: 셤 ò 8 원 ò 셤 à FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145

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204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
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 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITTLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PIC1
 CURRENT FILING DATE: 2001-09-26
PRIOR PELLICATION NUMBER: US/09/943,664
PRIOR PELLING DATE: 2001-09-26
PRIOR PELLING DATE: 2001-05-25
PRIOR PELLING DATE: 2001-05-25
PRIOR PELLING DATE: December 3, 1997
PRIOR PELLING DATE: December 11, 1997
PRIOR PELLING DATE: December 12, 1997
 FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,702
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,870
 APPLICATION NUMBER: 60/069,696
 APPLICATION NUMBER: 60/069,87
 Sequence 61, Application US/09943664 Publication No. US20040091972A1 GENERAL INFORMATION:
 FILING DATE: December 16, 199' APPLICATION NUMBER: 60/069,69
 FILING DATE: February 9, 1998
 FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,0
 APPLICATION NUMBER: 60/068,
 Godowski, Paul
Grimaldi, Christopher
 FILING DATE: December 18
 FILING DATE: December 17
 December 1
 Ferrara, Napoleone
Filvaroff, Ellen
 Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Goddard, Audrey
 Gerritsen, Mary
 Wood, William
 Roy, Margaret
Tumas, Daniel
 Napier, Mary
 FILING DATE:
 206
 566
 326
 APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
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 Length 440;
 0; Indels
 DB 10;
 94.3%; Sco...
100.0%; Pred. No. v,
... 0; Mismatches
 RELING DATE: February 9, 1998

DR APPLICATION NUMBER: 60/074, 092

R FILING DATE: February 9, 1998

R FILING DATE: February 25, 1998

DR FILING DATE: February 25, 1998

R FILING DATE: December 16, 1998

DR APPLICATION NUMBER: 60/113, 296

DR FILING DATE: December 22, 1998

DR APPLICATION NUMBER: 60/113, 296

DR FILING DATE: December 16, 1998

OR APPLICATION NUMBER: 60/116, 222

OR FILING DATE: December 16, 1998

OR APPLICATION NUMBER: 07/US98/1910

OR FILING DATE: December 16, 1998

OR APPLICATION NUMBER: 09/216, 221

OR FILING DATE: December 16, 1998

OR APPLICATION NUMBER: 09/216, 221

OR FILING DATE: December 16, 1998

OR APPLICATION NUMBER: 09/216, 221

OR APPLICATION NUMBER: 09/216, 221

OR APPLICATION NUMBER: 09/216, 21

OR APPLICATION NUMBER: PET/US99/21090
 FILING DATE: December 1, 2000
APPLICATION NUMBER: PCT/US01/06520
FILING DATE: February 28, 2001
 FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: January 5, PRIOR FILING DATE: February 6, PRIOR APPLICATION NUMBER: 60) PRIOR FILING DATE: February 6, PRIOR FILING DATE: February 7, PRIOR FILING DATE: February 7, PRIOR PLILOG DATE: February 7, PRIOR PLILOG DATE: February 7, PRIOR PLILOG DATE: December 7, PRIOR PLILOG DATE: September 7, PRIOR PLILOG DATE: September 7, PRIOR PRILOG DATE: September 7, PRIOR PRILOG DATE: September 7, PRIOR PRILOG DATE: December 7, PRIOR PRILOG DATE: PEDVICATION NUMBER: PERIOR PRILOG DATE: PEDVICATION NUMBER: PERIOR PRILOG DATE: MAICH 30, PRIOR PRILOGATION NUMBER: PERIOR PRILOGATION NUMBER: PERI
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-584-61
 146
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/10/052,586

CURRENT PILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: 60/059266

PRIOR FILING DATE: 1997-09-18

PRIOR PILING DATE: 1997-0-18

PRIOR PLING DATE: 1997-0-17

PRIOR APPLICATION NUMBER: 60/063120

PRIOR PILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-10-21

PRIOR PILING DATE: 1997-10-28

 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
 APPLICATION NUMBER: 60/069335
FILING DATE: 1997-12-11
APPLICATION NUMBER: 60/069425
 Sequence 34, Application US/10052586 Publication No. US20020127584A1 GENERAL INFORMATION:
 PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063734
PRIOR FILING DATE: 1997-10-29
 FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063870
 APPLICATION NUMBER: 60/064103
FILING DATE: 1997-10-31
 PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063564
 APPLICATION NUMBER: 60/065311
 Watanabe, Colin K. Wood, William I.
 FILING DATE: 1997-11-13
 FILING DATE: 1997-10-31
 Gurney, Austin L
 Smith, Victoria
 Goddard, Audrey
 Godowski, Paul
 Zhang, Zemin
 US-10-052-586-34
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 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 86 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 84 FRDFRPLKDSRPQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
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 26 LRLLLLLPSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 94.3%; Score 417; DB 11; Length 440; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels
 OR FILING DATE: February 9, 1998
OR APPLICATION NUMBER: 60/012,955
OR FILING DATE: February 25, 1998
OR PILING DATE: February 25, 1998
OR PILING DATE: February 25, 1998
OR FILING DATE: December 16, 1998
OR FILING DATE: December 22, 1998
OR PELING DATE: 0112 28, 1999
OR APPLICATION NUMBER: 60/146,222
OR FILING DATE: September 16, 1998
OR PILING DATE: December 16, 1998
OR FILING DATE: December 16, 1998
OR FILING DATE: December 16, 1998
OR FILING DATE: December 16, 1998
OR PILING DATE: December 16, 1998
OR APPLICATION NUMBER: 09/216,021
OR FILING DATE: December 12, 1998
OR PILING DATE: December 15, 1999
OR APPLICATION NUMBER: PCT/US99/28409
OR FILING DATE: September 15, 1999
OR APPLICATION NUMBER: PCT/US99/28409
OR FILING DATE: September 15, 1999
OR APPLICATION NUMBER: PCT/US99/28409
OR FILING DATE: September 15, 1999
OR APPLICATION NUMBER: PCT/US99/28409
OR APPLICATION NUMBER: PCT/US99/28409
OR APPLICATION NUMBER: PCT/US99/28409
OR APPLICATION NUMBER: PCT/US99/28009
 TELING DATE: December 16, 1999

R APPLICATION NUMBER: PCT/USO0/03565

R FILING DATE: Pebruary 11, 2000

R FILING DATE: February 22, 2000

R APPLICATION NUMBER: PCT/USO0/04414

R FILING DATE: March 2, 2000

R APPLICATION NUMBER: PCT/USO0/08419

R FILING DATE: March 2, 2000

R FILING DATE: March 3, 2000

R FILING DATE: March 30, 2000
 DR APPLICATION NUMBER: PCT/USO0/14042
DR FILING DATE: May 22, 2000
DR APPLICATION NUMBER: PCT/USO0/20710
DR FILING DATE: July 28, 2000
DR APPLICATION NUMBER: PCT/USO0/32678
DR FILING DATE: December 1, 2000
DR APPLICATION NUMBER: PCT/USO1/06520
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR PILING DATE: February 25, 1998
PRIOR PILING DATE: February 25, 1998
PRIOR PILING DATE: February 25, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 17, 1999
PRIOR PILING DATE: December 15, 1999
PRIOR PILING DATE: MUMBER: PCT/US99/28301
PRIOR PILING DATE: MUNBER: PCT/US99/28301
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: PEDRUARY 11, 2000
PRIOR PILING DATE: PEDRUARY 12, 2000
PRIOR PILING DATE: PEDRUARY 12, 2000
PRIOR PILING DATE: PEDRUARY 28, 2001
 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
 US-09-943-664-61
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| 1997-<br>NUMBER<br>NUMBER<br>NUMBER<br>1998-<br>NUMBER<br>1998-<br>NUMBER<br>1998-<br>NUMBER                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 1998-03-20 1998-03-20 1998-03-20 1998-03-21 1998-03-21 1998-03-31 1998-03-31 1998-04-01 1998-04-01 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1098-04-08 1098-04-08 1098-04-08 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18 1098-04-18                                                                                   | NUMBER: 60/083322 1998-04-29 NUMBER: 60/083495 1998-04-29 NUMBER: 60/083496 1998-04-29 1998-04-29 NUMBER: 60/08359 1998-04-29 NUMBER: 60/08359 1998-05-05 1998-05-05 NUMBER: 60/084640 1998-05-07 NUMBER: 60/084640 NUMBER: 60/085579                                                                           |
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| OR FILING DATE OR APPLICATION OR PILING DATE OR RELING DATE OR APPLICATION OR FILING DATE OR RELING DATE OR APPLICATION OR FILING DATE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TELLING DATE OR APPLICATION OR FILING DATE | OR APPLICATION OR APPLICATION OR FILING DATE: OR APPLICATION OR PILING DATE: OR PILING DATE: OR APPLICATION OR PILING DATE: OR APPLICATION OR PILING DATE: OR APPLICATION OR PILING DATE: |
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PRIOR APPLICATION NUMBER: 60/086033
PRIOR PALICATION NUMBER: 60/086486
PRIOR PALICATION NUMBER: 60/086486
PRIOR PLICATION NUMBER: 60/08708
PRIOR PLING DATE: 1998-65-28
PRIOR PLING DATE: 1998-65-28
PRIOR PLING DATE: 1998-65-28
PRIOR PLING DATE: 1998-65-28
PRIOR PLING DATE: 1998-66-02
PRIOR PLING DATE: 1998-66-02
PRIOR PLING DATE: 1998-66-02
PRIOR PLING DATE: 1998-66-03
PRIOR PLING DATE: 1998-66-04
PRIOR PLING DATE: 1998-66-05
PRIOR PLING DATE: 1998-66-10
PR

DB 13; Length 440;

94.3%; Score 417;

Query Match

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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Godowski, Paul
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gorney, Austin L.
APPLICANT: Ban, Jame
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Zhang, Zemin I.
APPLICANT: Zhang, Zemin I.
APPLICANT: Zhang, Zemin I.
APPLICANT: Alang, Zemin I.
APPLICANTON: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RIC104
CURRENT APPLICATION NUMBER: US/10/176, 758
CURRENT APPLICATION EMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 146 NIMIDIQKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 264 TCEAIGKPQPVMVTWYRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 146 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 144 NLMIDIQXDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 266 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 PAMLCLIIILGRYFARHKGTYFTHEAKGADDAADAAINAEGGGNNSEEKKEYFI 440
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 86 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 FRDFRPLKDSRFQLLNPSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHI QMTYPLQGLTREGDALEL
 26 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
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 Length 440;
 Indels
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 14;
 94.3%; bcc...
100.0%; Pred. No. c,
... 0; Mismatches
 Score 417; DB
Pred. No. 0;
 ; Sequence 34, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
 Query Match
Best Local Similarity 100.0
Matches 417; Conservative
 APPLICANT: Baker, Kevin P.
 ORGANISM: Homo Sapien
US-10-176-758-34
 US-10-176-758-34
 LENGTH: 440
 SEQ ID NO 34
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 APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Garney, Austin L.
APPLICANT: San, James
APPLICANT: San, James
APPLICANT: Smith, Victoria
APPLICANT: Wood, William I.
APPLICANT: Tang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: US/10/174,590
CURRENT APPLICATION NUMBER: 2002-06-18
 FRDFRPLADSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDFPQGESYTTITVLVPPR 143
 FRDFRPLKDSRFQLLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 NLMIDIQKDTAVEGERIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNINKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTT388AGEEGSIRAVDHAVIGGVVAVVV 385
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 24 LRILILIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEEKKEYFI 442
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVIQLLNPNRQTIY
 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 Gaps
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0
 DB 14; Length 440;
 0; Indels
 0; Indels
 Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
 tch 94.3%; Score 417; DB sal Similarity 100.0%; Pred. No. 0; 417; Conservative 0; Mismatches
 Pred. No. 0;
Mismatches
 ; Sequence 34, Application US/10174590; Publication No. US20030008352A1; GENERAL INFORMATION:
100.0%; Pre-
 417; Conservative
 APPLICANT: Baker, Kevin P.
 TYPE: PRT
ORGANISM: Homo Sapien
 Best Local Similarity
Matches 417; Conserv
 US-10-174-590-34
 Query Match
Best Local S
Matches 417
 98
 84
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 326
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 SEQ ID NO 34
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APPLICANT:
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APPLICANT:
 Sequence 34, Application US/10175737
Publication No. US20030013153A1
GENERAL INFORMATION:
JAPPLICANT: Desnoyers, Luc
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godweki, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Shing, Zemin
TITLE OF INVENTION: SCRETEB AND TRANSMEMBRANE POLYPEPTIDES AND NUCLBIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT PILICATION NUMBER: US/10/175,737
CURRENT PILICATION TEMORY - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 84 FRDFRPLKDSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL 265
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 83
 FAMLCLIIIGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 440
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 24 LRILILIESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 ö
 94.3%; Score 417; DB 14; Length 440; 100.0%; Pred. No. 0; Nismatches 0; Indels
 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
 RESULT 36
US-10-175-737-34
 US-10-175-737-34
 SEQ ID NO 34
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RESULT 37

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Sequence 34, Application 10/10174581

Publication No. US20030017540A1

APPLICANT: BAREA. KWA'IN P.

APPLICANT: BAREA. AND TRANSHERANE POLIPPETIDES AND WOLEIC

TITLE BY BERNER. DAYLORGE RICOLIN THE SAME

TITLE BY APPLICANTON WINSER: 10/10174.581

TITLE BY APPLICANTON WINSER: 10/10174.581

TRID BY APPLICANTON WINSER: 10/102586

PRIOR PELING DAYE: JOJO-06-18

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; PRIOR APPLICATION NUMBER: 60/087827

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R FILING DATE: 1998-03-27

R APPLICATION NUMBER: 60/079786

R FILING DATE: 1998-03-27

R APPLICATION NUMBER: 60/080107

R FILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080194

R APPLICATION NUMBER: 60/080194

R APPLICATION NUMBER: 60/080337

R FILING DATE: 1998-04-01

R APPLICATION NUMBER: 60/080333

R FILING DATE: 1998-04-01

R APPLICATION NUMBER: 60/080333

R APPLICATION NUMBER: 60/080333

R FILING DATE: 1998-04-01
 RAPPLICATION NUMBER: 60/08582
R FILING DATE: 1998-05-15
R FILING DATE: 1998-05-15
R FILING DATE: 1998-05-15
R APPLICATION NUMBER: 60/086023
R APPLICATION NUMBER: 60/086023
R APPLICATION NUMBER: 60/086392
R FILING DATE: 1998-05-18
R FILING DATE: 1998-05-22
R APPLICATION NUMBER: 60/086486
R FILING DATE: 1998-05-22
R APPLICATION NUMBER: 60/087098
R FILING DATE: 1998-05-28
R APPLICATION NUMBER: 60/087098
R FILING DATE: 1998-06-28
R APPLICATION NUMBER: 60/087609
R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087609
R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087609
R FILING DATE: 1998-06-02
 R FILING DATE: 1998-05-06
R APPLICATION NUMBER: 60/084639
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084640
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084643
R FILING DATE: 1998-05-07
 FILING DATE: 1998-04-08
APPLICATION UNMBER: 60/081195
FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081838
 APPLICATION NUMBER: 60/082569
FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704
 FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
 APPLICATION NUMBER: 60/085573
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079664
 APPLICATION NUMBER: 60/081070
 FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21
 FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
 APPLICATION NUMBER: 60/083495
FILING DATE: 1998-04-29
 FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083499
FILING DATE: 1998-04-29
 APPLICATION NUMBER: 60/084414
 FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085580
FILING DATE: 1998-05-15
 FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082797
 APPLICATION NUMBER: 60/083496
 APPLICATION NUMBER: 60/083559
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|---|------|---------|------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
|   |      | FAIOR   | FILLING DAILS: 1998-0  | 20000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     |
|   | ٠. ٠ | A CLOS  |                        | NUMBER: 60/088025<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     |
| _ | - •  | PRIOR   |                        | : 1230-00-01<br>: NIMBER: 60/088028                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |     |
|   | ٠.   | PRIOR   |                        | FILING DATE: 1998-06-04                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |     |
|   | •    | PRIOR   |                        | NUMBER: 60/088029                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
|   | • •  | PRIOR   |                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |
|   | • •- | PRIOR   |                        | NUMBER: 60/088033                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
|   | •-   | PRIOR   |                        | 1: 1998-06-04                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |     |
|   | ••   | PRIOR   |                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |
|   | ••   | PRIOR   |                        | : 1998-06-05                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |     |
|   | ••   | PRIOR   |                        | NUMBER: 60/088202                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
|   |      | PRICK   |                        | FILING DATE: 1998-06-05                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |     |
|   | •    | PRIOR   |                        | · ·                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |     |
|   |      | PRIOR   | APPLICATION            | NUMBER: 60/088217                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
|   |      | PRIOR   | FILING DATE            | : 1998-06-05                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |     |
|   | ٠-   | PRIOR   | APPLICATION            | APPLICATION NUMBER: 60/088326                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |     |
|   | -    | PRIOR   |                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |
|   | •-   | PRIOR   |                        | NUMBER: 60/088655                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
|   |      | PRIOR   |                        | 60-5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |     |
|   | •-   | PRIOR   |                        | NUMBER: 60/088722                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
|   | •    | A CLOS  | ADDITONATION NUMBER 60 | 70007                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     |
|   | ٠. ٠ | DETOG   |                        | 7 088 / 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |     |
|   | - •  | PRIOR   |                        | : 1336-06-10<br>  NIMBER: 60/088740                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |     |
| _ | • •• | PRIOR   |                        | FILING DATE: 1998-06-10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |     |
|   |      | PRIOR   |                        | APPLICATION NUMBER: 60/088811                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |     |
|   | •-   | PRIOR   |                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |
|   | •-   | PRIOR   |                        | APPLICATION NUMBER: 60/088824                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |     |
| _ | •-   | PRIOR   |                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |
|   | •- • | PRICK   |                        | APPLICATION NUMBER: 60/088825                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |     |
| _ | •- • | A 5     |                        | :: TYYB=U=-0-1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |
|   | ٠. ٠ | PRIOR   |                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |
| _ | - •  | PRIOR   |                        | :: 1338-06-10<br>  MTMREP: 60/08861                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |     |
|   | - •  | PRIOR   |                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |
|   | ٠.   | PRIOR   |                        | NUMBER: 60/08863                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |     |
|   |      | PRIOR   |                        | 6-11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |     |
|   | ••   | PRIOR   | APPLIC                 | NUMBER: 60/088876                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
|   | ••   | PRIOR   | FILING DATE: 1998-0    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |
|   | ٠. ٠ | PRIOR   |                        | NUMBER: 60/089090                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
|   | ••   | PRIOR   | APPLICA                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |
|   | ٠.   | PRIOR   |                        | DATE: 1998-06-12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |     |
|   |      | PRIOR   |                        | NUMBER: 60/089512                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
|   | •-   | PRIOR   | FILING DATE:           | 6-16                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |     |
|   | •-   | PRIOR   | APPLICATION NUMBER:    | NUMBER: 60/089514                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
|   | ٠. ٠ | PRIOR   | PILING DATE:           | DATE: 1998-06-16<br>TION NUMBED: 60/089538                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |     |
|   | - •  | PRIOR   | FILING DATE:           | FILING DATE: 1998-06-17                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |     |
|   |      | PRIOR   |                        | NUMBER: 60/089598                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
|   | •    | PRIOR   |                        | 7,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |     |
|   | •-   | PKIOK   |                        | NOMBER: 60/089653                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
|   |      | Query N | Match                  | 94.3%; Score 417;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
|   |      | Matches | al Sımı<br>417:        | 100.0%;<br>vative                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 0   |
|   |      |         |                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |
|   | ò    |         | 26 LRLLLLI             | LRILILILESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY E                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 82  |
| _ | Ω    |         | 24 LRLLLL              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 83  |
|   | δ    |         | 86 FRDFRPI             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 145 |
|   | 7    |         |                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |
|   | đ    |         | 84 FRDFRPI             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 143 |
|   | ò    |         | 146 NLMIDIC            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 205 |
|   | ź    |         | TOTAL VAL              | NI WID OKUMAN SKBATTI BENEKCATTI KOKSBATTI BENEKCATTI | 503 |
|   | 3    | _       | אומזויייט גגו          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |
| _ | ò    |         | 206 MLKVHK             | 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 265 |

| Qy 386 FAMLCLLIILGRYPARHKGTYFTHEAKGADDAADTAIINAEGGONNSEEKKEYPI 442  Db 384 FAMLCLLIILGRYPARHKGTYFTHEAKGADDAADDTAIINAEGGONNSEEKKEYPI 440  RESULT 39  US-10-176-149-34  Sequence 34, Application US/10176749  Publication No. US20030017542A1  GENERAL INFORMATION:  APPLICANT: Baker, Kevin P.  APPLICANT: Chen, Jian  APPLICANT: Chen, Jian  APPLICANT: Goddard, Pudce  APPLICANT: G | APPLICANT: Gurney, Austin L. APPLICANT: Ban, James APPLICANT: Ban, James APPLICANT: Matanabe, Colin K. APPLICANT: Watanabe, Colin K. APPLICANT: Wood, William I. APPLICANT: Zhang, Zemin I. TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1076 CURRENT APPLICATION NUMBER: US/10/176,749 CURRENT PILING DATE: 2002-06-20 FILE REFERENCE: SEQ ID NOS: 612 SEQ ID NO 34 LENGTH: 440 TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT COGNANISM: Homo Sapien US-10-176-749-34                                           | Query Match  Best Local Similarity 100.0%; Pred. No. 0,  Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 26 LRILLLERSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 85  Db 24 LRILLLERSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83  Qy 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145  Db 24 LRILLLERSAAALIPTGDGQNLFTKDVTVINTSSDEGRYFCQLYTDPPQESYTTITVLVPPR 145  Db 24 LRILLLERSAAALIPTGDGQNLFTKNSTTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145 | 146 NIMIDIOKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDNYTVTSQL 1141 NIMIDIOKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDNYTVTSQL 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL                                                                                                                                                      | QY         266 TCEALGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325           Db         264 TCEALGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323           QY         326 YMLYVYDPPTTIPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | Qy 386 FAMLCLLIILGRYPARHKGTYFTHEAKGADDAADDTALINAEGGONNSEEKKEYF1 442                                                                                                                                                                                                                                                                                    |
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| Db 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263  Qy 266 TCEALGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNINKTDNGTYRCEASNIVGKAHSD 325  Db 264 TCEALGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNINKTDNGTYRCEASNIVGKAHSD 323  Qy 326 YMLYVDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | RESULT 38 US-10-176-483-34 i Sequence 34, Application US/10176483 i Publication No. US20030017541A1 general INFORMATION: US20030017541A1 general INFORMATION: Desnoyers, Luc h APPLICANT: Desnoyers, Luc h APPLICANT: Goddard, Audrey h APPLICANT: Godowski, Paul J. h APPLICANT: Gurney, Austin L. h APPLICANT: Smith, Victoria h APPLICANT: Smith, Victoria h APPLICANT: Wood, William I. h APPLICANT: Wood, William I. h APPLICANT: Anang, Zemin K. h APPLICANT: Anang, Zemin K. h APPLICANT: Anang, Zemin K. h APPLICANT: Anang, Zemin I. h APPLICANT: Alang, Zemin I. h APPLICANT: Alang, Zemin I. | ; TITLE OF INVEXTION: ACIDS ENCODING THE SAME; FILE REFERENCE: P3430R1C68; CURRENT APPLICATION NUMBER: US/10/176,483; CURRENT APPLICATION NUMBER: US/2002-06-20; Prior application removed - See File Wrapper or Palm; NUMBER OF SEQ ID NOS: 612; SEQ ID NO 34; LANGTH: 440; TYPE: PRT; ORGANISM: Homo Sapien; US-10-176-483-34                                                                                                                                                                                                                               | Query Match  94.3%; Score 417; DB 14; Length 440;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps  26 IRLLLLESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLANPNRQTIY  24 IRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLANPNRQTIY  25 IRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY | 86 FRDFRPLKOSRFOLLNFSSSELKVSLTNVSISDEGRYFCOLYTDPPOGESYTTITVLVPPR                                                                                                                                                                                 | Oy 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265  Db 204 MLKVHKEDDGVPVICQVEHPAVTGNLGTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263  Co 266 TCEAIGKPQPVMYTWVRVDDEMPQHAVLSGPNLFINNLMKTDNGTYRCEASNIVGKAHSD 325  Co 326 TCEAIGKPQPVMTWVRVDDEMPQHAVLSGPNLFINNLMKTDNGTYRCEASNIVGKAHSD 323  Co 326 XMLXVYDPPTTPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT |

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86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT3388
 324 YMLYVYDPPTTIPPPTTTTTTTTTTTTTLTITDSRAGEEGSIRAVDHAVIGGVVAVVV 383
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 384 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADAADTAIINAEGGQNNSEEKKEYFI 440
 386 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 144 NLMIDIQKDTAVEGEBIEVNCTAMASKPATTIRWFKGNTELKGKSEVEBWSDMYTVTSQL
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
 APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C7
CURRENT APPLICATION NUMBER: US/10/173,706
CURRENT PILING DATE: 2002-06-17
PPIOR APPLICATION TEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
ILENGTH: 440
TYPE: PRT
CURRENT HOMO Sapien
US-10-173-706-34
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 24 LRILILIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 Query Match 94.3%; Score 417; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches 0; Indels (
 or Palm
 FILE REFERENCE: P3430R1C110
CURRENT APPLICATION NUMBER: US/10/176,915
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper NUMBER OF SEQ ID NOS: 612
LENGTH: 440
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 Sequence 34, Application US/10173706; Publication No. US20030022293A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 TYPE: PRT
CORGANISM: Homo Sapien
US-10-176-915-34
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 APPLICANT:
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 NLMIDIQKDTAVEGEBIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL 263
 96 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 85
 24 LRILILILERSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY 83
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 Gaps
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 DB 14; Length 440;
 0; Indels
 94.3%; Score 417; DB 100.0%; Pred. No. 0; ive 0; Mismatches
 Sequence 34, Application US/10176915; Publication No. US20030017544A1; GENERAL INFORMATION: APPLICANT: Baker.Kevin P. APPLICANT: Chen, Jian
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
 Watanabe, Colin K. Wood, William I.
 Gurney, Austin L.
 Matches 417; Conservative
 Pan, James
Smith, Victoria
 TYPE: PRT
ORGANISM: Homo Sapien
 Chen, Jian
 Query Match
Best Local Similarity
 US-10-176-914-34
 RESULT 41
US-10-176-915-34
 APPLICANT:
APPLICANT:
APPLICANT:
 146
 206
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MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTLTITDSRAGEBGSIRAVDHAVIGGVVAVVV 385
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 144 NIMIDIQKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 144 NIMIDIQXOTAVEGEEIEVNCTAMASKPATTIRMFKGNTELKGKSEVEEWSDMYTVTSQL
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 APPLICANT: Watenabe, Colin K.
APPLICANT: Watenabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemn I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPRENCE: P3430R1C60
CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
 24 IRILILIPSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 0; Gaps
 Length 440;
 Indels
 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 ö
 Query Match 94.3%; Score 417; DB 14; Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches 0;
 ; Sequence 34, Application US/10175752; Publication No. US20030022295A1; GENERAL INFORMATION:
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Desmoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ORGANISM: Homo Sapien
 RESULT 44
US-10-175-752-34
 LENGTH: 440
 US-10-175-752-34
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 APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Alang Zemin
ITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITLE OF INVENTION: ACIDE ENCODING THE SAME
FILE REPERENCE: P3430R1C45
CURRENT PILING DATE: 2002-06-19
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 145
 205
 265
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTBEEGSIRAVDHAVIGGVVAVVV 383
 24 LRILLILPSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY 83
 83
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 LRILLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
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 Length 440;
 DB 14; Length 440;
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 94.3%; Score ...,
100.0%; Pred. No. 0;
tive 0; Mismatches
 94.3%; Score 417; DB
100.0%; Pred. No. 0;
iive 0; Mismatches
 Sequence 34, Application US/10175738
Publication No. US203002294A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
 al Similarity 100.
417; Conservative
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
 US-10-175-738-34
 SEQ ID NO 34
 204
 326
 98
 84
 206
 266
 264
 324
 386
 384
 26
 86
 146
 Query Match
Best Local (
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 APPLICANT: Gurney, Austin L.
APPLICANT: Ban, James
APPLICANT: Ban, James
APPLICANT: Ban, James
APPLICANT: Matanabe, Colin K.
APPLICANT: Wacanabe, Colin K.
APPLICANT: Wacanabe, Colin K.
APPLICANT: Applicant: Zhang, Zemin
ITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C70
CURRENT APPLICATION NUMBER: US/10/176,482
CURRENT APPLICATION NUMBER: US/10/176,482
CURRENT APPLICATION TEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NOS: 612
 ö
264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT3385
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 144 NLMIDIQKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 83
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 PAMLCLIILGRYFARHKGTYFTHEAKGADDAADADATAIINAEGGQNNSEEKKEYFI 440
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADDTAIINAEGGONNSEEKKEYFI 442
 24 LRILLILESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 ;
0
 DB 14; Length 440;
 0; Indels
 94.3%; Score 417; DB
100.0%; Pred. No. 0;
tive 0; Mismatches
 ; Sequence 34, Application US/10176482; Publication No. US20030022296A1; GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers Luc
APPLICANT: Goddard, Audrey;
APPLICANT: Goddwski, Paul J.
 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-482-34
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 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTT3388
 203
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPWVYTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 324 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 383
 83
 HTLE OF INVENTION. SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P34-30R1C66 CURRENT APPLICATION NUMBER: US/10/176,757 CURRENT FILING DATE: 2002-06-20 FILE WIRDER OF SEQ ID NOS: 612 SEQ ID NOS: 612 SEQ ID NOS: 612 LENGTH-
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 146 NLMIDIQKDTAVEGEBIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 24 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 ö
 Ouery Match 94.3%; Score 417; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches 0; Indels 0
 Sequence 34, Application US/10176913
Fublication No. US20030022298A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Genovers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.
Sequence 34, Application US/10176757; Publication No. US20030022297A1; GENERAL INFORMATION:
 APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-757-34
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Prior Application removed
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
TYPE: PRT
 Zhang, Zemin
 , ORGANISM: Homo Sapien
US-10-180-552-34
 ORGANISM: Homo Sapien
 US-10-180-557-34
 US-10-180-557-34
 LENGTH: 440
TYPE: PRT
 APPLICANT:
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APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Anny-Zemin
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITILE OF INVENTION: ALIDE BNCODING THE SAME
FILE REFERENCE: P3430R1C66
CURRENT APPLICATION NUMBER: US/10/176, 913
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: AND
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 145
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 MIKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 82
 83
 FAMLCLLILLGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 FAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLLNPNRQTI Y
 Gaps
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 DB 14; Length 440;
 0; Indels
 94.3%; Score 417; DB
100.0%; Pred. No. 0;
:ive 0; Mismatches
 Best Local Similarity 100.
Matches 417; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-913-34
 RESULT 48
US-10-180-552-34
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 145
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 205
 265
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL 263
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 83
 442
 384 FAMLCLLIIIGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 440
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIBGEVATISCQVNKSDDSVIQLLNPNRQTIY
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P3430FIC147
CURRENT APPLICATION NUMBER: 105/10/180,557
CURRENT FILING DATE: 2002-06-25
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 Gaps
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI
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 Query Match 94.3%; Score 417; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches 0; Indels
 Length 440;
 Indels
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
- See File Wrapper or Palm
 ö
 Query Match 94.3%; Score 417; DB 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0;
 Sequence 34, Application US/10180557
Publication No. US20030022301A1
GENERAL INFORMATION:
 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Godowski, Paul J.
 Gurney, Austin L.
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
ORGANISM: Homo Sapien
 US-10-174-572-34
 APPLICANT:
APPLICANT:
APPLICANT:
 326
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 APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Coddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Wood, William I.
APPLICANT: Ananabe, Colin K.
APPLICANT: All Second Secreted and TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDE ENCODING THE SAME
FILE REFERENCE: P3430R1C14
CURRENT APPLICATION NUMBER: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRNPKGNTELKGKSEVEEWSDMYTVTSQL 203
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 83
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 85
 83
 442
 24 LRILILIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
LRLLLLLFSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLLNPNRQTI Y
 Gaps
 FAMLCLLI ILGRYFARHKGTYFTHEAKGADDAADADTAI INAEGGONNSEEKKEYFI
 ô
 DB 14; Length 440;
 0; Indels
 94.3%; Score 417; DE 100.0%; Pred. No. 0; ive 0; Mismatches
 Sequence 34, Application US/10173700; Publication No. US20030027262A1; GENERAL INFORMATION:
 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ; ORGANISM: Homo Sapien
US-10-173-700-34
 96
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 SEQ ID NO 34
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APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Shang, Zemin I.
APPLICANT: Shang, Zemin I.
APPLICANT: Shang, Zemin I.
APPLICANT: Color SEGRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITTLE OF INVENTION: SEGRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC CURRENT APPLICATION NUMBER: US/10/174,572
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEG ID NOS: 612
SEQ ID NO 34
TWATTLE ALAD
 325
 145
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 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTT338AGEEGSIRAVDHAVIGGVVAVVV 385
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 MIKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 264 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 82
 83
 442
 440
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
 264 TCEAIGKPQPVWVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 NLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHI QMTYPLQGLTREGDALEL
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 24 LRILILIESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
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 94.3%; Score 417; DB 14; Length 440;
 0; Indels
 0; Mismatches
 Pred. No
 Sequence 34, Application US/10174572; Publication No. US20030027263A1; GENERAL INFORMATION:
 Best_Local Similarity 100.0%;
Matches 417; Conservative 0
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Publication No. US20030027265A1
 RESULT 54
US-10-174-588-34
 SEQ ID NO 34
LENGTH: 440
 386
 APPLICANT:
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 APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Swith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin I.
APPLICANT: Zhang, Zemin I.
APPLICANT: APPLICATION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND CURRENT APPLICATION NUMBER: US/10/174,579
CURRENT APPLICATION NUMBER: US/10/174,579
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTŢIPPPTŢTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 83
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 24 LRILLILESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 26 LRLLLLLFSAAALIPTGDGQNLFTXDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 ö
 DB 14; Length 440;
 0; Indels
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 94.3%; Score 417; DE ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
 ; Sequence 34, Application US/10174579; Publication No. US20030027264A1; GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-579-34
 Similarity
 RESULT 52
US-10-174-579-34
 417;
 Query Match
Best Local S:
Matches 417,
 386
 98
 204
 324
 386
 146
 206
 266
 264
 326
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RESULT 53 US-10-174-582-34 ; Sequence 34, Application US/10174582

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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Zhang, Zemin
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBNCE: P3430R1C36
CURRENT APPLICATION NUMBER: US/10/174,582
CURRENT FILING DATE: 2002-06-18
Frior Application removed - See File Wrapper or Palm
NUMBER: OF SEQ ID NOS: 612
 145
 205
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 265
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRXLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 264 TCEAIGKPQPVMVTMVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 82
 83
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 384 FAMLCLIIILGRYFARHKGTYFTHEAKGADDAADADIAIINAEGGONNSEEKKEYFI 440
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 24 LRILLILFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 Gaps
 ó
 Query Match 94.3%; Score 417; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches 0; Indels
 Sequence 34, Application US/10174588; Publication No. US20030027266A1; GENERAL INFORMATION:
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Pan, James
Smith, Victoria
Watanabe, Colin K.
 Godowski, Paul J.
Gurney, Austin L.
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc APPLICANT: Goddard, Audre
APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ORGANISM: Homo Sapien US-10-174-582-34
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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us-10-622-237-2.oligo.rapb

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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-739-34
 JS-10-175-740-34
 SEQ ID NO 34
 326
 84
 146
 206
 566
 386
 384
 APPLICANT:
APPLICANT:
 APPLICANT:
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 PRDPRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 203
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT3385
 83
 384 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
APPLICANT: Wood, william I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ALIDS ENCODING THE SAME
FILE REPERENCE: P3430RLC28
CURRENT APPLICATION NUMBER: US/10/174,588
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NOS: 612
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Chang, Zemin I.
APPLICANT: Chang, Zemin I.
APPLICANT: Chang, Zemin I.
APPLICANT: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/175,739
CURRENT FILING DATE: 2002-06-19
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 24 LRLILLIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 ö
 DB 14; Length 440;
 0; Indels
 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
 94.3%; Score 417; DB 100.0%; Pred. No. 0; ive 0; Mismatches
 Sequence 34, Application US/10175739; Publication No. US20030027267A1; GENERAL INFORMATION:
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Best Local Similarity 100.
Matches 417; Conservative
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
) ORGANISM: Homo Sapien
US-10-174-588-34
 98
 146
 264
 TYPE: PRT
 84
 206
 266
 326
 386
 Query Match
 APPLICANT:
APPLICANT:
APPLICANT:
 LENGTH:
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YMLYVYDPPTTIPPPTTTTTTTTTTTTTLTILTIDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKKGNTELKGKSEVEEWSDMYTVTSQL 203
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 82
 83
 83
 APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERBNCE: 1943OR1C61
CURRENT APPLICATION NUMBER: US/10/175,740
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 26 IRLILLIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
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 94.3%; Score 417; DB 14; Length 440; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels (
 14; Length 440;
 Indels
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Query Match 94.3%; Score 417; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
 Sequence 34, Application US/10175740 Publication No. US20030027268A1 GENERAL INFORMATION:
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Godowski, Paul J.
Gurney, Austin L.
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddweki, Paul J
APPLICANT: Gutney, Austin L
APPLICANT: Pan, James
 Goddard, Audrey
 ; ORGANISM: Homo Sapien
US-10-175-740-34
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R FILING DATE: 1997-11-24

R APPLICATION NUMBER: 60/069335

R FILING DATE: 1997-12-11

R FILING DATE: 1997-12-12

R APPLICATION NUMBER: 60/069425

R APPLICATION NUMBER: 60/069870

R FILING DATE: 1997-12-17

R APPLICATION NUMBER: 60/06917

R FILING DATE: 1997-12-18

R APPLICATION NUMBER: 60/068017

R APPLICATION NUMBER: 60/068017
 R FILING DATE: 1998-03-10
R APPLICATION NUMBER: 60/077632
R APPLICATION NUMBER: 60/077649
R APPLICATION NUMBER: 60/077649
R FILING DATE: 1998-03-11
R APPLICATION NUMBER: 60/078886
R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/078993
 R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080194
R APPLICATION NUMBER: 60/080327
R APPLICATION NUMBER: 60/080327
R FILING DATE: 1998-04-01
R FILING DATE: 1998-04-01
R FILING DATE: 1998-04-01
R FILING DATE: 1998-04-01
 R FILING DATE: 1998-04-15
R APPLICATION NUMBER: 60/082568
R FILING DATE: 1998-04-21
R APPLICATION NUMBER: 60/08269
R FILING DATE: 1998-04-21
R FILING DATE: 1998-04-22
R FILING DATE: 1998-04-22
R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION UNMERS: 60/083499
PRIOR PILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR PILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084366
PRIOR PILING DATE: 1998-05-05
 R FILING DATE: 1998-04-08

R APPLICATION NUMBER: 60/081070

R FILING DATE: 1998-04-08

R APPLICATION NUMBER: 60/081195

R APPLICATION NUMBER: 60/081838
 PRIOR APPLICATION NUMBER: 60/084414 PRIOR FILING DATE: 1998-05-06 PRIOR APPLICATION NUMBER: 60/084639 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084640
 FILING DATE: 1998-04-28
APPLICATION WINBER: 60/083495
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083496
 FILING DATE: 1997-11-21
APPLICATION UNDRER: 60/066466
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/066772
 PILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/080107
 FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/083322
APPLICATION NUMBER: 60/064103
 FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/065311
 FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066120
 FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079664
 Sequence 34, Application US/1017543

Sequence 34, Application US/1017543

GENERAL INPOMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Andrey
APPLICANTION NUMBER: GO/G05263
PRIOR FILING DATE: 1007-00-18
PRIOR FILING DATE: 1007-00-18
PRIOR FILING DATE: 1007-00-18
PRIOR PRILING DATE: 1007-10-18
PRIOR FILING DATE: 1007-10-18
PRIOR FILING DATE: 1007-10-18
PRIOR FILING DATE: 1007-10-28
PRIOR APPLICATION NUMBER: GO/G05364
PRIOR FILING DATE: 1007-10-29
PRIOR APPLICATION NUMBER: GO/G05364
PRIOR FILING DATE: 1007-10-21
PRIOR PRILING DATE: 1007-10-21
PRIOR APPLICANTON NUMBER: GO/G05364
PRIOR PRILING DATE: 1007-10-21
PRIOR APPLICATION NUMBER: GO/G05364
PRIOR PRILING DATE: 1007-10-21
PRIOR PRILING DATE: 1007-10-21
PRIOR PRILING DATE: 1007-10-21
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTT388GEEGSIRAVDHAVIGGVVAVVV 385
 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADDTAIINAEGGONNSEEKKEYFI 440
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
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205
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 203
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 83
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 440
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P343.0RTC119
CURRENT APPLICATION NUMBER: US/10/176,488
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
EBNGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 NLMIDIOKOTAVEGELIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 26 LRILLILLESAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 ;
0
 DB 14; Length 440;
 Indels
 ö
 Query Match
94.3%; Score 417; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches
 PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR PLING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
 Sequence 34, Application US/10176488
Publication No. US20030027271A1
GENERAL INFORMATION:
APPLICATION NUMBER: 60/089512
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William I.
 Zhang, Zemin
 JS-10-176-488-34
 US-10-176-488-34
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94.3%; Score 417; DB 14; Length 440;

Query Match

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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Ban, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: ALONG, William I.
APPLICANT: Zhang, Zemin
ITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITLE OF INVENTION: ACIDE ENCODING THE SAME
ITLE OF INVENTION: ACIDE ENCODING THE SAME
FILE REFERENCE: P3430R1C92
CURRENT APPLICATION NUMBER: US/10/176,747
CURRENT APPLICATION NUMBER: US/10/176,747
CURRENT APPLICATION NUMBER: See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNINKTDNGTYRCEASNIVGKAHSD 323
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 266 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 384 FAMLCLIIIGRYFARHKGTYFTHEAKGADDAADDAINAEGGQNNSEEKKEYFI 440
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 84 FRDFRPLKDSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 144 NLMIDIQXDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 24 LRILLILFSAAALIPTGGGONLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 NLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 ;
 Query Match 94.3%; Score 417; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches 0; Indels
 Sequence 34, Application US/10176747
Publication No. US20030027273A1
GENERAL INFORMATION:
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ORGANISM: Homo Sapien
 US-10-176-747-34
 US-10-176-747-34
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 206
 APPLICANT:
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 APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Alang, Zemin
TITLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3440RICL07
CURRENT APPLICATION NUMBER: US/10/176, 492
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 NEMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
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 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 TCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 82
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 83
 442
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNDNRQTIY
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 LRITITI FSAAALI PTGDGONLFTKDVTVI EGEVATI SCOVNKSDDSVI OLLNPNROTI Y
 LRILLILFSAAALI PTGDGONLFTKDVTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIY
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVIQLLNPNRQTIY
 Gaps
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 FAMLCLLI ILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI
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 DB 14; Length 440;
 0; Indels
 0; Indels
 Query Match
94.3%; Score 417; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches
100.0%; Pred. No. 0;
ive 0; Mismatches
 ; Sequence 34, Application US/10176492; Publication No. US20030027272A1; GENERAL INFORMATION:
 Matches 417; Conservative
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Desnoyers, Luc
 TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-492-34
 Best Local Similarity
 SEQ ID NO 34
 96
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 APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Ban, James
APPLICANT: Smith, Victoria
APPLICANT: Wood, William I.
APPLICANT: APPLICANT: Scain
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED
TITLE REFERENCE: P3439NICLO3
TITLE REFERENCE: P3439NICLO3
CURRENT APPLICATION NUMBER: US/10/176,750
CURRENT FILING DATE: 2002-06-21
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 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADDAAJINAEGGGONNSEEKKEYFI
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 DB 14; Length 440;
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 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
 Query Match 94.3%; Score 417; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
 ; Sequence 34, Application US/10176750; Publication No. US20030027274A1; GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-750-34
 US-10-176-750-34
 SEQ ID NO 34
 266
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goodwafi, Paul J.
APPLICANT: Goodwafi, Paul J.
APPLICANT: Goodwafi, Paul J.
APPLICANT: Garney, Austin L.
APPLICANT: Garney, Austin L.
APPLICANT: Watanabe, Colin-K.
APPLICANT: Watanabe, Colin-K.
APPLICANT: Wood, William I.
APPLICANT: Bang, Zemin ACIDS ENCODING THE SAME
FILE REFERENCE: Pal30R1C99
CURRENT APPLICATION NUMBER: US/10/176,985
CURRENT FILING DATE: 2002-06-21
Frior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
EBNOTH: 440
TYPE: PRT
TTYLE PRESENCE: DATE: Consense
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 266 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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 83
 PAMLCLLI ILGRYFARHKGTYFTHEAKGADDAADAAI INAEGGONNSEEKKEYFI 440
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 24 LRILILIFSAAALIPTGDGQNLFTKOVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
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 DB 14; Length 440;
 Indels
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 Query Match 94.3%; Score 417; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
 ; Sequence 34, Application US/10176987; Publication No. US20030027278A1; GENERAL INFORMATION:
Sequence 34, Application US/10176985 Publication No. US20030027277A1
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
 GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
 ; ORGANISM: Homo Sapien
US-10-176-985-34
 US-10-176-987-34
 326
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US-10-176-993-34
; Sequence 34, Application US/10176993
; Publication No. US20030027280A1
; GENERAL INFORMATION:
; APPLICANT: Baker Kevin P.
; APPLICANT: Chen, Jian
 APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 TYPE: PRT
ORGANISM: Homo Sapien
 US-10-176-992-34
 US-10-176-993-34
 APPLICANT:
APPLICANT:
 SEQ ID NO 34
SEQ ID NO 34
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 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
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 TCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTLTIITDSRAGEEGSIRAVDHAVIGGVVAVVV 383
 83
 APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: APOLYPEPTIDES AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: RECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENT PAPLICATION NUMBER: US/10/176,987
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 24 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C100
CURRENT APPLICANTION NUMBER: US/10/176,992
CURRENT PILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
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 Length 440;
 0; Indels
 14;
 <u>18</u>
 94.3%; Score 417; DB 100.0%; Pred. No. 0; ive 0; Mismatches
 ; Sequence 34, Application US/10176992; Publication No. US20030027279A1; GENERAL INFORMATION:
 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
CORGANISM: Homo Sapien
US-10-176-987-34
 324
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 APPLICANT:
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 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNINKTDNGTYRCEASNIVGKAHSD 323
 82
 83
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
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 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
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 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C89
CURRENT APPLICATION NUMBER: US/10/176,993
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 Query Match
94.3%; Score 417; DB 14; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0; Indels
 DB 14; Length 440;
 Indels
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Query Match
94.3%; Score 417; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches
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Sequence 34, Application US/10176991; Publication No. US20030027324A1; GENERAL INFORMATION:
 Query Match
Best Local Similarity 100.0
Matches 417; Conservative
 APPLICANT: Baker, Kevin P.
 LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
 US-10-176-991-34
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 APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Goddard, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Ban, James
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Matanabe, Colin K.
APPLICANT: Arang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDE ENCODING THE SAME
FILE REFERENCE: P3430R1C226
CURRENT APPLICATION NUMBER: US/10/184,658
CURRENT APPLICATION NUMBER: US/10/184,658
CURRENT APPLICATION NUMBER: US/2002-06-28
FILE APPLICATION NUMBER: US/2003-06-28
SPIOT APPLICATION NUMBER: US/2003-06-28
SPIOT APPLICATION NUMBER: US/2003-06-28
SPIOT APPLICATION NUMBER: US/2003-06-28
SPIOT NO 34
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 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 NIMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
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 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTLTISRAGEEGSIRAVDHAVIGGVVAVVV 385
 24 LRILLLESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY 83
 FAMLCLIIILGRYFARHKGTYFTHBAKGADDAADDTAIINAEGGONNSEEKKEYFI 442
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 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 ó
 Length 440;
 0; Indels
 DB 14;
 94.3%; Score 417; DB 100.0%; Pred. No. 0; cive 0; Mismatches
 ; Sequence 34, Application US/10184658; Publication No. US20030027281A1; GENERAL INFORMATION:
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
 TYPE: PRT
ORGANISM: Homo Sapien
 US-10-184-658-34
 US-10-184-658-34
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
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APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Aughin L.
APPLICANT: Gurney, Aughin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: APPLICANT: ALT STANGY Zenin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PASSORICALZ
CURRENT APPLICATION NUMBER: US/10/176,991
CURRENT PILLING DATE: 2002-06-21
CURRENT PILLING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
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205
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 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
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 83
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
 24 LRILILILFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 26 LRLLLLLFSAAALI PTGDGQNLFTKDVTVIEGEVATI SCQVNKSDDSVIQLLNPNRGTIY
 Gaps
 FAMLCLI I I GRY FARHKGTY FTHEAKGADDAADADTAI I NAEGGONNSEEKKEY FI
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 DB 14; Length 440;
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 94.3%; Score 417; DB 100.0%; Pred. No. 0; ive 0; Mismatches
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Baker, Kevin P.

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 Sequence 34, Application US/10173695
; Sequence 34, Application US/10173695
; Publication No. US2030032101A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Goddard, Audrest, Lo.
; APPLICANT: Goddard, Audrest, Lo.
; APPLICANT: Goddard, Audrest, Lo.
; APPLICANT: Godwski, Paul J.
; APPLICANT: Smith, Victoria
; APPLICANT: Matenabe, Colin K.
; APPLICANT: Watenabe, Colin K.
; APPLICANT: Watenabe, Colin K.
; APPLICANT: Adapt, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C3
; CURRENT APPLICATION NUMBER: US/10/173, 695
; CURRENT APPLICATION NUMBER: US/10/173, 695
; CURRENT APPLICATION NUMBER: US/2-06-17
; PATIOR APPLICATION NUMBER: OS See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; FERNATE: ...
; SEQ ID NOS: 612
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 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
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 83
 440
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 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI 442
 24 LKLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 Gaps
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 94.3%; Score 417; DB 14; Length 440;
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; Publication No. US20030032102A1
; GENERAL INFORMATION:
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
 US-10-173-695-34
 98
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 206
 146
 204
 266
 326
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86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 143
 202
 203
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
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 266 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 83
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
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 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 Gaps
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0
 Length 440;
 Indels
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 Query Match 94.3%; Score 417; DB 14; Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches 0;
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 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gonowski, Paul J
APPLICANT: Guney, Austin L
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin J
APPLICANT: Saith, Xocoria
APPLICANT: Saith, Xocoria
APPLICANT: Saith, Xocoria
APPLICANT: Zhang, Zemin
 ; ORGANISM: Homo Sapien
US-10-173-697-34
Chen, Jian
 US-10-173-705-34
 326
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US-10-174-576-34
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 144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTT388AGEEGSIRAVDHAVIGGVVAVVV 385
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 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC FITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430RIC18 CURRENT APPLICATION NUMBER: US/10/173,705
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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 APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Hold, William I.
APPLICANT: Anang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT FILING DATE: 2002-06-18
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 Gaps
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 Length 440;
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 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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100.0%; Pred. No. 0;
iive 0; Mismatches 0;
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 Godowski, Paul J. Gurney, Austin L.
 Conservative
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
CORGANISM: Homo Sapien
US-10-173-705-34
 TYPE: PRT
ORGANISM: Homo Sapien
 Query Match
Best Local Similarity
Matches 417; Conserv
 LENGTH: 440
 SEQ ID NO 34
 84
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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
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 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 144 NLMIDIOKOTAVEGEEIEVNCTAMASKPATTIRWPKGNTELKGKSEVEEWSDMYTVTSOL 203
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 83
 83
 386 PAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R.037
CURRENT APPLICATION NUMBER: US/10/174,585
CURRENT FILING DATE: 2002-06-18
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 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
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 94.3%; Score 417; DB 14;
100.0%; Pred. No. 0;
tive 0; Mismatches 0;
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 Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
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 94.3%; Score 417; DB
100.0%; Pred. No. 0;
ive 0; Mismatches
 Sequence 34, Application US/10174585
Publication No. US20030032105A1
GENERAL INFORMATION:
 Watanabe, Colin K.
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Best Local Similarity 100.(
Matches 417; Conservative
 Goddard, Audrey
Godowski, Paul J.
 Gurney, Austin L
 Wood, William I.
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 Pan, James
Smith, Victoria
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Desnoyers, Luc
 ORGANISM: Homo Sapien
 RESULT 72
US-10-174-585-34
 US-10-174-585-34
 APPLICANT:
APPLICANT:
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 APPLICANT:
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| TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P3430RICHE SENCEDING THE SAME FILE REPERENCE: P3430RICHE SONG-06-19
| CURRENT FILING DATE: 2002-06-19
| PRIOR PELICATION NUMBER: 00/05266 |
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| PRIOR PLILING DATE:
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Publication No. US20030032107A1
GENERAL INFORMATION:
 APPLICATION NUMBER: 60/069335
FILING DATE: 1997-12-11
APPLICATION NUMBER: 60/069425
 APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
 Godowski, Paul J.
Gurney, Austin L.
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 US-10-175-747-34
 APPLICANT:
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 APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Ban, James
APPLICANT: Ban, James
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: SEGRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C24
CURRENT APPLICATION: NUMBER: US/10/174,586
CURRENT FILING DATE: 2002-06-18
FILE REPERENCE: SEGRETED
NUMBER: OF SEG ID NOS: 612
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 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
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 MLKVHKEDDGVPVI COVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 Gaps
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 DB 14; Length 440;
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 Query Match 94.3%; Score 417; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
 Sequence 34, Application US/10174586; Publication No. US20030032106A1; GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
ORGANISM: Homo Sapien
US-10-174-586-34
 SEQ ID NO 34
 266
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 386
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| 1997-<br>NUMBER<br>1997-<br>NUMBER<br>1998-<br>NUMBER<br>1998-<br>NUMBER<br>1998-<br>NUMBER<br>1998-<br>NUMBER<br>1998-<br>NUMBER | 1998-03-( NUMBER: 6 NUMBER: 6 1998-03-( NUMBER: 6 1998-03-( NUMBER: 6 1998-04-( NUMBER: 6 | NUMBER: 60/0833<br>1998-04-29<br>NUMBER: 60/0834<br>1998-04-29<br>NUMBER: 60/0834<br>1998-04-29<br>NUMBER: 60/0835<br>1998-04-29<br>NUMBER: 60/0843<br>1998-05-05<br>NUMBER: 60/0846<br>1998-05-05<br>NUMBER: 60/0846<br>1998-05-07<br>NUMBER: 60/0846<br>1998-05-07<br>NUMBER: 60/0846<br>1998-05-07<br>NUMBER: 60/0846<br>1998-05-07<br>NUMBER: 60/0855<br>1998-05-15<br>NUMBER: 60/0855<br>1998-05-15<br>NUMBER: 60/0855<br>1998-05-15<br>NUMBER: 60/0855<br>1998-05-15<br>NUMBER: 60/0855<br>1998-05-15<br>NUMBER: 60/0855<br>1998-05-15<br>NUMBER: 60/0855                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
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PRIOR APPLICATION NUMBER: 60/086392
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PRIOR PLINIO DATE: 19

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GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin
 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 265
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
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 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
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 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 24 LRILILIFSAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 440
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 Gaps
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100.0%; Pred. No. 0;
tive 0; Mismatches 0; Indels
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 Sequence 34, Application US/10176481
Publication No. US20030032108A1
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 TYPE: PRT CORGANISM: Homo Sapien US-10-176-481-34
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265
 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTLITITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
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 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEEKKEYFI 442
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 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
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US-09-30-61

US-09-778-510-22

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100.0%; Score 442; Dest Local Similarity 100.0%; Pred. No. 0; Matches 442; Conservative 0; Mismatches
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; ORGANISM: Homo sapien
US-09-778-510-20
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 Sequence 2, Appli
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Sequence 15507, A
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Sequence 120, Appli
Sequence 110, Appl
Sequence 12, Appli
Sequence 14, Appli
Sequence 6, Appli
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 -09-248-796A-21225
-09-270-767-34513
 US-09-270-767-60061
US-09-248-796A-27877
 US-09-270-767-49730
US-09-513-999C-6366
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US-09-778-510-20
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Gaps

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Sequence 20, Application US/09778510
; Sequence 20, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
APPLICANT:
Baum, Peter
CURRENT ELING NUMBER:
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE:
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR PILING DATE:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS:
SOFTWARE:
SOFTWARE:
PATENT FILING DATE:
NUMBER OF SEQ ID NOS:
SOFTWARE:
FLENGTH: 442
 ык: PCT/US99/17906
1999-08-05
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Sequence 1, Application US/09930803

Sequence 1, Application US/09930803

GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: YOSHINORI, Muramaki
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILE REFERENCE: JUHIT70-1
CURRENT APPLICATION NUMBER: US/09/930,803
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
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100.0%; Pred. No. 0;
live 0; Mismatches
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Best Local Similarity 100.
Matches 442; Conservative
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-803-1
 RESULT 2
US-09-930-803-1
 61
 SEQ ID NO 1
 LENGTH:
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265 263

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE SERERENCE: P2548P1C1
CURRENT PAPLICATION NUMBER: US/09/944,457
CURRENT APPLICATION NUMBER: US/06/928
PRIOR PILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
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 FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
 Sequence 61, Application US/09944457 Patent No. 6734288
 FILING DATE: February 9, 1998
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
 Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
 Gurney, Austin
Hillan, Kenneth
 Gerritsen, Mary
 Goddard, Audrey
 Kljavin, Ivar
Napier, Mary
Roy, Margaret
 Tumas, Daniel
Wood, William
 GENERAL INFORMATION:
 326
 APPLICANT:
APPLICANT:
APPLICANT:
 206
 204
 APPLICANT:
APPLICANT:
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 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
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 APPLICANT: Hillah, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Najer, Mary
APPLICANT: Noy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PIC1
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CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 120
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 94.3%; Score 417; DB
100.0%; Pred. No. 0;
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 Sequence 61, Application US/09866028
Patent No. 6642360
GENERAL INFORMATION:
 Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 al Similarity 100.
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 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Gerritsen, Mary
Goddard, Audrey
 Godowski, Paul
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61
 Eaton, Dan
 -09-866-028-61
 APPLICANT:
APPLICANT:
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GENERAL INFORMATION:
APPLICANT: Well, Gary
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for TITLE OF INVENTION: H. capsulatum
FILE REFERENCE: BJCH 9986
CURRENT APPLICATION NUMBER: US/09/060,767B
CURRENT FILING DATE: 1997-04-15
PRIOR FILING DATE: 1997-04-15
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NUMBER OF SEQ ID NOS: 9
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APPLICATION

TITLE OF INVENTION: Molecules Designated B711

FILE REPERBENCE: 2844-08

CURRENT APPLICATION NUMBER: US/09/778,510

CURRENT FILING DATE: 2001-02-07

PRIOR PILING DATE: 1999-08-05

PRIOR PILING DATE: 1999-08-05

PRIOR FILING DATE: 06/095,663

PRIOR FILING DATE: 1998-08-07

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 22

LENGTH: 423

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US-09-778-510-22
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Best Local Similarity
Matches 150; Conserv
 JS-09-778-510-22
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 TYPE: PRT
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 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDBGRYFCQLYTDPPQESYTTITVLVPPR 143
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PRIOR APPLICATION NUMBER: 60/074,092
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Best Local Similarity 100.
Matches 417; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
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Sequence 14, Application US/09588995A

Sequence 14, Application US/09588995A

GENERAL INFORMATION:

APPLICANT: PETERSEN. CAROLYN

APPLICANT: BETERSEN.

APPLICANT: BETERSEN.

TITLE OF INVENTION: INTECTION OF CRYPTOSPORIDIUM SPECIES AND

TITLE OF INVENTION: INTECTIONS

TITLE OF INVENTION: INTECTIONS

TITLE OF INVENTION: INTECTIONS

TITLE OF INVENTION: INTECTIONS

TITLE OF INVENTION: UNMER: US/09/588,995A

CURRENT APPLICATION NUMBER: US/09/589,995A

CURRENT FILING DATE: 1997-09-12

PRIOR PELING DATE: 1997-09-12

PRIOR FILING DATE: 1997-09-14

PRIOR FILING DATE: 1996-08-14

SOFTWARE: PATENTIN VOWER: 08/700,651

PRIOR FILING DATE: 1996-08-14

SOFTWARE: PATENTIN VOWER: 08/700,651

PRIOR FILING DATE: 1996-08-14

SOFTWARE: PATENTIN VOWER: 08/700,651
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 Length 130;
 DB 4; Length 130; 2.2e-05;
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 Indels
 Score 14; DB 3; Le
Pred. No. 2.2e-05;
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELEPHONE: 650-324-1677
TELEPHONE: 650-324-1677
TELEPRAX: 650-324-1677
TELEPRAX: 650-324-1677
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 ; Sequence 12, Application US/08700651B
 ; ORGANISM: Cryptosporidium parvum US-09-588-995A-14
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 340 PITITITITIT 353
 48 PITITITITIT 61
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Best Local Similarity 100.0
Matches 14; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
 US-08-928-361B-14
 RESULT 10
US-08-700-651-12
 SEQ ID NO 14
LENGTH: 130
 48
 TYPE: PRT
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 Sequence 14, Application US/08928361B

Sequence 14, Application US/08928361B

Patent No. 6071518

GENERAL INFORMATION:
PAPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
 DNAS AND RNAS
 GENERAL INPORMATION:

GENERAL INPORMATION:

APPLICANT: PETERSEN, CAROLYN

APPLICANT: LEECH, JAMES

APPLICANT: LEECH, JAMES

APPLICANT: MICHARD, C.

APPLICANT: GUT, JIRI

TITLE OF INVENTION: VOR PROPHYLAXIS AND TREATMENT OF CRYPCOSPORTIGUM PARVUM

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: WHERE: US/08/700,651B

CURRENT APPLICATION NUMBER: US/08/700,651B

CURRENT PILING DATE: 1995-04-03

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PALCHIN VEY: 2.0

SEQ ID NO 9

LENGTH: 130
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 Gaps
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 3.2%; Score 14; DB 3; Length 130;
100.0%; Pred. No. 2.2e-05;
tive 0; Mismatches 0; Indels
 3.4%; Score 15; DB 4; Length 41;
100.0%; Pred. No. 8.2e-07;
tive 0; Mismatches 0; Indels
 COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-9
 RESULT 7
US-08-700-651-9
Sequence 9, Application US/08700651B
Patent No. 6015882
 TYPE: PRT
ORGANISM: Cryptosporidium parvum
 339 PPTTTTTTTTTT 353
 340 PITITITITIT 353
 Best Local Similarity 100.
Matches 15; Conservative
 Best Local Similarity 100. Matches 14; Conservative
; ORGANISM: Leishmania
US-09-060-7678-5
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 US-08-928-361B-14
 STATE:
 Query Match
 Query Match
 FEATURE:
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Sequence 21069, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WINBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
FRIOR FILING DATE: 1998-02-13
FRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 21669
LENGTH: 197
 GENERAL INCURCATION:
CARDICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
FAPPLICANT: BARNES, DEBRA A.
FAPPLICANT: BARNES, DEBRA A.
FAPPLICANT: BARNES, DEBRA A.
FAPPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT PELING DATE: 1997-06-16
FRIOR PELING DATE: 1997-03-27
FRIOR PELING DATE: 1997-09-17
FRIOR PELING DATE: 1997-09-14
FRIOR FILING DATE: 1996-08-14
FRIOR FILING DATE: 1996-08-14
FRIOR FILING DATE: 1996-08-14
FRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE PATENTIN VET: 2.1
 Gaps
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 Query Match 3.2%; Score 14; DB 4; Length 175; Best Local Similarity 100.0%; Pred. No. 2.9e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 3.2%; Score 14; DB 3; Length 175; 100.0%; Pred. No. 2.9e-05; tive 0; Mismatches 0; Indels
 Sequence 17, Application US/09588995A Patent No. 6514697
 , ORGANISM: Cryptosporidium parvum
US-09-588-995A-17
 87 PTTTTTTTTT 100
 340 PITITITITIT 353
 340 PTTTTTTTTTT 353
 Query Match 3.2%
Best Local Similarity 100.0°
Matches 14; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-928-361B-17
TYPE: amino acid STRANDEDNESS:
 GENERAL INFORMATION:
 RESULT 13
US-09-248-796A-21069
 US-09-588-995A-17
 SEQ ID NO 17
LENGTH: 175
TYPE: PRT
 8
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 g
 APPLICANT: PETERSEN, CAROLYN
APPLICANT: PETERSEN, CAROLYN
APPLICANT: PETERSEN, CAROLYN
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
TITLE OF INVENTION: INFECTIONS
FILE REPERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: 08/017-014
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATCHIN VET. 2.0
 GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: SPECIES INFOCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
 ö
 Gaps
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0
 Query Match 3.2%; Score 14; DB 3; Length 175; Best Local Similarity 100.0%; Pred. No. 2.9e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 CUMPRY: USA

ZIP: 94306-1840

COMPUTER READBLE FORM:
MEDIUM TYPE: FIDEPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION 12-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
ATTONNEY/AGENT INFORMATION:
NAME: VETNY HANA
REGISTRATION NUMBER: 30,518
REFERENCE/POCKET UNBER: 30,518
REFERENCE/POCKET UNBER: 480.76-1(HV)
TELEPPHONE: 650-324-1677
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-12
 ; Sequence 17, Application US/08928361B ; Patent No. 6071518
 ORGANISM: Cryptosporidium parvum
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
 87 Pririririririr 100
 340 PTITITITITI 353
 175 amino acids
 RESULT 11
US-08-928-361B-17
 ర్
 SEQ ID NO 12
LENGTH: 175
 STATE:
 TYPE: PRT
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us-10-622-237-2.oligo.rai

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PERTIDES, POLYPEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
 APPLICANT: PETERERSH, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: 08/827,171
PRIOR APPLICATION NUMBER: 08/927,171
PRIOR PILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR PILING DATE: 1997-09-12
PRIOR PILING DATE: 1996-08-14
PRIOR PILING DATE: 1996-08-15
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 3.2%; Score 14; DB 3; Length 216; 100.0%; Pred. No. 3.5e-05;
 CUMITAL:

ZIP: 94306-1840

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: Patent PC-DOS/MS-DOS

SOFTWARING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,361B

FILING DATE: 12-SEP-1997
 TITLE OF INVENTION: PEPTIDES,
TITLE OF INVENTION: PERTIDES,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS
TITLE OF INVENTION: FOR TREATMENT AND DETECT
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
 0; Mismatches
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
 Sequence 8, Application US/09588995A
Patent No. 6514697
GENERAL INFORMATION:
 340 PTTTTTTTTTT 353
 LENGTH: 216 amino acids
TYPE: amino acid
STRANDEDNESS:
 Query Match
Best Local Similarity 100.0
Matches 14; Conservative
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 MOLECULE TYPE: protein
 TOPOLOGY: linear
 USA
 J
 US-08-928-361B-27
 RESULT 16
US-09-588-995A-8
 COUNTRY:
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 VARIANTS, ANALOGS AND FRAGMENTS
 PERFIDES, POLYBEPTIDES, GLYCOPROTEINS, PERFIDES, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DEFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
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 Score 14; DB 4; Length 197;
Pred. No. 3.2e-05;
 Score 14; DB 3; Length 216;
Pred. No. 3.5e-05;
 0; Indels
 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILLING DATE: 12-SEP-1997
 APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS
TITLE OF INVENTION: FOR TREATMENT AND DETECT
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
 3.2%; Scor.
100.0%; Pred. No. 3.-...
0; Mismatches
 0; Mismatches
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKTA NUMBER: 480.76-1 (HV)
TELECOMUNICATION INFORMATION:
TELECHONE: 650-324-1677
 ; Sequence 27, Application US/08928361B; Patent No. 6071518; GENERAL INFORMATION:
 Sequence 8, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
 3.2%; S
100.0%;
 113 TTTTTTTTTTT 126
 341 TTTTTTTTTTI 354
 340 PTTTTTTTTTT 353
 LENGTH: 216 amino acids
TYPE: amino acid
STRANDEDNESS:
 Query Match
Best Local Similarity 100.0
watches 14; Conservative
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21069
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Best Local Similarity 100.
Matches 14; Conservative
 , MOLECULE TYPE: protein US-08-928-361B-8
 linear
 STATE: CA
COUNTRY: USA
ZIP: 94306-1840
 US-08-928-361B-27
 TOPOLOGY:
 US-08-928-361B-8
 Query Match
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Sequence 20, Application US/09588995A

Patent No. 6514697

GENERAL INFORMATION:
APPLICANT: PETERSEN
APPLICANT: BARNES, DEBRA A.
APPLICANT: GUT, JIMI
APPLICANT: GUT, JIMI
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT APPLICATION NUMBER: US/00-06-06
CURRENT APPLICATION NUMBER: US/00-06-06
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 Query Match 3.2%; Score 14; DB 4; Length 249; Best Local Similarity 100.0%; Pred. No. 4e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 Score 14; DB 3; Length 249; Pred. No. 4e-05; 0; Mismatches 0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
FILING DATE: 13-SEP-1996
ATTORNEY APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY AGENT INFORMATION:
NAME: Verry, Hana
REGISTRATION NUMBER: 480.76-1(HV)
TELEPHONE: 650-324-1678
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1678
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
 3.2%; Scc...
100.0%; Pred. No. ...
... 0; Mismatches
 PRIOR APPLICATION NUMBER: 08/827,171
PRIOR FILING DATE: 1997-03-27
PRIOR PELING DATE: 1997-03-27
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR PILING DATE: 1996-08-14
PRIOR PILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-15
SOFTWARE: PALENELIN VET. 2.1
SOFTWARE: PALENELIN VET. 2.1
SEQ ID NO 20
LENGTH: 249
 TYPE: PRT Cryptosporidium parvum US-09-588-995A-20
 165 PTTTTTTTTTT 178
 340 PTTTTTTTTTT 353
 165 Pririririririr 178
 340 PTTTTTTTTT 353
 LENGTH: 249 amino acids
TYPE: amino acid
STRANDEDNESS:
 3.2%
Best Local Similarity 100.0
Matches 14; Conservative
 MOLECULE TYPE: protein
 linear
 US-08-928-361B-20
 US-09-588-995A-20
 TOPOLOGY:
 Best Local
Matches
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 Sequence 15. Application US/08700651B
Fatent No. 601582
Fatent No. 601582
Fatent No. 601582
Fatent No. 601582
FAPLICANT: DETERBEN, CAROLYN
APPLICANT: DETERBEN, CAROLYN
TITLE OF INVENTION: VACINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: VACINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND TITLE OF INVENTION: WACRITIONS
TITLE OF INVENTION: 105 04 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
 US-08-928-361B-20
| Sequence 20, Application US/08928361B
| Patent No. 6071518
| Patent No. 6071518
| Patent No. 6071518
| APPLICANT: Petersen, Carolyn TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS TITLE OF INVENTION: PREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM TITLE OF INVENTION: SPECIES INFECTIONS NUMBER OF SEQUENCES: 30
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: PETERS, VERNY, JONES & BIKSA STREET: 385 Sherman Avenue, Suite 6
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 Gaps
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 3.2%; Score 14; DB 3; Length 249; llarity 100.0%; Pred. No. 4e-05; Conservative 0; Mismatches 0; Indels
 Score 14; DB 4; Length 216;
Pred. No. 3.5e-05;
 0; Indels
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-15
 3.2%; Score 14; DB ilarity 100.0%; Pred. No. 3.5 Conservative 0; Mismatches
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 TYPE: PRT
ORGANISM: Cryptosporidium parvum
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 340 PTTTTTTTTTT 353
 340 PTTTTTTTTTT 353
 70 PITITITITI 83
 SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 216
 NUMBER OF SEQ ID NOS: 115
 Query Match
Best Local Similarity
Matches 14; Conserv
 Best Local Similarity
Matches 14; Conserv
 COUNTRY: USA
ZIP: 94306-1840
 RESULT 17
US-08-700-651-15
 US-09-588-995A-8
 SEQ ID NO 15
LENGTH: 249
 Query Match
 FEATURE:
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Sequence 6, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PREPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS;
TITLE OF INVENTION: SPECIES INFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
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 Query Match 3.2%; Score 14; DB 3; Length 1721; Best Local Similarity 100.0%; Pred. No. 0.00024; Matches 14; Conservative 0; Mismatches 0; Indels
 3.2%; Score 14; DB 3; Length 1721; 100.0%; Pred. No. 0.00024;
 Indels
 ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
 100.0%; Prec. ...
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMONICATION INFORMATION:
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-08-700-651-5
 307 PTTTTTTTTTT 320
 340 PITITITITIT 353
 TTT 353
 Prirrirririri 320
 TELEPHONE: 650-324-1677
 Best Local Similarity 100.0
Matches 14; Conservative
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS
 650-324-1678
 MOLECULE TYPE: protein
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 3
 TYPE: amino acid
STRANDEDNESS:
 linear
 340 PTTTTTT
 USA
 ð
 TOPOLOGY:
 SEQ ID NO 5
LENGTH: 1721
 RESULT 22
US-08-928-361B-6
 US-08-928-361B-6
 COUNTRY:
 LENGTH:
 307
 Query Match
 RESULT 23
 8
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 셤
 DNAS AND RNAS
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 APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND
TITLE OF INVENTION: POR PROPHILAXIS AND TREATMENT OF Cryptosporidium parvum
FILE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
 Gaps
 GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
 ö
 Score 14; DB 1; Length 887;
Pred. No. 0.00013;
 0; Indels
 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION NUMBER: WC/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: R.CE-0002
TELECHOMMUNICATION INFORMATION:
TELECHOME: 215-568-3100
 Mismatches
 PC-DOS/MS-DOS
 3.2%; Scc.
100.0%; Pre
0;
 Sequence 5, Application US/08700651B
Patent No. 6015882
GENERAL INFORMATION:
 Sequence 3, Application US/07867106
Patent No. 5389526
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
 TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 250 PTTTTTTTTT 263
 340 PTTTTTTTTT 353
 : 887 amino acids
AMINO ACID
 Query Match
Best Local Similarity 100.0
Marches 14; Conservative
 COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
 TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-867-106-3
 US-08-700-651-5
 US-07-867-106-3
 LENGTH:
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APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION UNMBER: US/09/588,995A
CURRENT APPLICATION NUMBER: US/09/28,361
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SEQ ID NO S
LENGTH: 1837
 Gaps
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0
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 Query Match 3.2%; Score 14; DB 3; Length 1837; Best Local Similarity 100.0%; Pred. No. 0.00026; Matches 14; Conservative 0; Mismatches 0; Indels
 Length 1837;
 0; Indels
 DB 4; Le
 US-09-205-258-953
) Sequence 953.
Patent No. 6525174
) GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION:
TITLE OF INVENTION 207 Human Secreted Proteins;
FILE REPRENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
) CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER PILING DATE: 1998-06-04
 Query Match 3.2%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 14; Conservative 0; Mismatches
 Sequence 5, Application US/09588995A Patent No. 6514697
 ORGANISM: Cryptosporidium parvum
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-324-1677
FILEPRAX: 650-324-1678
INFORMATION FOR SEO ID NO: 5: SEQUENCE CHARACTERISTICS:
 LENGTH: 1837 amino acids
 340 PTTTTTTTTT 353
 340 PTTTTTTTTTT 353
 378 Priritriritrii 391
 378 Prirrirriri 391
 GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
 TOPOLOGY: linear; MOLECULE TYPE: protein US-08-928-3618-5
 TYPE: amino acid
STRANDEDNESS:
 US-09-588-995A-5
 US-09-588-995A-5
 RESULT 26
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 US-08-928-361B-5

Sequence 5, Application US/08928361B

Sequence 5, Application US/08928361B

Patent No. 6071518

SENERAL INFORMATION:
Patent No. 6071518

TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRACMENTS

TITLE OF INVENTION: PRETIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: SPECIES INFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESSE: PETERS, VERNY, JONES & BIKSA

STREET: 385 Sharman Avenue, Suite 6

CITY: Palo Alto
 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
BARNES, DEBRA A.
APPLICANT:
APPLICANT:
BARNES, DEBRA A.

APPLICANT:
TITLE OF INVENTION:
ISOLATES AND FOR DETECTION OF CRYPTOSPORIDIUM
FILLE OF INVENTION:
INFECTIONS
FILLE REFERENCE: 480.19-5
CURRENT FILLING DATE: 1097-09-12
FRIOR FILLING DATE: 1097-09-12
FRIOR APPLICATION NUMBER: 08/227,171
FRIOR FILLING DATE: 1997-09-12
FRIOR FILLING DATE: 1997-09-12
FRIOR FILLING DATE: 1996-08-14
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 Gaps
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 Score 14; DB 4; Length 1721;
Pred. No. 0.00024;
 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CONFURE: PatentIn Release #1.0, Version #1.30
SOGTWARE: PatentIn Release #1.0, Version #1.30
FILING DATE: 12-SEP-1997
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
 Mismatches
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
 Sequence 6, Application US/09588995A
Patent No. 6514697
 : Cryptosporidium parvum
 3.2%; Scillarity 100.0%; P. Conservative 0;
 rrrr 353
 307 PTTTTTTTTTTTT 320
 Local Similarity
nes 14; Conserv
 USA
 J
 340 PTT
 STATE: CA
US-09-588-995A-6
 US-09-588-995A-6
 TYPE: PRT
 Query Match
 Best Loca
Matches
 RESULT 24
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 à
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BARLIER APPLICATION NUMBER: 60/048, 885
BARLIER PALLOADION NUMBER: 60/046, 375
BARLIER PAPLICATION NUMBER: 60/046, 375
BARLIER PAPLICATION NUMBER: 60/048, 381
BARLIER PAPLICATION NUMBER: 60/048, 886
BARLIER PAPLICATION NUMBER: 60/048, 896
BARLIER APPLICATION NUMBER: 60/048, 896
BARLIER APPLICATION NUMBER: 60/048, 896
BARLIER APPLICATION NUMBER: 60/048, 897
BARLIER PAPLICATION NUMBER: 60/048, 997
BARLIER PAPLICATION NUMBER: 60/048, 915
BARLIER PAPLICATION NUMBER: 60/048, 917
BARLIER
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 Gaps
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 TITLE OF INVENTION:

PAPPLICANT: Bard, Jonathan A.

TITLE OF INVENTION: USAS THEREOF

TITLE OF INVENTION: USAS THEREOF

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEB: Cooper & Dunham Lip

STREET: 1185 Avenue of The Americas

CITY: New York

COUNTRY: U.S.A.

ZIP: 11036

COMPUTER: New York

COUNTRY: BADABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: TAM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PRECENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/900,230

FILING DATE: 23-UUL-1997

CLASSIFICATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678

TELEFORMINICATION INFORMATION:

TELEFORM: TELEFORE TELEFOR: TELEFORMINICATION INFORMATION:

TELEFORMINICATION INFORMATION:

TELEFORM: TELEFORE CHARACTERISTICS:

LENGTH: 57 amino acids

LENGTH: 57 amino acids
 ;
0
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 Length 44;
 Length 57;
 0; Indels
 IndelB
 Score 13; DB 4; L
Pred. No. 7.1e-05;
 2.9%; Score 13; DB 3; L. 100.0%; Pred. No. 9.1e-05;
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 7.1 Matches 13; Conservative 0; Mismatches
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 9.1 Matches *13; Conservative 0; Mismatches
EARLIER FILING DATE: 1997-12-18
EARLIER PELING DATE: 1997-12-18
EARLIER PLING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOTUMARE: PARENTIN Ver. 2.0
 US-08-900-230-59; Sequence 59, Application US/08900230; Patent No. 6329197; GENERAL INFORMATION:
 419 DADTAIINAEGGQ 431
 341 TTTTTTTTTT 353
 21 DADTAIINAEGGO 33
 ; ORGANISM; Homo sapiens
US-09-205-258-953
 TYPE: amino acid STRANDEDNESS: sin
 linear
 ; ANTI-SENSE: NO
US-08-900-230-59
 TOPOLOGY:
 LENGTH: 44
TYPE: PRT
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Sequence 19, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PER FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: SPECIES INFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF ADDRESS: 30
CORRESPONDENCES: 30
CORRESPONDENCES: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
 DNAS AND RNAS
 APPLICANT: BETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: BELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS;
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: LOS ROCHITAXIS AND TREATMENT OF Cryptosporidium parvum
TITLE OF INVENTION INPERE: US/08/700, 651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: US/08/15,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTION OF: 2.0
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 Score 13; DB 4; Length 75;
Pred. No. 0.00012;
0; Mismatches 0; Indels
 DB 3; Length 91;
0.00014;
hes 0; Indels
 FEATURE: OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-14
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 25289
LENGTH: 75
 Sequence 14, Application US/08700651B Patent No. 6015882
 ORGANISM: Cryptosporidium parvum
1999-02-12
 341 TTTTTTTTTT 353
 341 TTTTTTTTTT 353
 7 řiřiřiřiřiřiří 19
 ORGANISM: Candida albicans
CURRENT FILING DATE:
 CITY: Palo Alto
 GENERAL INFORMATION:
 US-09-248-796A-25289
 US-08-928-361B-19
 US-08-700-651-14
 STATE:
 TYPE: PRT
 RESULT 32
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 US-09-248-796A-23083

Sequence 23083, Application US/09248796A

Sequence 23083, Application US/09248796A

Sequence 23083, Application US/09248796A

GENERAL INCORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/248, 796A

CURRENT APPLICATION NUMBER: US/09/248, 796A

CURRENT FILING DATE: 1998-02-13

PRIOR PRILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096, 409

PRIOR APPLICATION NUMBER: US 60/096, 409

PRIOR SEQ ID NOS: 28208

SEQ ID NO 23083
 Sequence 25289, Application US/09248796A

Sequence 25289, Application US/09248796A

Patent No. 6747137

GENERAL NO. 6747137

APPELCANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A
 Sequence 9, Application US/09060767B

| Sequence 9, Application US/09060767B
| Sequence 9, Application US/09060767B
| General No. 6720152
| General Information:
| APPLICANT: Weil, Gary
| APPLICANT: Chandrashekar, Ramaswamy
| TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for TITLE OF INVENTION: H. capsulatum
| FILE REFERENCE: BJCH 9986
| CURRENT APPLICATION NUMBER: US/09/060,767B
| CURRENT FILING DATE: 1996-04-15
| PRIOR FILING DATE: 1997-04-15
| NUMBER OF SEQ ID NOS: 9
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 9
| LENGTH: 57
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 Score 13; DB 4; Length 63;
Pred. No. 0.0001;
0; Mismatches 0; Indels
 Length 57;
 0; Indels
 Score 13; DB 4; Lo
Pred. No. 9.1e-05;
 100.0%; Prec.
 2.9%; Score 13; DB ilarity 100.0%; Pred. No. 9.1 Conservative 0; Mismatches
 ; TYPE: PRT
; ORGANISM: Histoplasma Capsulatum
US-09-060-7678-9
 2.98;
 340 PTTTTTTTTT 352
 338 PPPTTTTTTT 350
 16 PPPTTTTTTTT 28
 : Candida albicans
 Prirriririri 48
 Best Local Similarity 100.
Matches 13; Conservative
 Query Match
Best Local Similarity
 RESULT 30
US-09-248-796A-25289
 US-09-248-796A-23083
 RESULT 28
US-09-060-767B-9
 13;
 TYPE: PRT ORGANISM:
 36
 Query Match
 Matches
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US-08-700-651-11; Sequence 11, Application US/08700651B; Patent No. 6015882; GENERAL INFORMATION:
 ; ORGANISM: Drosophila melanogaster
US-09-270-767-51409
 ; ORGANISM: Drosophila melanogaster US-09-270-767-36192
 341 TTTTTTTTTT 353
 341 TTTTTTTTTT 353
 341 TTTTTTTTTT 353
 18 ririririririi 30
 US-09-270-767-51409
 TYPE: PRT
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 Sequence 19, Application US/09588995A

Sequence 19, Application US/09588995A

Sequence 19, Application US/09588995A

GENERAL INFORMATION:

APPLICANT: PETERSEN, CARCLYN

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: GIV. JIRI

TITLE OF INVENTION: INFECTION OF CRYPTOSPORIDIUM

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: UNBER: US/09/588,995A

CURRENT APPLICATION NUMBER: US/09/588,995A

CURRENT APPLICATION NUMBER: US/09/651

PRIOR FILING DATE: 1997-03-27

PRIOR FILING DATE: 1997-03-12

PRIOR FILING DATE: 1996-08-14

PRIOR FILING DATE: 1996-08-14

PRIOR FILING DATE: 1996-08-14

PRIOR FILING DATE: 1995-04-12

NUMBER OF SEQ ID NOS: 115

SEQ ID NO 19

LENGTHARE: PALEGATIN VET: 2.1

LENGTHARE: PALEGATIN VET: 2.1
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 Gaps
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 2.9%; Score 13; DB 4; Length 91; 100.0%; Pred. No. 0.00014; tive 0; Mismatches 0; Indels
 2.9%; Score 13; DB 3; Length 91; 100.0%; Pred. No. 0.00014;
 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILLING DATE: 12-SEP-1997
CLASSIFICATION:
 Query Match 2.9%; Score 13; DB. Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REGISTRATION INFORMATION:
TELEPHONE: 650-324-1677
ITELEPHONE: 650-324-1677
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 aming acids
 . TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-19
 341 TTTTTTTTTT 353
 18 riririririr 30
 Query Match 2.9
Best Local Similarity 100.
Matches 13; Conservative
 MOLECULE TYPE: protein
 TYPE: amino acid STRANDEDNESS:
 TOPOLOGY: linear
 94306-1840
 US-08-928-361B-19
COUNTRY:
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JARBACH, INCOMATI: PETEREEN, CAROLYN
APPLICANT: DEECH, JAMES
APPLICANT: DEECH, JAMES
APPLICANT: DEECH, JAMES
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS TITLE OF INVENTION: POR PROPHYLAXIS AND TREATMENT OF CRYPCOSPORIGIUM PARVUM TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4(HV)
 ö
 Sequence 51409, Application US/09270767

Facent No. 6703491

GENERAL INFORMATION:
FACENTY Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51409
LENGTH: 106
TYPE: RT
Sequence 36192.
Sequence 36192.
Sequence 36192. Application US/09270767.
Sequence 36192. Application US/09270767.
Sequence 36192. Application US/09270767.
Sequence 36192. Application US/09270767.
TITLE OF INVENTION:
NUCLEIC OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.
FILE REFERENCE: File Reference: 7326-094.
CURRENT APPLICATION NUMBER: US/09/270.767.
CURRENT FILING DATE: 1999-03-17.
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 36192.
LENGTH: 106
 Gaps
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 Query Match 2.9%; Score 13; DB 4; Length 106; Best Local Similarity 100.0%; Pred. No. 0.00016; Matches 13; Conservative 0; Mismatches 0; Indels
 Query Match 2.9%; Score 13; DB 4; Length 106; Best Local Similarity 100.0%; Pred. No. 0.00016; Matches 13; Conservative 0; Mismatches 0; Indele
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APPLICANT: DETERREN, CAROLYN
APPLICANT: DETERREN, CAROLYN
APPLICANT: DETERGON, RICHARD, C.
APPLICANT: DETERGON, RICHARD, C.
APPLICANT: OUT JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS;
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
FILE REPERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 128
 APPLICANT: BERNES, DEBRA A.
APPLICANT: BLEASEA, A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BULSON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
FILE REFERENCE: 480.19-5
CURRENT PAPLICATION NUMBER: US/09/588,995A
CURRENT PILING DATE: 1997-03-27
PRIOR PILING DATE: 1997-03-27
PRIOR PILING DATE: 1997-09-12
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SEQ ID NO 16
LENGTH: 124
 DB 3; Length 128;
 Length 124;
 Indels
 Y Match 2.9%; Score 13; DB 4; Le Local Similarity 100.0%; Pred. No. 0.00019; hes 13; Conservative 0; Mismatches 0;
 CTHER INFORMATION: mutant/variant of SEQ ID NO:5 US-08-700-651-7
 2.9%; Score 13;
 RESULT 38
US-09-588-995A-16
Sequence 16, Application US/09588995A
Fatent No. 6514697
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
 Sequence 7, Application US/08700651B Patent No. 6015882 GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-16
 ORGANISM: Cryptosporidium parvum
 341 TTTTTTTTTT 353
 341 TITITITITI 353
 33 TTTTTTTTTTT
 US-08-700-651-7
 TYPE: PRT
 Query Match
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 Sequence 16, Application US/08928361B
Patent No. 6071518
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
NUMBER OF SEQUENCES: 30
CORRESPONDENCE 30
CORRESPONDENCE ADDRESS:
ADDRESSE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
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 Gaps
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 2.9%; Score 13; DB 3; Length 124;
100.0%; Pred. No. 0.00019;
tive 0; Mismatches 0; Indels
 Query Match 2.9%; Score 13; DB 3; Length 124; Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 13; Conservative 0; Mismatches 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIMP FC compatible
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: VETTY, HARA
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
REGISTRATION INFORMATION:
TELEPHONE: 650-324-1677
 OTHER INFORMATION: mutant/variant of SEQ ID NO:5
CURRENT APPLICATION NUMBER: US/08/700,6518
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
LENGTH: 124
 TYPE: PRT
ORGANISM: Cryptosporidium parvum
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acids
STRANDEDNESS:
 341 TTTTTTTTTT 353
 rrrrrrrrrr 45
 Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
 Best Local Similarity
Matches 13; Conserva
 USA
 US-08-928-361B-16
 US-08-700-651-11
 COUNTRY:
 33
 Query Match
 FEATURE:
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Gaps

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US-08-700-651-8

US-08-700-651-8

Sequence 8, Application US/08700651B

Patent No. 6015882

GENERAL INFORMATION:
APPLICANT: DETERSEN, CAROLYN
APPLICANT: LEECH, JAMES

APPLICANT: GUT, JIRI
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: 1NFECTIONS
TITLE OF INVENTION UNMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
FILE REPERBENCE: 480.19-5
CURRENT PEDLICATION NUMBER: 08/995A
CURRENT FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 08/827,171
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR PILING DATE: 1997-09-12
PRIOR PILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SEQ ID NO 12
 ..
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 APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
 Score 13; DB 4; Length 128; Pred. No. 0.00019;
 Length 130;
 Indels
 Indels
 Query Match 2.9%; Score 13; DB 3; Le. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 13; Conservative 0; Mismatches 0;
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5 US-08-700-651-8
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 US-08-928-361B-13; Sequence 13, Application US/08928361B Patent No. 6071518; GENERAL INFORMATION:
 ORGANISM: Cryptosporidium parvum US-09-588-995A-12
 ORGANISM: Cryptosporidium parvum
 341 TITITITITIT 353
 SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 130
 341 TITTTTTTT 353
 37 rrrrrrrrrrrr 49
 39 TTTTTTTTTT 51
 TYPE: PRT
 TYPE: PRT
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 1, Carolyn, PEPTIDES, GLYCOPROTEINS, FERTIDES, POLYPEPTIDES, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATHENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INPECTIONS
 ô
 Sequence 12, Application US/09588995A
PREENT NO. 6514697
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLIN
APPLICANT: BARNES, DEBRA A.
APPLICANT: NELGON, RICHARD C.
APPLICANT: NELGON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
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 2.9%; Score 13; DB 3; Length 128; 100.0%; Pred. No. 0.00019;
 0; Indels
 0; Indels
 COMPUTAT: USA

ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
 100.0%; Pred. No. 0.00019; tive 0; Mismatches 0;
 100.0%; Prec. ...
 3: PETERS, VERNY, JONES & BIKSA 385 Sherman Avenue, Suite 6
 REPERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 Sequence 12, Application US/08928361B
Patent No. 6071518
 341 TITITITITI 353
 LENGTH: 128 amino acids TYPE: amino acid
 341 TTTTTTTTTT 353
 Best Local Similarity 100.
Matches 13; Conservative
 37 rriririririr 49
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 TTTTTTTTT 49
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Petersen, Car
TITLE OF INVENTION: PEPT
TITLE OF INVENTION: FOR
TITLE OF INVENTION: SPEC
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
 13; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
 Best Local Similarity
Matches 13; Conserv
 Palo.Alto
 USA
 STRANDEDNESS:
 ADDRESSEE:
 RESULT 41
US-09-588-995A-12
 RESULT 40
US-08-928-361B-12
 US-08-928-361B-12
 COUNTRY:
 STREET:
 STATE:
 37
 Query Match
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DNAS AND RNAS

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 US-08-700-651-10
 CITY: E
 SEQ ID NO 13
 RESULT 45
 RESULT 46
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TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Allo
 Sequence 13, Application US/09588995A

Patent No. 6514697

GENERAL INPORMATION:
APPLICANT: BETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
TITLE OF INVENTION: METHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: INFECTION
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: OWNBER: US/09/588,995A
CURRENT APPLICATION NUMBER: 08/82,171
PRIOR FILING DATE: 1997-03-27
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/128,361
PRIOR FILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/128,361
PRIOR APPLICATION NUMBER: 08/144,751
PRIOR APPLICATION NUMBER: 08/14,751
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 Gaps
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 2.9%; Score 13; DB 3; Length 130;
100.0%; Pred. No. 0.0002;
lve 0; Mismatches 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM Forms
MEDIUM TYPE: Floppy disk
COMPUTER: ISM Forms
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verry, Hana
REGISTRATION NUMBER: 30 518
REFERENCE/DOCKET NUMBER: 480.76-1 (HV)
TELECOMMULCATION INFORMATION:
TELEPHONE: 650-324-1677
 Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS:
 341 TTTTTTTTTT 353
 NUMBER OF SEQ ID NOS: 115
SOFTWARE: PatentIn Ver. 2.1
 39 řřřřřřřřřřřř 51
 MOLECULE TYPE: protein
 linear
 USA
 S
 US-08-928-361B-13
 US-09-588-995A-13
 TOPOLOGY:
 STATE: C. COUNTRY:
 Query Match
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Sequence 10, Application US/08700651B
Fatent No. 6015882
GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: BETSON, RICHARD, C.
APPLICANT: GUT, JIR.
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS;
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: 1NPECTIONS
FILE REFERENCE: 480.19-4 (HV)
CURRENT FILING DATE: 1997-08-14
EARLIER PILING DATE: 1997-08-14
SEALLIER PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 138
 SQUENCE 15. Application US/08928361B

| Sequence 15. Application US/08928361B
| Patent No. 607151B
| Patent No. 60
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 Length 130;
 2.9%; Score 13; DB 3; Length 138;
100.0%; Pred. No. 0.00021;
iive 0; Mismatches 0; Indels
 0; Indels
 DB 4; I
 FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-10
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
LENGTH: 130
TYPE: PRT
CRGANISM: Cryptosporidium parvum
US-09-588-995A-13
 TYPE: PRT
ORGANISM: Cryptosporidium parvum
 341 TITITITITI 353
 341 TTTTTTTTT 353
 47 TTTTTTTTT 59
 39 TTTTTTTTTTT 51
 Query Match
Best Local Similarity 100.0
Matches 13; Conservative
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ö
 Length 150;
 0; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/08/928,361B FILING DATE: 12-SEP-1997
 Score 13; DB 3; L
Pred. No. 0.00022;
 CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 60/026,062
PILING DATE: 13-SEP-1996
ATTORNEY/AGENT INPORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKTY NUMBER: 480.76-1(HV)
TELECOMMINICATION INPORMATION:
TELEPHONE: 650-324-1677
 0; Mismatches
 PRIOR APPLICATION NUMBER: 08/827,171
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/928,361
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
 INFORMATION FOR SEQ ID NO: 18:
 100:08;
 ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS:
 341 TTTTTTTTTT 353
 Query Match
Best Local Similarity 100:0
Matches 13; Conservative
 62 rrrrrrrrrrrr 74
 650-324-1678
 TOPOLOGY: linear
MOLECULE TYPE: protein
 USA
 JS-08-928-361B-18
 US-08-928-361B-18
 US-09-588-995A-18
 COUNTRY:
 g
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 US-09-588-995A-15

i Sequence 15, Application US/09588995A

j Sequence 15, Application US/09588995A

j GENERAL INFORMATION:

j APPLICANT: PETERSEN, CAROLYN

APPLICANT: BERES.

APPLICANT: BERES.

APPLICANT: BERES.

APPLICANT: BERES.

TITLE OF INVENTION: INFECTION OF CRYPTOSPORIDIUM SPECIES AND

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: UNFECTIONS

TITLE OF INVENTION: 08/09/588,995A

CURRENT APPLICATION NUMBER: 08/827,171

PRIOR FILING DATE: 1997-03-27

PRIOR PELING DATE: 1997-03-12

PRIOR FILING DATE: 1997-03-14

PRIOR FILING DATE: 1997-03-14

PRIOR FILING DATE: 1997-03-14

PRIOR FILING DATE: 1997-03-15

SPRIOR FILING DATE: 1997-03-15

SPRIOR FILING DATE: 1995-04-03

NUMBER OF SEQ ID NOS: 115

SEQ ID NO IS

LENGTH: 138

"LENGTH: 138
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 Score 13; DB 3; Length 138;
Pred. No. 0.00021;
 Length 138;
 0; Indels
 0; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
 Query Match 2.9%; Score 13; DB 4; Le Best Local Similarity 100.0%; Pred. No. 0.00021; Matches 13; Conservative 0; Mismatches 0;
 2.9%; bcc.
100.0%; Pred. No.
0; Mismatches
 REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-324-1677
TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY, AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
 ; ORGANISM: Cryptosporidium parvum
US-09-588-995A-15
 341 TTTTTTTTT 353
 341 TITITITITIT 353
 Query Match
Best Local Similarity 100.
 47 TITITITITI 59
 47 riririririris 59
 TOPOLOGY: linear MOLECULE TYPE: protein
 STRANDEDNESS
 US-08-928-361B-15
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Sequence 18, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
PATENTE NO. FORTICANT: PETERSON.
TITLE OF INVENTION: PRETIDES, POLYPEPTIDES, GLYCOPROFEINS,
TITLE OF INVENTION: PRETIDES, POLYPEPTIDES, GLYCOPROFEINS,
TITLE OF INVENTION: PRETINENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: PETERS, VERNY, JONES & BIKSA
STAFET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto ö Bequence 18, Application US/09588995A

Patent No. 6514697

GENERAL INFORMATION:
APPLICANT: BETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: MELSON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: INFECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
FILE REPRENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 2000-06-06
CURRENT FILING DATE: 2000-06-06
CURRENT PAILOR OF CANADOM CONTINUED CONTINUE Gaps

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US-09-248-796A-16058
US-09-248-796A-16058
Sequence 16058, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANN:
TITLE OF INVENTION: WUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR PILING DATE: 1999-02-13
PRIOR PILING DATE: 1999-02-13
PRIOR PILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
SEQ ID NOS: 28208
:ENGTH: 207
 LOCATION: (204)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknow
US-09-248-796A-16058
 Sequence 3, Application US/09060767B

Fatent No. 6720152

GENERAL INFORMATION:
APPLICANT: Weil, Gary
APPLICANT: Chandrashekar, Ramaswamy
ITLE OF INVENTION: H. capsulatum
FILLE OF INVENTION: H. capsulatum
FILLE REFERENCE: BJCH 9986
CURRENT FILLON DATE: 1998-04-15
CURRENT FILLON DATE: 1998-04-15
FRIOR FILLING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE PAPELICATION NOWER: 60/043,332
FRIOR FILLING DATE: 1997-04-15
SEQ ID NO 3
LENGTH: 211
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 Query Match
2.9%; Score 13; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 13; Conservative 0; Mismatches 0; Indels
 2.9%; Score 13; DB 4; Length 207; 100.0%; Pred. No. 0.0003; tive 0; Mismatches 0; Indels
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
; FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-13
 ; ORGANISM: Histoplasma capsulatum
US-09-060-767B-3
 341 TTTTTTTTTT 353
 341 TTTTTTTTTT 353
 76 TTTTTTTTT 88
 61 TTTTTTTTT 73
 ORGANISM: Candida albicans
 Query Match 2.9
Best Local Similarity 100.
Matches 13; Conservative
 NAME/KEY: UNSURE
 RESULT 53
US-09-060-767B-3
 LENGTH: 162
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 US-09-248-796A-21631

i Sequence 21631, Application US/09248796A

i Patent No. 6747137

j Patent No. 6747137

i Patent No. 6747137

i TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

i FILE REFERENCE: 107196_132

i CURRENT APPLICATION NUMBER: US 60/074,725

i PRIOR APPLICATION NUMBER: US 60/074,725

i PRIOR PLING DATE: 1998-08-13

i NUMBER OF SEQ ID NOS: 28208

i NUMBER OF SEQ ID NOS: 28208

i ENGTH: 159

i LENGTH: 159
 APPLICANT: PETERSEN, CARCLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: USECH, JAMES
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: PREPHYLAXIS AND TREATMENT OF CRYPCOSPORTION
TITLE OF INVENTION: INPECTIONS
FILE REFERENCE: 480.19-4 (HV)
CURRENT PELLOR NUMBER: US/08/700,651B
CURRENT PILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER PALENCE: SEQ ID NOS: 15
SOFTWARE: PALENTING DATE: 2.0
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 Gaps
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 2.9%; Score 13; DB 4; Length 150;
100.0%; Pred. No. 0.00022;
ive 0; Mismatches 0; Indels
 Length 159;
 0; Indels
 0; Indels
 Score 13; DB 4; Lo
 Mismatches
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR FILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER: OF SEQ ID NOS: 115
SEQ ID NO 18
 US-08-700-651-13
; Sequence 13, Application US/08700651B
; Patent No. 6015882
; GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-18
 Query Match
Best Local Similarity 100.0%; P. Matches 13; Conservative 0;
 342 TITITITITI 354
 341 TTTTTTTTT 353
 Query Match
Best Local Similarity 100.0
Matches 13; Conservative
 62 TTTTTTTTTT 74
 ; ORGANISM: Candida albicans
US-09-248-796A-21631
 52 rrrrrrrrrii 64
 13;
 TYPE: PRT
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Sequence 341, Application US/09216393B

Sequence 341, Application US/09216393B

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Michael James
TIPLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER FILE REFERENCE: TX-1-C2
CURRENT APPLICATION NUMBER: US/09/216,393B
CURRENT PILING DATE: 1998-12-18
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-19
RIOR FILING DATE: 1997-12-19
SEQ ID NO 341
LENGTH: 288
 Sequence 344, Application US/09216393B
Patent No. 6514694
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER FILE REFERENCE: TX-1-C2
CURRENT APPLICATION NUMBER: US/09/216,393B
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: Patentin version 3.1
 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
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 Gaps
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 Length 288;
 2.9%; Score 13; DB 4; Length 288; 00.0%; Pred. No. 0.00041;
 0; Indels
 0; Indels
 Score 13; DB 4; Le Pred. No. 0.00041;
 Query Match
2.9%; Score 13; C. Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 Query Match
2.9%; Score 13; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 13; Conservative 0; Mismatches
 CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
 US-09-248-796A-25055
; Sequence 25055, Application US/09248796A
; Patent No. 6747137
 ; SEQ ID NO 344

; LENGTH: 288

; TYPE: PRT

; ORGANISM: Toxoplasma gondii

US-09-216-393B-344
 341 TTTTTTTTTT 353
 164 TTTTTTTTTT 176
 164 TTTTTTTTTTT 176
 ORGANISM: Toxoplasma gondii
US-09-216-393B-341
 341 TTTTTTTTTT 353
 US-09-216-393B-344
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 US-09-248-796A-24111
US-09-248-796A-24111
Sequence 24111, Application US/09248796A
Facent No. 6747137
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
FIENCH OF SEQ ID NOS: 28208
FIRMALIANT OF SEQ ID NOS: 28208
FIRMALIANT OF SEQ ID NOS: 28208
 Sequence 17391, Application US/09248796A
Patent No. 6747137

APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17391
LENGTH: 216
 ; NAME/KEY: UNSURE
; LOCATION: (212)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknq
US-09-248-796A-17391
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 Gaps
 Gaps
 Gaps
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Query Match 2.9%; Score 13; DB 4; Length 211; Best Local Similarity 100.0%; Pred. No. 0.00031; Matches 13; Conservative 0; Mismatches 0; Indels
 2.9%; Score 13; DB 4; Length 247;
100.0%; Pred. No. 0.00036;
tive 0; Mismatches 0; Indels
 Length 216;
 0; Indels
 Query Match
2.9%; Score 13; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 13; Conservative 0; Mismatches 0;
 338 PPPTTTTTTT 350
 341 TTTTTTTTTT 353
 341 TTTTTTTTTT 353
 37 PPPTTTTTTTT 49
 TYPE: PRT
ORGANISM: Candida albicans
 74 rrrrrrrrrr 86
 : Candida albicans
 Best Local Similarity 100.
Matches 13; Conservative
 RESULT 54
US-09-248-796A-17391
 US-09-248-796A-24111
 Query Match
 ORGANISM
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APPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
 Gaps
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0
 Query Match 2.9%; Score 13; DB 4; Length 398; Best Local Similarity 100.0%; Pred. No. 0.00056; Matches 13; Conservative 0; Mismatches 0; Indels
 CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT PILING DATE: 2001-07-17
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-16
PRIOR PILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-09-17
 PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
 PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/23089
 PRIOR APPLICATION NUMBER: PCT/US99/28214
 US-09-907-794A-84; Sequence 84, Application US/09907794A; Patent No. 6635468
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 Kljavin, Ivar J.
Mather, Jannie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
 FILING DATE: 1999-10-05
 375 DADTAIINAEGGQ 387
 419 DADTAIINAEGGQ 431
 Goddard, A.
 US-09-778-510-6
 APPLICANT:
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 ; LOCATION: (287), (288), (289)
; OTHER INFORMATION: Identity of 'amino acid sequences at the above locations are unkno
US-09-248-796A-25055
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 Gaps
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 Query Match 2.9%; Score 13; DB 4; Length 398; Best Local Similarity 100.0%; Pred. No. 0.00056; Matches 13; Conservative 0; Mismatches 0; Indels
 2.9%; Score 13; DB 4; Length 292; 100.0%; Pred. No. 0.00042; ive 0; Mismatches 0; Indels
 Baum, Peter
Baum, Peter
TTON: Molecules Designated B7L1
 Molecules Designated B7L1
 APPLICANT:
TITLE OF INVENTION:
FILE REPERENCE:
CURRENT APPLICATION WUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
FRIOR PRIOR PLICATION NUMBER: PCT/US99/17906
FRIOR APPLICATION NUMBER: PCT/US99/17906
FRIOR APPLICATION NUMBER: 60/095,663
FRIOR APPLICATION NUMBER: 60/095,663
FRIOR APPLICATION NUMBER: 1998-08-07
NUMBER OF SQ ID NOS: 1998-08-07
NUMBER OF SQ ID NOS: 200
SQFTWARE: Patentin Ver. 2.0
SGFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGINE SD A
 Sequence 4, Application US/09778510

Fatent No. 6512095
GENERAL INFORMATION:
APPLICANT:
Baum, Peter
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT FILING DATE:
PRIOR APPLICATION NUMBER:
FRICK APPLICATION NUMBER:
FRICK FILING DATE:
PRIOR FILING DATE:
PRIOR FILING DATE:
PRIOR FILING DATE:
PRIOR FILING DATE:
SOFTWARE:
FRICK APPLICATION NUMBER:
FRICK PRIOR FILING DATE:
SOFTWARE:
FRICK APPLICATION NUMBER:
FRICK PRIOR FILING DATE:
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FRICK PRIOR FILING DATE:
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FRICK PRIOR PRI
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 25055
LENGTH: 292
TYPE: PRT
 Sequence 6, Application US/09778510; Patent No. 6512095; GENERAL INFORMATION:
 375 DADTAIINAEGGQ 387
 341 TITITITITIT 353
 419 DADTAIINAEGGQ 431
 Best Local Similarity 100.
Matches 13; Conservative
 TYPE: PRT
CORGANISM: Mus musculus
US-09-778-510-4
 TYPE: PRT
ORGANISM: Homo sapien
 NAME/KEY: UNSURE
 SEQ ID NO 4
LENGTH: 398
 RESULT 59
US-09-778-510-4
 Query Match
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FILING DATE: 1999-09-15

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APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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 2.9%; Score 13; DB 4; Length 398;
100.0%; Pred. No. 0.00056;
 100.0%; Pred. ...
 PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/309511
PRIOR PLILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30991
 CURRENT APPLICATION NUMBER: US/09/902,775A CURRENT FILING DATE: 2001-07-10
 PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/USOO/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
 PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
 Sequence 84, Application US/09902775A Patent No. 6686451 GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher J.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Gurney, Austin L.
Hillan, Kenneth, J
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerber, Hanspeter
Gerritsen, Mary E.
 Paoni, Nicholas F.
 Kljavin, Ivar J.
Mather, Jennie P.
 419 DADTAIINAEGGQ 431
 375 DADTAIINAEGGQ 387
 13; Conservative
 Wei-Qiang
 Eaton, Dan L.
 TYPE: PRT ORGANISM: Homo sapiens
 Goddard, A.
 Pan, James
 Query Match
Best Local Similarity
Matches 13; Conserv
 JS-09-902-775A-84
 US-09-905-125A-84
 APPLICANT
 APPLICANT
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 ö
 ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
 ö
 Query Match 2.9%; Score 13; DB 4; Length 398; Best Local Similarity 100.0%; Pred. No. 0.00056; Matches 13; Conservative 0; Mismatches 0; Indels
 CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT APPLICATION NUMBER: US/09/905,125A
PRIOR FILING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PRILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PRILING DATE: 1999-09-15
PRIOR PRILING DATE: 1999-09-15
Sequence 84, Application US/09905125A Patent No. 6664376
 Godowski, Paul J.
Grimaldi, Christopher J.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
 Gurney, Austin L.
Hillan, Kenneth, J.
 Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
 Gerritsen, Mary E.
Goddard, A.
 Gerber, Hanspeter
 419 DADTAIINAEGGQ 431
 375 DADTAIINAEGGO 387
 Desnoyers, Luc
Eaton, Dan L.
 Matches
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APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Wood, William.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 1016-6-14
CURRENT APPLICATION WOMER: US/09/906,700
CURRENT APPLICATION WOMER: US-00/1-24
REIOR APLIACATION WOMER: US-00/1-24
REIOR APPLICATION WOMER: PCT/US-9/2054
REIOR FILING DATE: 1999-00-15
REIOR APPLICATION WOMER: PCT/US-9/2054
REIOR FILING DATE: 1999-00-15
REIOR REIOR DATE: 1999-10-05
REIOR REIOR DATE: 1999-10-15
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REIOR RELIOR DATE: 1999-10-05
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REIOR RELIOR DATE: 1999-11-29
REIOR RELIOR DATE: 1999-11-29
REIOR RELIOR DATE: 1999-11-20
REIOR RELIOR DATE: 1999-12-10
REIOR RELIOR DOTE: 100-00-10-10
REIOR RELIOR DOTE: 100-00-10-10
REIOR RELIOR DOTE: 100-00-10-10
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 Length 398;
 Indels
 Query Match 2.9%; Score 13; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 13; Conservative 0; Mismatches 0;
 Sequence 84, Application US/09903603A
Patent No. 6767995
GENERAL INFORMATION:
Stewart, Timothy A.
 Ferrara, Napoleone
Filvaroff, Ellen
 Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
 419 DADTAIINAEGGQ 431
 375 DADTAIINAEGGO 387
 APPLICANT: Geneticch, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napole
APPLICANT: Filvaroff, Eller
APPLICANT: Forg, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
 Fong, Sherman
Gao, Wei-Qiang
 TYPE: PRT
CRGANISM: Homo sapiens
US-09-906-700-84
 US-09-903-603A-84
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 Score 13; DB 4; Length 398;
Pred. No. 0.00056;
 0; Indels
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 PRIOR FILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
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PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 RESULT 64
US-05-906-700-84
'Sequence 84, Application US/09906700
'Patent No. 6725335
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
 Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
 Gerritsen, Mary E.
 GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Betstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
 Gerber, Hanspeter
 375 DADTAIINAEGGQ 387
 419 DADTAIINAEGGO 431
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-84
 Goddard, A.
 APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/904,920A
CURRENT FILING DATE: 2001-07-13
 FRIOR AFFLICATION UNGER: PCI/US9/20214

PRIOR AFFLICATION UNGER: PCI/US99/20313

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-30

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-05

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1999-12-16

PRIOR PLING DATE: 1999-12-16

PRIOR PLING DATE: 1999-12-16

PRIOR PLING DATE: 1999-12-16

PRIOR AFPLICATION UNDER: PCT/US99/30991

PRIOR PLING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30999

 PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR PLILING DATE: 2001-07-13
PRIOR PLILING DATE: 2000-02-22
PRIOR PELICATION NUMBER: PCT/USO0/04414
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PLILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-13
PRIOR PLILING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/28214
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 sequence 84, Application US/09904920A
 errara, Napoleone
 Paoni, Nicholas F.
 Gerritsen, Mary E
 Gerber, Hanspeter
 Kljavin, Ivar J.
Mather, Jennie P.
 Genentech, Inc.
Ashkenazi, Avi
Botstein, David
 ong, Sherman
 Goddard, A.
 Рап, Јашев
 ## PRPLICANTY Wood, William, I TITLE OF INVENTION: Sected and Transmembrane Polypeptides and Nucleic FILE OF INVENTION: Acids Encoding the Same FILE REFERENCE: GNR.16182CL2
CURRENT APPLICATION NUMBER: US/09/903,603A
FRIOR APPLICATION NUMBER: US/09/903,603A
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PLILING DATE: 1999-07-07-28
PRIOR PLILING DATE: 1999-07-07-28
PRIOR PLILING DATE: 1999-07-08
PRIOR PLILING DATE: 1999-09-13
PRIOR PELICATION NUMBER: PCT/US99/21090
PRIOR PELICATION NUMBER: PCT/US99/22014
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PRIOR APPLICATION NUMBER: PCT/US99/22014
PRIOR PLILING DATE: 1999-11-20
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PRIOR PRIOR PLILING DATE: 1999-12-02
PRIOR PRIOR PLILING DATE: 1999-12-02
PRIOR PRIOR PLILING DATE: 1999-12-03
PRIOR PLILING DATE: 1999-10-03
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 Gaps
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 2.9%; Score 13; DB 4; Length 398;
100.0%; Pred. No. 0.00056;
 0; Indels
 0; Mismatches
 Godowski, Paul J.
Grimaldi, Christopher
 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 100.08;
 Roy, Margaret Ann
Stewart, Timothy A.
 Pan, James
Paoni, Nicholas F.
 rritsen, Mary E
Gerber, Hanspeter
 419 DADTAIINAEGGQ 431
 Best Local Similarity 100.
Matches 13; Conservative
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-603A-84
 Query Match
 APPLICANT
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375 DADTAIINAEGGQ 387

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RESULT 66 US-09-904-920A-84

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APPLICANT: Paoni, Nicholas F.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-114
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/USO0/04414
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 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
PRIOR PLINGATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
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PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
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PRIOR PELING DATE: 1999-09-08
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 PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 398
 APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/30911
 Sequence 84, Application US/09905381A Patent No. 6818746
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerritsen, Mary E.
 Gerber, Hanspeter
 Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
 375 DADTAIINAEGGQ 387
 419 DADTAIINAEGGO 431
 Desnoyers, Luc
Eaton, Dan L.
 Fong, Sherman
Gao, Wei-Qiang
 TYPE: PRT
CRGANISM: Homo sapiens
US-09-909-064-84
 Goddard, A.
 GENERAL INFORMATION
 US-09-905-381A-84
 PRIOR
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 APPLICANT: Milawin, Nemicul, O.
APPLICANT: Milawin, Nemicul, O.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, Jawin, Nicholas F.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
APPLICANT: Wood, WINGER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
 Gaps
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 Length 398;
 0; Indels
 Score 13; DB 4; L
Pred. No. 0.00056;
 Mismatches
 FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
 FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
 FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
 APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
 APPLICATION NUMBER: PCT/US99/28564
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 Sequence 84, Application US/09909064
Patent No. 681849
GENERAL INFORMATION:
 Query Match 2.9%; Scc
Best Local Similarity 100.0%; Pr
Matches 13; Conservative 0;
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
 Gao, Wei-Qiang
Gerber, Hanspeter
 Gerritsen, Mary E
 Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
 419 DADTAIINAEGGO 431
 375 DADTAIINAEGGO 387
 Eaton, Dan L.
 Goddard, A.
 US-09-909-064-84
 CURRENT APPL.
CURRENT FILLING
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 Sequence 1, Application US/08659984A
; Sequence 1, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
 APPLICANT: Sinds Sukanto
 APPLICANT: Sinds Sukanto
 TITLE OF INVENTION: Inhibition
 TITLE OF INVENTION: Inhibition
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE Townsend and Townsend and Crew LLP
 STREET: Two Enhancedero Ctr., 8th Floor
 STREET: Two Enhancedero Ctr., 8th Floor
 STATE: California
 COUNTRY: USA
 COUNTRY: USA
 MEDIUM TYPE: Floppy disk
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 COMPUTER: IBM PC Compatible
 COMPUTER: IBM PC Compatible
 COMPUTER: IBM PC Compatible
 2.9%; Score 13; DB 4; Length 398;
100.0%; Pred. No. 0.00056;
 Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-UN-1996
CLASSIFICATION: 436
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 PRIOR PELICATION NUMBER: DCT/US99/20594
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-08
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
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PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
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PRIOR PELING DATE: 1999-12-03
PRIOR PELING DATE: 1999-12-03
PRIOR PELING DATE: 1999-12-03
PRIOR PELING DATE: 1999-13-03
PRIOR PELING DAT
 375 DADTAIINAEGĞQ 387
 419 DADTAIINAEGGQ 431
 ORGANISM: Homo sapiens
US-09-906-618-84
 US-08-659-984A-1
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 APPLICANT: ROY, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thuas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
 Gaps
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 Score 13; DB 4; Length 398;
Pred. No. 0.00056;
 0; Indels
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
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PRIOR PLILING DATE: 2990-11-25
PRIOR PLILING DATE: 2990-11-25
PRIOR PLILING DATE: 2990-11-25
PRIOR PLILING DATE: 2990-11-20
 FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/906,618

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07
 Godowski, Paul J.
Grimaldi, Christopher J.
 Sequence 84, Application US/09906618
Patent No. 6828146
GENERAL INFORMATION:
 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Ferrara, Napoleone
Filvaroff, Ellen
 Pan, James
Paoni, Nicholas F.
 Gao, Wei-Qiang
Gerber, Hanspeter
 Gerritsen, Mary E
 419 DADTAIINAEGGQ 431
 Desnoyers, Luc
 Fong, Sherman
 Eaton, Dan L.
 TYPE: PRT; ORGANISM: Homo sapiens
US-09-905-381A-84
 Goddard, A.
 -09-906-618-84
 APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
APPLICANT:
 PPLICANT
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 Sequence 5, Application US/08659984A

Sequence 5, Application US/08659984A

Patent No. 594240

GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukano

APPLICANT: Sinha, Sukano

TITLE OF INVENTION: Assays for Detecting Beta-Secretase

TITLE OF INVENTION: Inhibition

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Ctr., 8th Floor

COUNTRY: California

COUNTRY: USA
 Query Match 2.9%; Score 13; DB 3; Length 421; Best Local Similarity 100.0%; Pred. No. 0.00059; Matches 13; Conservative 0; Mismatches 0; Indels
 Query Match 2.9%; Score 13; DB 4; Length 432; Best Local Similarity 100.0%; Pred. No. 0.0006; Matches 13; Conservative 0; Mismatches 0; Indels
 COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILLING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILLING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
 APPLICANT:
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
FILE REPERENCE: 1999-08-05
PRIOR PLING DATE: 1999-08-05
PRIOR PLING DATE: 1999-08-05
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VOICE: 1998-08-07
SEQ ID NO 2
LENGTH 432
TYPE: PRT
 Sequence 2, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 303 LNKTDNGTYRCEA 315
 409 DADTAIINAEGGQ 421
 272 LNKTDNGTYRCEA 284
 419 DADTAIINAEGGQ 431
 ORGANISM: Homo sapien
 RESULT 73
US-08-659-984A-5
 RESULT 72
US-09-778-510-2
 US-09-778-510-2
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 Score 13; DB 2; Length 421;
Pred. No. 0.00059;
0; Mismatches 0; Indels
 APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Reim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESCONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
 REGISTRATION NUMBER: 29,541
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPAK: 415-326-2400
TELEPAK: 415-326-2402
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acids
STRANDEDNESS: single
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: O'-JUN-1995
ATTORNEY/AGBNT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELEPHONE: 415-326-2400
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
 Sequence 1, Application US/08660531
Patent No. 6221645
 TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
 LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
 303 LNKTDNGTYRCEA 315
 272 LNKTDNGTYRCEA 284
 TOPOLOGY: linear MOLECULE TYPE: protein US-08-659-984A-1
 MOLECULE TYPE: protein
 linear
 COUNTRY: USA
ZIP: 94111-3834
 GENERAL INFORMATION:
 FILING DATE:
 US-08-660-531-1
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303 LNKTDNGTYRCEA 315

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 Query Match 2.9%; Score 13; DB 2; Length 444; Best Local Similarity 100.0%; Pred. No. 0.00062; Matches 13; Conservative 0; Mismatches 0; Indels
 Query Match 2.9%; Score 13; DB 3; Length 444; Best Local Similarity 100.0%; Pred. No. 0.00062; Matches 13; Conservative 0; Mismatches 0; Indels
 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/660,531

FILING DATE:

CLASSIFICATION A35

PROOF APPLICATION DATA:

PUBLICATION NUMBER: US/08/480,498

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INPORMATION:

NAME: Heslin, James M.

REGISTRATION NUMBER: 29,541

REGISTRATION NUMBER: 29,541

REGISTRATION NUMBER: 29,541

REGISTRATION NUMBER: 15270-002210US

TELEPHONE: 415-326-2400
 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Ctr., 8th Floor CITY: San Francisco STATE: California STATE: California ZIP: 94111-3834
REGISTRATION NUMBER: 29,541
REPERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPAX: 415-326-2420
INFORMATION FOR SEQ ID NO: 5: CONTROLL OF SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
 APPLICANT: Chrysler, Susanna M.S. APPLICANT: Sinha, Sukanto APPLICANT: Keim, Pamela S. APPLICANT: Anderson, John P. ITITLE OF INVENTION: Beta-Secretase NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 5, Application US/08660531; Patent No. 6221645; GENERAL INFORMATION:
 TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
 295 LNKTDNGTYRCEA 307
 303 LNKTDNGTYRCEA 315
 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 TOPOLOGY: linear
MOLECULE TYPE: protein
 single
 , MOLECULE TYPE: protein US-08-659-984A-5
 TYPE: amino acid
STRANDEDNESS: sir
 US-08-660-531-5
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CONTRIVE OF THE REFERENCE: 1079248796A

FILE OF INVENTION: Wolls.

FILE REFERENCE: 107196-132

CURRENT FILING DATE: 1999-02-13

FRIOR FILING DATE: 1998-02-13

FRIOR FILING DATE: 1998-03-13

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 Length 543;
 Query Match 2.9%; Score 13; DB 4; Length 543
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 13; Conservative 0; Mismatches 0; Indels
 Search completed: June 28, 2005, 10:22:30 Job time: 34.659 secs
 341 TITITITITIT 353
295 LNKTDNGTYRCEA 307
 ; ORGANISM: Candida albicans
US-09-248-796A-22504
 TYPE: PRT
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 28, 2005, 10:07:28; Search time 25.4289 Seconds (without alignments) 1600.529 Million cell updates/sec
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
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 283416
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
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 SUMMARIES
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 - protein search, using sw model
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|                                                                                     |                                                                                                                                                                                                                  |                                                                                                   | 749.7<br>749.130<br>740.134<br>741.759<br>741.759<br>741.759<br>726.166<br>726.166<br>839.615<br>839.615<br>839.615<br>839.615<br>839.615<br>839.615                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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## ALIGNMENTS

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C, Special protein Y43F8C.9 - Caenorhabditis elegans
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C, Accession: Tacksun 126880
R, Ainscough, R.
Submitted to the EMBL Data Library, October 1998
A, Reference number: 220279
A, Reference number: 220279
A, Reference number: 220279
A, Reference number: DNA
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Status: preliminary; translated from GB/EMBL/DDBJ
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A, Cross-references: UNIPPOT:09xWN0; EMBL:AL032637; PIDN:CAA21621.1; CESP:Y43F8C.9
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A, Gene: CESP:Y43F8C.9
A, Introns: 40/3
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Query Match

3.5%; Score 15; DB 2; Length 108;

probable WRKY-type DNA binding protein At2g38470 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein T19C21.4 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Dard-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004 C;Accession: T02498; D84805 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,

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promastigote surface antigen P2 (clone 4.6) precursor - Leishmania major (fragment) C,Species: Leishmania major C,Accesion: S20074; D41710 R;Murray, P.J.; Spithill, T.W.
J. Biol. Chem. 266, 24477-24484, 1991
A,Title: Variants of a Leishmania surface antigen derived from a multigenic family. A,Reference number: A41710; MUID:92105105; PMID:1761547
A,Reference number: A41710; MUID:92105105; PMID:1761547
A,Rolcoule type: MRNA
A,Residues: 1-327 AMURA
A,Residues: 1-327 AMURA
A,Cross-references: UNIPROT:Q25334; EMBL:X57135; NID:g9582; PID:g9583
C,Keywords: Dlocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage F;1-299/Product: promastigote surface antigen P2 (fragment) #status predicted APSA>F;300-327/Domain: carboxyl-terminal propeptide #status predicted carboxyl end (ASP) (in mature form)
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 Query Match 3.5%; Score 15; DB 2; Length 327; Best Local Similarity 100.0%; Pred. No. 6e-06; Matches 15; Conservative 0; Mismatches 0; Indels
 Query Match 3.3%; Score 14; DB 2; Length 304; Best Local Similarity 100.0%; Pred. No. 4.9e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 Indels
Pred. No. 2.4e-06;
; Mismatches 0;
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100.08;
 335
 335
 183 PPITITITITITI 197
 48 PPTTTTTTTTT 62
 322 PTTTTTTTTTT 335
 67 PTTTTTTTTT 80
 15; Conservative
 321 PPTTTTTTTTTT
 321 PPTTTTTTTTT
 Best Local Similarity
Matches 15; Conserv
 C,Genetics:
A,Gene: CESP:EEED8.11
A,Introns: 27/1; 242/2
 RESULT 2
 RESULT 3
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A, Residues: 1-518 < MIC>
A, Residues: 1-518 < MIC>
A, Cross-references: UNIPROT: 043753; EMBL: Z18952; MID: 918319; PIDN: CAA79477.1; PID: 918320
C; Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C; Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph F; 278/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
 C,Species: Dictyostelium discoldeum
C,Species: Dictyostelium discoldeum
C,Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 09-Jul-2004
C,Accession: A35679; S14202; S15811
R,Leiting, B.; Lindner, I.J.; Noegel, A.A.
R,Leiting, B.; Lindner, I.J.; Noegel, A.A.
A,Title: Biol. 10, 372-3735, 1990
A,Title: The extrachromosomal replication of Dictyostelium plasmid Ddp2 requires a cis-a. A;Reference number: A35679; MUID:90287164; PMID:2192261
 A;Residues: 1.889 <LBI>
A;Residues: 1.889 <LBI>
A;Cross-references: UNIPROT:023895; GB:M55298; NID:g167727; PIDN:AAA33191.1; PID:g167728
B;Slade, M.B.; Chang, A.C.M.; Williams, K.L.
Plasmid 24, 195-207, 1990
 mucin-like glycoprotein 900 - Cryptosporidium parvum
C;Species: Cryptosporidium parvum
C;Species: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T3lla,
R;Barnes, D.A.; Bonnin, A.; Huang, J.X.; Gousset, L.; Wu, J.; Gut, J.; Doyle, P.; Dubrem Mol. Biochem. Parasitol. 96, 93-110, 1998
A;Title: A novel multi-domain mucin-like glycoprotein of Cryptosporidium parvum mediates
A;Accession: T3ll13
 A,Title: The sequence and organization of Ddp2, a high-copy-number nuclear plasmid of Di
A,Reference number: S14202; MUID:91172902; PMID:2077544
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 A;Molecule type: DNA
A;Residues: 1-141,'I',143-353,'A',355-780,'E',782-885,'GY' <SLA2>
A;Cross-references: EMBL:X51478; NID:g7307; PIDN:CAA35843.1; PID:g7308
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0
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 rep protein - slime mold (Dictyostelium discoideum) plasmid Ddp2
 Length 518;
 Length 889
 0; Indels
 Indels
 DB 2; Le
 Score 14; DB 2; Le
Pred. No. 0.00012;
 ;Residues: 1-141,'I',143-780,'E',782-885,'GY' <SLA1>;Cross-references: EMBL:X51478;Slade, M.B.
 A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
 submitted to the EMBL Data Library, January 1990
A;Reference number: S15811
A;Accession: S15811
 100.0%; Pred.
 3.3%; Score 14;
.00.0%; Pred. No.
 322 PITITITITIT 335
 323 TTTTTTTTTT 336
 Trrrrrrrrrrr 472
 3.3%
Best Local Similarity 100.0
Matches 14; Conservative
 14; Conservative
 Query Match
Best Local Similarity
 Status: preliminary
 A, Molecule type: mRNA
 ;Molecule type: DNA
 ;Molecule type: DNA
 Accession: A35679
 Accession: S14202
 A; Genome: plasmid
 Genetics:
 Matches
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 Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
RiPark, K.Y.; Drory, A.; Woodson, W.R.
Plant Mol. Biol. 18, 377-386, 1992
A;Title: Molecular cloning of an 1-aminocyclopropane-1-carboxylate synthase from senesci
A;Reference number: S19252
A;Reference number: S19252
A;Reture: preliminary
A;Residues: 1-516 <PAR>A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
Cipate: UNIPROT:P27486; EMBL:M66619
C;Suparefamily: 1-aminocyclopropane-1-carboxylate synthase
C;Suparefamily: 1-aminocyclopropane thylene biosynthesis; phosphoprotein; pyridoxal phosph
F;276/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
 C;Species: Dianthus caryophyllus (clove pink)
C;Species: Dianthus caryophyllus (clove pink)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: 331442
Submitted to the EMBL Data Library, December 1992
Submitted to the EMBL Data Library, December 1892
A;Abscription: Isolation of petal senescence-associated cDNA clones encoding 1-aminocycl
A;Accession: S31442
 A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-512 «ROU»
A; Residues: 1-512 «ROU»
A; Rouses: cultivar Columbia
A; Experimental source: cultivar Columbia
B; Edin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Muture 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MulD:20083487; PMID:10617197
 ö
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submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.
A;Reference number: 214676
 A; Cross-references: GB: AE002093; NID: g6598471; PIDN: AAC67339.2; GSPDB: GN00139
 Gaps
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 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - clove pink
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 3.3%; Score 14; DB 2; Length 516; 100.0%; Pred. No. 7.7e-05; tive 0; Mismatches 0; Indels
 3.3%; Score 14; DB 2; Length 512;
100.0%; Pred. No. 7.6e-05; .
tive 0; Mismatches 0; Indels
 A;Gene: At2g38470; T19C21.4
A;Map position: 2
A;Introns: 74/3; 143/3; 321/2; 375/2
 323 TTTTTTTTTT 336
 457 Tritititititi 470
 122 Prirrirririri 135
 322 PTTTTTTTTT 335
 Query Match
Best Local Similarity 100.
Matches 14; Conservative
 14; Conservative
 Query Match
Best Local Similarity
 A Status: preliminary
A Molecule type: DNA
A, Residues: 1-512 <STO>
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C;Genetics:

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RESULT 6

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CJACCession: 339310

R) Ramassamy, R.; Ranasinghe, C.
submitted to the EMBL Data Library, November 1993

A; Description: Cycle ds DNA sequencing of a malaria parasite protein from infected blood

A; Reference number: S39310

A; Accession: S39310
 Rimarshall, V.M.; Coppel, R.L.; Anders, R.F.; Kemp, D.J.
Mol. Biochem. Parasitol. 50, 181-184, 1992
A;Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2)
A;Reference number: A45632; MUID:92178286; PMID:1542312
A;Contents: KF1916
A;Accession: A45632
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26868
R;Ainscough, R.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z20279
A;Accession: T2666
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T2656
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-245 < WIL>
A;Ross=references: UNIRROT:09XWP2; EMBL:AL032637; PIDN:CAA21609.1; CESP:Y43F8C.5
A;Experimental source: clone Y43F8C
 merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 22-Apr.1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45632
 merozoite surface antigen - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-278 <RAM>
A;Cross-references: UNIPROT:Q25862; EMBL:X76087; NID:g434996; PID:g836639
C;Superfamily: Epstein-Barr virus nuclear antigen
 A;Cross-references: UNIPROT:P50497; GB:M73810; NID:g160484; PID:g160485 A;Note: sequence extracted from NCBI backbone (NCBIN:85252, NCBIP:85257) C;Superfamily: Epstein-Barr virus nuclear antigen C;Keywords: surface antigen
 Length 245;
 Length 274;
 3.1%; Score 13; DB 2; Length 278;
 Indels
 0; Indels
 3.1%; Score 13; DB 2; Le:
ilarity 100.0%; Pred. No. 0.00035;
Conservative 0; Mismatches 0;
 Query Match
3.1%; Score 13; DB 2; Lv
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 13; Conservative 0; Mismatches 0;
 97 TTTTTTTTT 109
 321 PPTTTTTTT 333
 323 TTTTTTTTTTT 335
 C; Keywords: surface antigen
 Local Similarity
les 13, Conserv
 A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-274 < MAR>
 A; Gene: CESP:Y43F8C.5
A; Introns: 69/3; 163/2
 Query Match
 Query Match
 Best Loca
Matches
 C; Genetics:
 RESULT 13
 A45632
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 B56888

alkaline phosphatase (EC 3.1.3.1), intestinal type II - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 05-3na-1996 #sequence_revision 05-Jan-1996 #text_change 16-Aug-2004

C;Accession: B56888

R;Engle, M.J; Alpers, D.H.

Ciln. Chem. 38, 2506-2509, 1992

A;Title: The two mRNAs encoding rat intestinal alkaline phosphatase represent two distin

A;Reference number: A56888; MUID:93092310; PMID:1458592

A;Accession: B56888
 A,Cross-references: UNIPROT:096503; EMBL:AF068065; NID:94063041; PID:94063042; PIDN:AAC$
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 RESULT 10
Sol358
salivary glue protein ags-3 precursor - fruit fly (Drosophila simulans)
CiSpecies: Drosophila simulans
CiSpecies: Drosophila simulans
CiDate: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
CiSpecies: Mayers, A2988
Ascession: Sol358, A2988
A;Ritle: Evolution and expression of the Sgs-3 glue gene of Drosophila.
A;Reference number: Sol358, MUID:88332966; PMID:3138416
A;Recession: Sol358
A;Status: not compared with conceptual translation
 A; Experimental source: duodenal mucosa
A;Note: sequence extracted from NCBI backbone (NCBIN:121249, NCBIP:121252)
C;Superfamily: Alkaline phosphatase
C;Keywords: intestine; membrane protein; phosphoric monoester hydrolase
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 A;Cross-references: FlyBase:FBgn0012853
C;Superfamily: salivary glue protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-217/Product: salivary glue protein sgs-3 #status predicted
 Length 1832;
 Score 13; DB 2; Length 217;
Pred. No. 0.00032;
0; Mismatches 0; Indels
 3.1%; Score 13; DB 2; Length 67; larity 100.0%; Pred. No. 0.00012; Conservative 0; Mismatches 0; Indels
 Indels
 hypothetical protein Y43F8C.5 - Caenorhabditis elegans
 Query Match
3.3%; Score 14; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 14; Conservative 0; Mismatches 0;
 3.1%; Scor.
100.0%; Pred. No. v...
 A;Residues: 1-217 <MAR>
A;Cross-references: UNIPROT:P13729
C;Genetics:
 PTTTTTTTTT 335
 373 Priririririri 386
 TTTTTTTTTT 335
 323 TTTTTTTTTT 335
 rrrrrrrrrrr 61
 Best Local Similarity 100.
Matches 13; Conservative
 Local Similarity
nes 13; Conserv
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-67 <ENG>
 A; Molecule type:
 322
 323
 27
 Query Match
 A;Gene: Sgs-3
 Query Match
 49
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Best Loca Matches

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RESULT 11

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-517 <WIL>
A;Cross-references: UNIPROT:Q19269; EMBL:Z73896; PIDN:CAA98057.1; GSPDB:GN00022; CESP:FO
A;Experimental source: clone F09E8
C;Genetics:
A;Gene: CESP:F09E8.6
 alkaline phosphatase (EC 3.1.3.1) - rat
N;Alternate names: phytase
N;Alternate names: phytase
C;Species: Rattum norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S18408; S17576
R;Strom, M.; Krisinger, J.; DeLuca, H.F.
Biochim. Biophysa Acta 1090, 299-304, 1991
A;Title: Isolation of a mRNA that encodes a putative intestinal alkaline phosphatase reg
A;Reference number: S18408; MUID:92062729; PMID:1954251
 AjCross-references: UNIPROT:P51740
AjNote: the correct sequence of residues 144-160 is shown in Fig. 2; the corresponding c
R;Yang, W.J.; Matsuda, Y.; Sano, S.; Masutani, H.; Nakagawa, H.
Biochim. Biophys. Acta 1075, 75-82, 1991
 A;Cross-references: UNIPROT:Q09592; EMBL:Z46935; PIDN:CAA87049.1; GSPDB:GN00020; CESP:M1
A;Experimental source: clone M106
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 C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23739
 Gaps
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 A;Map position: 2
A;Introns: 47/2; 110/3; 185/2; 231/2; 270/2; 321/2; 347/3; 411/3; 452/3
C;Superfamily: Caenorhabditis elegans hypothetical protein M106.2
 ö
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 Length 517;
 Length 519;
 Indels
 Indels
 A;Map position: 4
A;Introns: 40/1; 110/3; 141/2; 219/3; 393/1
C;Superfamily: probable zinc metalloproteinase T04G9.2
 DB 2; Ler
. 0.00066;
ches 0;
 Query Match 3.1%; Score 13; DB 2; Le Best Local Similarity 100.0%; Pred. No. 0.00066; Matches 13; Conservative 0; Mismatches 0;
 aypothetical protein M106.2 - Caenorhabditis elegans
 R;Palmer, S.

Bubmitted to the EMBL Data Library, December 1994
ByReference number: Z19792
A;Accession: T23739
A;Status: prellnimary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-519 <WIL>
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 submitted to the EMBL Data Library, May 1996
A;Reference number: Z19307
A;Accession: T20658
 323 TTTTTTTTTTT 335
 323 TITITITITIT 335
 334 rrrrrrrrrrrr 346
 A;Molecule type: mRNA
A;Residues: 1-551 <STR>
 A;Status: preliminary
 A;Gene: CESP:M106.2
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 RESULT 18
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 submitted to the EMBL Data Library, February 1996
A;Reference number: Z19503
A;Accession: T22023
A;Status: Systy translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-284 <WIL>
A;Cross-references: UNIPROT:Q20202; EMBL:Z69792; PIDN:CAA93666.1; GSPDB:GN00028; CESP:F4
 A;Residues: 1-341 «KEM»
A;Cross-references: EMBL:AF045635; PIDN:AAC02556.1; GSPDB:GN00022; CESP:C05G6.3
A;Experimental source: strain Bristol N2; clone C05G6
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 RESULT 14
T12023
T120203
C) Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: L5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T22023
R; Smye, R.
 hypothetical protein C05G6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32949
 probable zinc metalloproteinase F09E8.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T20658
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 Query Match 3.1%; Score 13; DB 2; Length 284; Best Local Similarity 100.0%; Pred. No. 0.0004; Matches 13; Conservative 0; Mismatches 0; Indels
 Query Match 3.1%; Score 13; DB 2; Length 341; Best Local Similarity 100.0%; Pred. No. 0.00047; Matches 13; Conservative 0; Mismatches 0; Indels
 0; Indels
 Rikemp, K.

Bubmitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid C05G6.
A;Reference number: Z21252
A;Accession: T32949
100.0%; Pred. No. 0.00039;
tive 0; Mismatches 0;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
 A; Introns: 52/2; 110/1; 151/3; 195/1; 254/3; 295/3
 A;Map position: X
A;Introns: 34/3; 76/2; 141/3; 183/3; 240/3
 A; Experimental source: clone F40E10
 101 TTTTTTTTTT 113
 323 TITITITITI 335
 323 TTTTTTTTT 335
 91 TTTTTTTTTT 103
 323 TTTTTTTTT 335
 214 riririririri 226
 Matches 13; Conservative
Best Local Similarity
 C,Genetics:
A,Gene: CESP:F40E10.5
 A; Gene: CESP: C05G6.3
 A; Map position: 4
 RESULT 16
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A;Map position: 1
A;Introns: 29/2; 54/3; 93/3; 180/2; 236/1; 264/2; 471/3; 486/3; 583/3
 A, Experimental source: strain AX4 C, Genetics: A, Gene: docA
 323 TITITITITI 335
 323 TITITITITIT 335
 323 TITITITITI 335
 513 Trititititit 525
 672 říříříříříříříří 684
 Query Match
Best Local Similarity 100.C
Matches 13; Conservative
 A;Reference number: Z16456
A;Accession: T08611
 Local Similarity
les 13; Conserv
 A;Residues: 1-781 <ZHA>
 A; Gene: CESP: F55D12.5
 A;Status: preliminary A;Molecule type: DNA
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 Query Match
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Matches
 RESULT 21
 RESULT 22
 RESULT 23
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 RESULT 20
Tyll75
hypothetical protein FS5D12.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T21175, T22735
R;Mcmrray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19385
A;Accession: T21175
A;Accession: T21175
A;Residus: preliminary; translated from GB/EMBL/DDBJ
A;Residus: L-651 <WIL>
A;Residus: L-651 <WIL>
A;Cross-references: UNIPROT:Q19659; EMBL:Z75538; PIDN:CAA99842.1; GSPDB:GN00019; CESP:FF
R;McMurray, A.
A;Title: Purification and characterization of phytase from rat intestinal mucosa. A;Reference number: $17576; MUD:91370007; PMID:1654110
A;Accession: $17576
A;Molecule type: protein
A;Residues: 20-29 <XAN>
A;Note: 10-Val was also found
C;Superfamily: alkaline phosphatase
C;Keywords: phosphoric monoester hydrolase
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-560 <HEN>
A;Cross-references: EMBL:AF039047; PIDN:AAB94223.1; GSPDB:GN00023; CESP:KIID12.1
A;Experimental source: strain Bristol N2; clone K11D12
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 submitted to the EMBL Data Library, June 1996
A;Reference number: 219606
A;Reference number: 219606
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-651 <WI2>
A;Cressines: 1-651 <WI2>
A;Cressines: 1-651 <WI2>
A;Cressines: 1-651 <WI2>
A;Cressinental source: Clone F55D12
C;Genetics:
 hypothetical protein K11D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T32661
R;Henkhaus, J.; Wohldmann, P.; Gillam, B.
Submitted to the BMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid K11D12.
A;Reference number: Z21207
 A; Introns: 5/3; 48/3; 90/3; 127/3; 149/3; 190/1; 207/1; 233/3; 264/1; 480/1
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 Length 551;
 Query Match 3.1%; Score 13; DB 2; Length 560; Best Local Similarity 100.0%; Pred. No. 0.00071; Matches 13; Conservative 0; Mismatches 0; Indels
 0; Indels
 Query Match 3.1%; Score 13; DB 2; I Best Local Similarity 100.0%; Pred. No. 0.0007; Matches 13; Conservative 0; Mismatches 0;
 $11 TTTTTTTTTT 523
 323 TTTTTTTTTT 335
 323 TITITITITIT 335
 345 rrrrrrrrrrrr 357
 C;Genetics:
A;Gene: CESP:K11D12.1
A;Map position: 5
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C;Species: Ruminococcus flavefaciens
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51592.
Moritine: Martin, J:; Flint, H.J.
Mol. Gen. Genet. 245, 260-264, 1994
A;Title: Identification of non-catalytic conserved regions in xylanases encoded by the xy
A;Reference number: S51592; MUID:95115675; PMID:7816035
 A;Cross-references: UNIPROT:052753; EMBL:235226; NID:g516273; PIDN:CAA84537.1; PID:g51627: F;42-239/Domain: endo-1,4-beta-xylanase homology <XYL>F;258-401/Domain: Thermotoga xylanase A amino-terminal repeat homology <TXA>
 protein phosphatase 2C-like protein Spalten - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08606
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 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRMA
A;Residues: 1-831 cAUB>
A;Cross-references: UNIPROT:O15756; EMBL:AF020409; NID:g2425146; PID:g2425147
 hypochetical protein DocA - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Becies: Dictyostelium discoideum
C;Bece: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: 708611
R;Aubry, L.; Firtel, R.A.; Iranfar, N.
submitted to the EMBL Data Library, August 1997
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 3.1%; Score 13; DB 2; Length 781;
100.0%; Pred. No. 0.00094;
rative 0; Mismatches 0; Indels
 Length 831;
 Length 651;
 Indels
Query Match
3.1%; Score 13; DB 2; Les
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 13; Conservative 0; Mismatches 0;
 3.1%; Score 13; DB 2; Le ilarity 100.0%; Pred. No. 0.00099; Conservative 0; Mismatches 0;
 KynB precursor - Ruminococcus flavefaciens
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A;Molecule type: DNA
A;Residues: 1-1083 <WAD>
A;Cross-references: UNIPROT:Q12075; GB:D31909; GB:D17441; NID:g559718; PIDN:BAA06705.1; F
 phospholipase C - yeast (Candida albicans)
CiSpecies: Candida albicans
CiSpecies: Candida albicans
CiDate: 12-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiAccession: T18257
RiBennett, D.E.; Mccreary, C.E.; Coleman, D.C.
RiBennett, D.E.; Mccreary, C.E.; Coleman, D.C.
A;Title: Genetic characterization of a phospholipase C gene from Candida albicans: preser A;Reference number: Z18844; MUID:98129081; PMID:9467900
A;Accession: T18257
 A;Residues: 1-1099 <BEN>
A;Cross-references: UNIPROT:013433; EMBL:Y13975; NID:g2462981; PIDN:CAA74308.1; PID:g2465
 glycoprotein A - mouse
C.Species: Mus musculus (house mouse)
C.Jaces 102-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 15-Jun-2001
C.Jacession: JE0120
R.Haidaris, C.G.; Medzihradsky, O.F.; Gigliotti, P.; Simpson-haidaris, P.J.
DNA. Res. 5, 77-85, 1998
À;Title: Molecular characterization of mouse Pneumocystis carinii surface glycoprotein A
A;Reference number: JE0120; MUID:98344138; PMID:9679195
 A,Gene: PLC1
P;566-726/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
 C;Accession: JC2300
R;Wada, M.; Nakamura, Y.
DNA Res. 1, 165-168, 1994
A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis
A;Reference number: JC2299; MUID:96051989; PMID:8535973
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 C;Species: Pneumocystis carinii
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
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 C, Superfamily: Pneumocystis carinii major surface glycoprotein MSG100
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 Length 1083;
 Length 1099;
 Indels
 Indels
 C; Comment: This protein is a surface antigen of pneumonia.
 - Pneumocystis carinii
 3.1%; Score 13; DB 2; Le ilarity 100.0%; Pred. No. 0.0012; Conservative 0; Mismatches 0;
 3.1%; Score 13; DB 2; Le
100.0%; Pred. No. 0.0012;
ttive 0; Mismatches 0;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
 glycoprotein MSG100
 A,Molecule type: mRNA
A,Residues: 1-1282 <HAI>
A,Cross-references: GB:AF143102
 323 TTTTTTTTT 335
 323 TTTTTTTTTT 335
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 959 riririririri 971
 Conservative
 C, Keywords: glycoprotein
 Query Match
Best Local Similarity
Matches 13; Conserv
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les 13; Conserv
 A; Accession: JE0120
 A,Gene: MSG100
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 Query Match
Best Local
 cell surface
 C;Genetics:
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 RESULT 28
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 glutactin - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S12319
R;Olson, P.F.; Fessler, L.I.; Nelson, R.E.; Sterne, R.E.; Campbell, A.G.; Fessler, J.H.
BMBO J. 9, 1219-1227, 1990
A;Title: Glutactin, a novel Drosophila basement membrane-related glycoprotein with seque A;Reference number: S12519; MUID:90214632; PMID:2108864
 A;Accession: S12519
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1023 <OLS>
A;Cross-references: UNIPROT:P33438; EMBL:X53286; NID:g297084; PIDN:CAA37380.1; PID:g2970
 A; Molecule type: mRNA
A; Residues: 1-1076 < KIT>
A; Residues: 1-1076 < KIT>
A; Cross-references: UNIPROT: Q01830; DDBJ: D21827; NID: 9425784; PIDN: BAA04851.1; PID: d1005
C; Superfamily: Pneumocystis carinii major surface glycoprotein MSG100
C; Keywords: glycoprotein
 major surface glycoprotein 5 - Pneumocystis carinii
C;Species: Pneumocystis carinii
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JC2217
R;Kitada, K.; Wada, M.; Nakamura, Y.
B)NA Res. 1, 57-66, 1994
A;Title: Multi-gene family of major surface glycoproteins of Pneumocystis carinii: full-A;Reference number: JC2217, MUID:96051981; PMID:7584029
A;Accession: JC2217
 F;245,471,574,804,837/Binding site: carbohydrate (Asn) (covalent) #status predicted
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R;Aubry, L.; Firtel, R.A.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z16454
A;Accession: T08606
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: L-975 <AUB>
A;Cross-references: UNIPROT:O15743; EMBL:AF019985; NID:g2425120; PID:g2425121
A;Experimental source: strain AX3
C;Genetics:
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 3.1%; Score 13; DB 2; Length 1023; 100.0%; Pred. No. 0.0012; ive 0; Mismatches 0; Indels
 Score 13; DB 2; Length 1076;
Pred. No. 0.0012;
0; Mismatches 0; Indels
 3.1%; Score 13; DB 2; Length 975; Similarity 100.0%; Pred. No. 0.0011; 3; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. ...
 603 rrrrrrrrrrrr 615
 323 TITITITITIT 335
 323 TTTTTTTTTTT 335
 951 rrrrrrrrrrr 963
 Query Match 3.1
Best Local Similarity 100.
Matches 13; Conservative
 Best Local Similarity 100.
Matches 13; Conservative
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 A; Introns: 390/3
 Query Match
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 A, Gene: spnA
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C;Accession: S71628; S78068 — S. S. S. Simon, M.I. Schuster, S.C.; Neegell, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I. EMBO J. 15, 3880-3889; 1996 — S. S. Simon, M.I. S. Shalos S. S. Simon, M.I. S. Shalos S. S. Simon, M.I. Shalos S. S. Simon, S. Simon, S. S. Simon, S. S. Simon, A;Residues: 1-1670 SCH>
A;Cross-references: UNPROT:Q23901; EMBL:X96869
A;Experimental source: strain AX2; substrain 214
R;Schuster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I.
Bybnitted to the EMBL Data Library, March 1996
A;Description: The hybrid histidine kinase DokA is part of the osmotic response system of A;Reference number: S78068
 A Description: modulates cell response to changes in osmolarity; involved in spore format C. Keywords is phosphoprotein; signal transduction F;1520-1629/Domain: response regulator homology <RRH2> F;1568/Binding site: phosphate (Asp) (covalent) #status predicted
 A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1737 <GEI>
A;Residues: 1-1737 <GEI>
A;Cross-references: UNIPROT:09TW28; GB:AF090533; NID:g5714395; PIDN:AAD47903.1; PID:g5714.
 RiGeissler, H.; Schwarz, B.C.; Soldati, T. submitted to GenBank, September 1998
Alpescription: Identification of two novel and highly divergent myosins in Dictyostelium
A;Recension: A59235
A;Accession: A59235
 sensory transduction histidine kinase dokA - slime mold (Dictyostelium discoideum) C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
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 unconventional myosin heavy chain MyoM - slime mold (Dictyostelium discoideum)
 A;Molecule type: DNA
A;Residues: 1-149,'E',151-219,'TRVLKLIQSTNNWIYWY',238-1671 <SCW>
A;Cross-references: EMBL:X96869; NID:g1237201; PIDN:CAA65612.1; PID:g1237202
 C;Species: Dictyostelium discoideum
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A59235
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 Query Match 3.1%; Score 13; DB 2; Length 1671; Best Local Similarity 100.0%; Pred. No. 0.0018; Matches 13; Conservative 0; Mismatches 0; Indels
 Ouery Match 3.1%; Score 13; DB 2; Length 1737; Best Local Similarity 100.0%; Pred. No. 0.0018; Matches 13; Conservative 0; Mismatches 0; Indels
 A;Map position: 6, aldB-cabA2
F;62-874/Domain: myosin motor domain homology #status atypical
 1053 TTTTTTTTTTT 1065
 323 TTTTTTTTTT 335
 323 TITITITITI 335
 399 TTTTTTTTTT 411
 A, Accession: S78068
 C;Genetics:
A;Gene: dokA
 A;Gene: myoM
 RESULT 33
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 cell surface protein DTFA - slime mold (Dictyostelium discoideum)
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Species: Do-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T17456
B;Ginger, R.S.; Drury, L.; Baader, C.; Zhukovskaya, N.V.; Williams, J.G.
Development 125, 3343-3352, 1998
A;fitle: A novel Dictyostellum cell surface protein important for both cell adhesion and A;Reference number: Z18798; MUID:98359946; PMID:9693138
A;Accession: T17456
A;Accession: T17456
A;Accession: T17456
A;Accession: L1742
A;Residues: DNA
A;Residues: L-1402
A;Coss-references: UNIPROT:096668; EMBL:AF102575; NID:g4063399; PIDN:AACS
A;Coss-references: UNIPROT:096668; EMBL:AF102575; NID:g4063399; PIDN:AACS
A;Coss-references: UNIPROT:096668; EMBL:AF102575; NID:g4063399; PIDN:AACS
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Ross-references: UNFROT:017412; EMBL:AF026492; NID:g2564720; PID:g2564721; PIDN:AABB
C;Genetics: GTZ
A;Gene: CHTZ
A;Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100
C;Keywords: glycoprotein
F;248,612,717,779,1063/Binding site: carbohydrate (Asn) (covalent) #status predicted
 chitinase (EC 3.2.1.14) - yellow fever mosquito
C;Species: Aedes aegypti (yellow fever mosquito)
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14075
R;de la Vega, H: Specht, C.A.; Liu, Y.; Robbins, P.W.
R;de la Vega, H: Specht, C.A.; Liu, Y.; Robbins, P.W.
A;Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosophila.
A;Reference number: Z17872
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 Query Match 3.1%; Score 13; DB 2; Length 1282; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 13; Conservative 0; Mismatches 0; Indels
 Query Match
3.1%; Score 13; DB 2; Length 1402;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels
 3.1%; Score 13; DB 2; Length 1635; 100.0%; Pred. No. 0.0017; ive 0; Mismatches 0; Indels
 CiGenetics:
A;Gene: dtfA
C;Function:
A;Description: involved in the cell adhesion and cell sorting
 1158 TTTTTTTTTTT 1170
 323 TTTTTTTTT 335
 217 TTTTTTTTTT 229
 323 TTTTTTTTT 335
 323 TTTTTTTTTT 335
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 Conservative
 Best Local Similarity
Matches 13; Conserva
 A; Accession: T14075
 Query Match
 RESULT 29
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1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 2 - slime mold (Dictyostelium discoideum)

RESULT 31

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C;Species: Schistosoma mansoni
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Aug-2004
C;Accession: S33640; S27841
R;Webster, P.J.; Mansour, T.E.
 engrailed-like - fluke (Schistosoma mansoni)
 A; Introns: 8/3; 54/3; 112/3; 151/1
 134 rrrrrrrrrrr 145
 421 rrrrrrrrrr 432
 Best Local Similarity 100.
Matches 12; Conservative
 323 TTTTTTTTT 334
 323 TTTTTTTTT 334
 S33640 homeotic protein smox-2,
 A; Residues: 1-458 <WIL>
 C, Genetics:
A, Gene: CESP: Y57A10A.i
 A; Status: preliminary
 A; Accession: A54843
 322
 Query Match
 RESULT 37
A54843
 RESULT 38
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C;Species: Dictyostellum discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
Mol. Cell. Biol. 15, 5645-5656, 1995
Myl Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Bioly A;Reference number: 206411
A;Reference number: 206411
A;Accession: T18273
A;Accession: T18273
A;Accession: T18273
A;Accession: Dictyostellum discoideum: Bioly A;Accession: T18273
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A;Accession: Dictyostellum discoideum: Bioly A;Accession: T18273
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A;Accession
 hypothetical protein (clone AAC1) - slime mold (Dictyostelium discoideum) (fragment)
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Species: Janar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: S05358
R;Shaw, D.R.; Richter, H.; Giorda, R.; Ohmachi, T.; Ennis, H.L.
Mol. Gen. Genet. 218, 453-459, 1989
A;Fitle: Nucleotide sequences of Dictyostelium discoideum developmentally regulated cDNA
A;Reference number: S05355; MUID:90066348; PMID:2511421
A;Accession: S05358
 A;Molecule type: mRNA
A;Residues: 1-183 <SHA>
A;Cross-references: UNIPROT:P14195; EMBL:X16525; NID:g7172; PIDN:CAA34532.1; PID:g930011
 A;Reaiduea: 1-342 <GAT>
A;Cross-references: UNIPROT:Q22902; EMBL:U64858; PIDN:AAB18288.1; GSPDB:GN00023; CESP:C1
A;Experimental source: strain Bristol N2; clone C16D9
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 hyporhetical protein C16D9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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 Score 13; DB 2; Length 1858;
Pred. No. 0.0019;
 2.8%; Score 12; DB 2; Length 342;
100.0%; Pred. No. 0.004;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0024;
 0; Indels
 0; Indels
 C,Accession: T29557
R,Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, July 1996
A,Description: The sequence of C. elegans cosmid C16D9.
A,Reference number: Z20640
A,Accession: T29557
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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 323 TTTTTTTTTT 335
 A;Gene: PIK2
C;Keywords: phosphotransferase
 TTTTTTTTTT 334
 Conservative
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 Best Local Similarity
Matches 12; Conserve
 Local Similarity
ses 12, Conserv
 A; Map position: 5
A;Introns: 59/2; 316/3
 A; Gene: CESP:C16D9.1
 323
 Query Match
 Query Match
 C;Genetics:
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A;Cross-references: UNIPROT:Q9NA83; EMBL:AL117195; NID:e1549729; PIDN:CAB55014.1; CESP:Y!
A;Experimental source: clone Y57A10A
 R;Choi, K.W.; Benzer, S.
Call 78, 125-136, 1994
A;Title: Rotation of photoreceptor clusters in the developing Drosophila eye requires the
A;Reference number: A54843; MUID:94306509; PMID:8033204
 C;Superfamily; unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo: C;Keywords: alternative splicing; ATP
F;38-301/Domain: protein kinase homology <KIN>
F;46-54/Region: protein kinase ATP-binding motif
 A;Molecule type: mRNÅ
A;Residues: 1-477 <CHO>
A;Cross-references: UNIPROT:Q23993; GB:U12009; NID:g515669; PIDN:AAA21124.1; PID:g532558
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hypothetical protein Y57A10A.i - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31631
R;Smye, R.
 nemo, form I - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A54843
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 Length 458;
 Length 477;
 Query Match 2.8%; Score 12; DB 2; Length 477 Best Local Similarity 100.0%; Pred. No. 0.0053; Matches 12; Conservative 0; Mismatches 0; Indels
 0; Indels
 2.8%; Score 12; DB 2; I
100.0%; Pred. No. 0.0052;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
 submitted to the EMBL Data Library, September 1999
A;Reference number: Z21048
A;Accession: T31631
 100.0%; Prec. ...
 A; Cross-references: FlyBase: FBgn0011817
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regulatory protein CRAC - slime mold (Dictyostellum discoideum)
C;Species: Dictyostellum discoideum
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: A54796
R;Insall, R.; Kuspa, A.; Lilly, P.J.; Shaulsky, G.; Levin, L.R.; Loomis, W.F.; Devreotes, J. Cell Biol. 126, 1537-1545, 1994
A;Title: CRAC, a cytosolic protein containing a pleckstrin homology domain, is required i
 325 TTTTTTTTT 336
 259 Trititititii 270
 323
 C;Genetics:
 C; Genetics:
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 RESULT 43
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Mech. Dev. 38, 25-32, 1992

A,Title: Conserved classes of homeodomains in Schistosoma mansoni, an early bilateral me
A,Reference number: S33640; MUID:92399260; PMID:1356008
A,Rocession: S33640
A,Roseluci type: mRNA
A,Rosidues: 1-524 <WEB>
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 alkaline phosphatase (EC 3.1.3.1), intestinal - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 16-Aug-2004 C; Date: 28-Mar-1991 #text_change 16-Aug-2004 C; Accession B36307 K; Ziomek, C.A.; Millan, J.L. Genomics 8, 541-554, 1990 A; Title: Genomic structure and comparison of mouse tissue-specific alkaline phosphatase A; Accession: B36307 MUD:91139124; PMID:2286375 A; Accession: B36307 A;
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 hypothetical protein H17B01.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T32812 R;Gattung, S.; Maggi, L. R;Gattung, S.; Maggi, L. R;Gattung, S.; Maggi, L. A;Description: The sequence of C. elegans cosmid H17B01.
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 A;Gene: smox-2
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
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100.0%; Pred. No. 0.0061;
tive 0; Mismatches 0; Indels
 Query Match
Best Local Similarity 100.0
Matches 12, Conservative
 323 TTTTTTTTTT 334
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A,Gene: CESP:H17B01.2
 A; Accession: T32812
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23454
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C;Accession: T30546

R;Mei, O.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A.
Infect. Immun. 66, 4268-4273, 1998

A;Title: Characterization of major surface glycoprotein genes of human Pneumocystis cari.
A;Reference number: Z17905; MUID:98380374; PMID:9712777
 ;Molecule type: nucleic acid;
;Residues: 1-3712 <KUS.
;Cross-references: UNIPROT:Q00174; GB:M96388; NID:g157799; PIDN:AAA28662.1; PID:g157800
;Carrison, K.; MacKrell, A.J.; Fessler, J.H.
. Biol. Chem. 266, 22899-22904; 1991
;Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struct:;Reference number: S18253; MUID:92078147; PMID:1744083
 ;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hr; Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular r; 273-3310/Domain: laminin-type EGF-like homology cLEG>; 333-400/Domain: laminin-type EGF-like homology cLEG>; 541-584/Domain: laminin-type EGF-like homology cLEGI>
 MBO J. 11, 4519-4527, 1992

"Title: Laminin A chain: expression during Drosophila development and genomic sequence. Reference number: S28399; MUID:93049203; PMID:1425586
 Jaminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Acression: S28399; Si8253
C;Acression: S28399; Si8253
R;Kusche-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, L.I.; Fessler, J.H.
EMBO J. 11, 4519-4527, 1992
 A;Cross-references: EMBL:AF038556; NID:g3560524; PID:g3560526; PIDN:AAC34981.1
A;Experimental source: f.sp. hominis
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C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Jun-2001
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B EGF-like homology <
B EGF-like homology <
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F;2017-2061/Domain: laminin-type
F;2064-2109/Domain: laminin-type
 1859-1914/Domain: laminin-type
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 325 TITITITITI 336
 902 rrrrrrrrrri 913
 tatus: preliminary
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 Accession: S18253
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C;Species: Ruminococcus flavefaciens
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C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A36910
R;Flint, H.J.; Martin, J.; McPherson, C.A.; Daniel, A.S.; Zhang, J.X.
Bacteriol. 175, 2943-2951, 1993
A;Title: A bifunctional enzyme, with separate xylanase and beta(1,3-1,4)-glucanase domai A;Reference number: A36910; MuID:9325938; PMID:8491715
A;Accession: A36910
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A;Residues: 1-802 ·FLI>
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C;Date: 15-Oct-1999 #text_change 09-Jul-2004
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R;Nhan, M:; Hawkins, J.
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ive 0; Mismatches 0; Indels
 Rinhar, M.; Hawkins, J.
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A;Description: The sequence of C. elegans cosmid C12D12.
A;Reference number: Z20656
A; Reference number: A54796; MUID:94375528; PMID:8089184
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Chin, C.W.; Chung, M.K.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudbes, B.; Hudzar, L.
Chin, C.W.; Hudbes, B.; Hudzar, L.
Mature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maytin, E.; Kim, C.C., Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Rooney, T.; Rowley, D.; Sakano, H.; Schuthwick, A.M.; Sun, H.; Tallon, II A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II A;Reference number: A86441; MulD:21016719; PMID:11130712
A;Reference number: A86441; MulD:21016719; PMID:11130712
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C;Accession: C90029
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchaa, A.; Mizuteani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; F.C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
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 probable auxin-induced protein, 50455-50036 [imported] - Arabidopsis thaliana
 hypothetical protein SA2097 [imported] - Staphylococcus aureus (strain N315)
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C;Accession: T26561
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Matches 11, Conservative
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Matches 11; Conservative
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A; Residues: 1-164 <WIL>
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 A; Map position: 1
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ankyrin 3, long splice form - human
N.Alternate names: ankyrin G
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A55575
R;Kordeli, E.; Lambert, S.; Bennett, V.
J. Biol. Chem. 270, 2352-2359, 1995
A;Reference number: A55575; MUID:95138209; PMID:7836469
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F;73-105/Domain: ankyrin repeat homology <ANU1>
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 322 PTTTTTTTT 333
 TTTTTTTTTT 334
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F;729-761/Domain:
 F;795-827/Domain:
 97/Domain:
 30/Domain:
 53/Domain:
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C;Species: Drosophila yakuba
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C;Date: 30-59p-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
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C;Accession: T29596
 C.Species: Ictalurus punctatus (channel catfish)
C.Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
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 156 rrrrrrrrr 166
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Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Réference number: A89758; MUID:21311952; PMID:11418146
A;Recession: C90029
A;Status: preliminary
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A;Residues: 1-166 <KUR>
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A;Experimental source: strain N315
C;Genetics:
A;Gene: SA2097
 C;Accession: T46896
R;Prescott, N.; Stowers, A.W.; Cheng, Q.; Bobogare, A.; Rzepczyk, C.M.; Saul, A.
Mol. Biochem. Parasitol. 63, 203-212, 1994
A;Title: Plasmodium falciparum genetic diversity can be characterized using the polymorp A;Reference number: 224128; MUID:94277144; PMID:8008018
 merozoite surface antigen 2 [imported] - malaria parasite (Plasmodium falciparum) (fragm
C;Species: Plasmodium falciparum
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
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 A;Cross-references: EMBL:AL110480; NID:e1542182; PIDN:CAB54379.1; CESP:Y24F12A.c A;Experimental source: clone Y24F12A
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C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 08-Sep-2000
C;Accession: T26560
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A;Introns: 12/2; 55/1; 200/1
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992

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A;Cross_references: UNIPROT:P17955; GB:X52583; NID:g57640; PIDN:CAA36813.1; PID:g57641
R;D'Onofrio, M.; Starr, C.M.; Park, M.K.; Holt, G.D.; Haltiwanger, R.S.; Hart, G.W.; Hanc Proc. Natl. Acad. Sci. U.S.A. 85, 9559-9599, 1988
A;Title: Partial CDNA sequence encoding a nuclear pore protein modified by O-linked N-ace A;Reference number: A31762; MUID:89071743; PMID:3200844
 C.Accession: A56573 Richard C. Accession: A56573 MUID:9200745; PRID:1915419
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C;Date: 09-Nov-1990 #sequence revision 09-Nov-1990 #text_change 09-Jul-2004
C;Date: 09-Nov-1990 #sequence revision 09-Nov-1990 #text_change 09-Jul-2004
C;Datesion: A35596; A31762; B5336; B1666
R;Starr, C.M.; D'Onofrio, M.; Park, M.K.; Hanover, J.A.
J. Cell Biol. 110, 1861-1871, 1990
A;Title: Primary sequence and heterologous expression of nuclear pore glycoprotein p62.
A;Reference number: A35596; MUID:90277705; PMID:2190987
 A56573
nuclear pore complex glycoprotein p62 - mouse
nuclear pore complex glycoprotein p62 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
 Rib'čnofrio, M.; Lee, M.D.; Starr, C.M.; Miller, M.; Hanover, J.A.
J. Balol. Chem. 266, 11980-11985, 1991
A;Title: The gene encoding rat nuclear pore glycoprotein p62 is intronless.
A;Reference number: I55336; MUID:91268076; PMID:2050692
 Gaps
 A;Molecule type: mRNA
A;Residues: 370, FR', 373-525 <DON>
A;Cross-references: GB:J04143; NID:g623564; PIDN:AAA60741.1; PID:g623565
A;Experimental source: hepatic
 A; Reaidues: 1-525 < RES>
A; Cross-references: GB:M62992; NID:g205953; PIDN:AAA41789.1; PID:g205954
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 DB 2; Lens.
3. 0.047;
0; Indels
 Length 525;
 Indels
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 DB 2;
0.05;
 Query Match 2.6%; Score 11; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
 Match 2.6%; Score 11; DB Local Similarity 100.0%; Pred. No. 0.C es 11; Conservative 0; Mismatches
 C;Superfamily: octopamine receptor type I C;Keywords: G protein-coupled receptor
 A;Status: translated from GB/EMBL/DDBJ
 A;Introns: #status absent
C;Keywords: coiled coil; glycoprotein
 nuclear pore glycoprotein p62 - rat
 A, Experimental source: hepatic
 323 TITITITITI 333
 350 rrrrrrrrrr 360
 323 TTTTTTTTT 333
 274 rrrrrrrrrr 284
 Molecule type: mRNA; Residues: 1-525 <STA>
 Status: preliminary
 A;Status: preliminary A;Molecule type: mRNA
 A; Molecule type: DNA
 Accession: I55336
 Query Match
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 RESULT 58
558868
G protein-coupled receptor GCR1 - migratory locust
C; Species: Locusta migratoria (migratory locust)
C; Date: 15-Pbb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C; Date: 15-Pbb-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004
C; Date: 15-Pbb-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004
A; Title: Characterization of a cloned locust tyramine receptor cDNA by functional express A; Reference number: S58868
A; Residues: 1-884 *CVAN>
A; Residues: 1-484 *CVAN>
A; Cross references: UNIPROT: Q25321; EMBL: X69520; NID: G871404; PIDN: CAA49268.1; PID: G871407
A; Molecule type: mRNA
A; Residues: 1-307, 'D', 309-338, 'K', 340-484 *CVA2>
A; Cross references: EMBL: X69521; NID: G871406; PIDN: CAA49269.1; PID: G871407
Riliu, Z.; Li, P.; Kocabas, A.; Karsi, A.; Ju, Z.
Biochem. Biophys. Res. Commun. 289, 317-324, 2001
Aritle: Microsatellite-containing genes from the channel catfish brain: Evidence of tri A;Reference number: JC7783
A;Contents: Brain
A;Accession: JC7783
A;Accession: JC7783
A;Molecule type: mRNA
A;References: UNIPROT:Q7LZR8
C;Comment: This protein with a polythreonine tract, has importance in the nucleotide exc
 Nypothetical protein F52G3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32467
R;Blanchard, M.; Gattung, S.; Sansone, J.
Submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F52G3.
A;Reference number: Z21173
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-415 cBLA>
A;Residues: 1-415 cBLA>
A;Residues: 1-415 cBLA>
A;Cross-references: UNIPROT: O9GZH9; EMBL;AF026212; PIDN: AAB71300.1; GSPDB:GN00028; CESP:
A;Experimental source: strain Bristol N2; clone F52G3
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 A;Nap position: X
A;Introns: 31/1; 49/1; 104/1; 117/1; 220/1; 241/2; 307/1; 370/3
 Length 415;
 2.6%; Score 11; DB 2; Length 385; 100.0%; Pred. No. 0.038; ive 0; Mismatches 0; Indels
 0; Indels
 Query Match 2.6%; Score 11; DB 2;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 11; Conservative 0; Mismatches 0
 11; Conservative
 323 TTTTTTTTT 333
 203 TTTTTTTT 213
 323 TTTTTTTTT 333
 114 TTTTTTTTT 124
 Local Similarity
 C;Genetics:
A;Gene: CESP:F52G3.5
 C;Genetics:
A;Gene: rad23b
A;Introns: 76/3
 Query Match
 Matches
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A;Residues: 1-569 <THA>
A;Cross-references: UNIPROT:Q83183; EMBL:X77798; NID:g535195; PIDN:CAA54825.1; PID:g5351£
C;Superfamily: murine cytomegalovirus gp88 protein
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-649 <WIL.>
A;Cross-treferences: UNIPROT:Q22225; EMBL:Z66500; PIDN:CAA91305.1; GSPDB:GN00020; CESP:T0^c
A;Experimental source: clone T05C12
C;Genetics:
 CJACCESSION: JASISS
RHAUSEY, F.; Hoffmann, W.
J. Biol. Chem. 267, 24620-24624, 1992
Ajrile: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C.1
Ajreference number: A45155; MUID:93077556; PMID:1447205
 A;Cross-references: UNIPROT:Q05049; GB:L02115; NID:g214147; PIDN:AAA74725.1; PID:g951460
 GP88 protein - murine cytomegalovirus
C;Species: murine cytomegalovirus, murine herpesvirus 1
C;Species: murine cytomegalovirus, murine herpesvirus 1
C;Species: murine cytomegalovirus, murine herpesvirus 1
C;Species: murine cytomegalovirus, 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47277
A;Reference number: S47277
A;Accession: S47277
A;Status: preliminary
A;Molecule type: D.M.A.
 hypothetical protein T05C12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 mucin FIM-C.1 - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
 A;Map position: 2
A;Introns: 28/3; 48/3; 103/3; 156/3; 192/3; 249/3; 408/3; 495/3; 623
C;Superfamily: Caenorhabditis elegans hypothetical protein T05C12.4
 Length 649;
 Length 569;
 Query Match 2.6%; Score 11; DB 2; Length 569
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 11; Conservative 0; Mismatches 0; Indels
 0; Indels
 DB 2;
 RjBurton, J. submitted to the EMBL Data Library, October 1995 A; Reference number: Z19901 A; Accession: T24505
 2.6%; Score 11; DB
100.0%; Pred. No. 0.0
ive 0; Mismatches
 F;162-202/Domain: trefoil homology <TRF1>
F;307-347/Domain: trefoil homology <TRF2>
F;354-394/Domain: trefoil homology <TRF3>
 Query Match 2.6
Best Local Similarity 100.
Matches 11; Conservative
 323 TTTTTTTT 333
 473 rrrrrrrrrr 483
 326 TTTTTTTT 336
 355 rrrrrrrrri 365
 A;Molecule type: mRNA
A;Residues: 1-662 <HAU>
 A;Gene: CESP:T05C12.4
 A;Status: preliminary
 C; Accession: T24505
 RESULT 65
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 translocated intimin receptor Tir [imported] - Escherichia coli (strain O157:H7, substra C; Species: Escherichia coli
C; Species: Bscherichia coli
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
B; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
A; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Hattori, M.; Shinagawa, H.
BNA Res. 8, 11-22, 2001
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Residues: 1-558 cHAYA
 A;Cross-references: UNIPROT:Q63850; GB:S59342; NID:g236260; PIDN:AAB19953.1; PID:g236261 A;Note: sequence extracted from NGBI Dackbone (NGBN:59342, NGBPF:59343) C;Comment: The amino end of this protein contains O-linked N-acetylglucosamine additions C;Keywords: glycoprotein; nuclear membrane; peripheral membrane protein
 A;Accession: E86045
A;Status: preliminary
A;Nolecule type: Dns.
A;Reaidues: 1-558 <STO>
A;Reaidues: 1-558 <STO>
A;Coss-references: UNIPROT:Q9R396; GB:AE005174; NID:g12518449; PIDN:AAG58825.1; GSPDB:C
C;Genetics:
A;Genetics:
A;Gene: tir
 probable translocated intimin receptor protein tir [imported] - Escherichia coli (strain c)Species: Escherichia coli (c)Species: Escherichia (c)Species: Escherichia (c)Species: Escherichia (c)Species: Escherichia (c)Species: Escherichia coli (c)Spe
 A;Cross-references: UNIPROT:O9R396; GB:BA000007; PIDN:BAB37984.1; PID:g13364036; GSPDB:C
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC84561
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 Query Match 2.6%; Score 11; DB 2; Length 526; Best Local Similarity 100.0%; Pred. No. 0.05; Matches 11; Conservative 0; Mismatches 0; Indels
 2.6%; Score 11; DB 2; Length 558; 100.0%; Pred. No. 0.053; tive 0; Mismatches 0; Indels
 2.6%; Score 11; DB 2; Length 558;
100.0%; Pred. No. 0.053;
iive 0; Mismatches 0; Indels
 Query Match 2.6
Best Local Similarity 100.
Matches 11; Conservative
 Conservative
 323 TTTTTTTTT 333
 274 İTİTİTİTİTİ 284
 323 TTTTTTTT 333
 TTTTTTTTT 333
 TTTTTTTTT 403
 393 TTTTTTTT 403
 Query Match
Best Local Similarity
Matches 11; Conserva
A;Residues: 1-526 <COR>
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C;Accession: C69493
R;Klenk, H.E.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woose, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MUID:98049343; PMID:9389475
 A, Accession: C69493
A, Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-816 < KLE>
A; Cross-references: UNIPROT:028331; GB:AE000968; GB:AE000782; NID:g2689291; PIDN:AAB8930E
 Sipuloy, A. submitted to the EMBL Data Library, July 1995
Alpescription: The sequence of C. elegans cosmid F32A5.
A) Reference number: Z18482
A) Accession: T16232
A) Accession: T16232
A) Returns preliminary; translated from GB/EMBL/DDBJ
A) Rolecule type: DNA
A) Residues: 1-977 < RAU>
A) Residues: 1-977 < RAU>
A) Residues: SPAD>
A) Residues: BMBL:U20864; NID:g669026; PID:g669033; PIDN:AAC46666.1; CESP:F32A5.2
A) Experimental source: strain Bristol N2
 1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 4 - slime mold (Dictyostelium discoideum) C; Species: Dictyostelium discoideum C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Accession: T18275 F; Emr. S.D.; Firtel, R.A. Mol. Cell. Biol. 15, 5645-5656, 1995 A; Fittle: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Biol A; Reference number: Z06411 A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Biol A; Accession: T18275
 A;Molecule type: DNA
A;Residues: 1-1093 <ZHO>
A;Cross-references: UNIPROT:P54677; EMBL:U23479; NID:g733527; PID:g733528; PIDN:AAA85725
 C;Genetics:
A;Gene: CESP:F32A5.2
A;Introns: 23/1; 58/3; 102/3; 136/2; 277/2; 380/2; 422/1; 502/1; 580/2; 648/1; 935/2
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 hypothetical protein F32A5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 hypothetical protein AF1948 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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 Query Match 2.6%; Score 11; DB 2; Length 816; Best Local Similarity 100.0%; Pred. No. 0.072; Matches 11; Conservative 0; Mismatches 0; Indels
 Query Match

2.6%; Score 11; DB 2; Length 977;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 11; Conservative 0; Mismatches 0; Indels
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 322 PITITITIT 332
 159 Pririririr 169
 320 PPPTTTTTT 330
 357 PPPTTTTTT 367
 C, Accession: T16232
 C, Genetics:
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 RESULT 69
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 Submitted to the EMBL Data Library, August 1996
A; Description: The sequence of C. elegans cosmid ZC13.
A; Description: The sequence of C. elegans cosmid ZC13.
A; Reference number: Z20113
A; Accession: T25937
A; Accession: T25937
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-732 < BRA>
A; Residues: 1-732 < BRA>
A; Residues: 1-732 < BRA>
A; Cxoss-references: UNIPROT: O95Q40; EMBL: U67953; PIDN: AAB07581.1; GSPDB: GN00028; CESP: ZC
A; Experimental source: strain Bristol N2; clone ZC13
A; Experimental source: strain Bristol N2; clone ZC13
A; Experimental source: strain Bristol N2; clone ZC13
A; Experimental S2/2; 86/1; 169/1; 301/1; 365/1; 401/3; 506/2; 528/2; 553/1; 683
 A;Cross-references: UNIPROT:Q20908; EMBL:Z74473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:F5
A;Experimental source: clone F56H9
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 RESULT 67
T22808
Hypothetical protein F56H9.1 - Caenorhabditis elegans
Cypecies: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22808
R;Burton, J.
R;Burton, J.
R;Reference number: Z19618
A;Reference number: Z1
 RESULT 66
T25303
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 Query Match 2.6%; Score 11; DB 2; Length 662; Best Local Similarity 100.0%; Pred. No. 0.061; Matches 11; Conservative 0; Mismatches 0; Indels
 2.6%; Score 11; DB 2; Length 770;
100.0%; Pred. No. 0.069;
ive 0; Mismatches 0; Indels
 2.6%; Score 11; DB 2; Length 732;
100.0%; Pred. No. 0.066;
tive 0; Mismatches 0; Indels
 C,Genetics:
A,Gene: CESP:F56H9.1
A,Map position: 5
A;Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2
F;526-566/Domain: trefoil homology <TRF4>
F;573-613/Domain: trefoil homology <TRF5>
F;621-661/Domain: trefoil homology <TRF6>
 Query Match
Best Local Similarity 100.
Matches 11; Conservative
 Best Local Similarity 100.
Matches 11; Conservative
 322 PTTTTTTT 332
 214 TITTTTTTTT 224
 323 TTTTTTTTT 333
 643
 323 TTTTTTTTT 333
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N;Alternate names: protein T20KI4 210
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51538
R;Sato, S; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew submitted to the Protein Sequence Database, August 2000
 larval glue protein Lgp-1 precursor - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Accession: A60095; S50126; S44060
R;Swida, U.; Lucka, L.; Kress, H.
Beet-openert 108, 269-280, 1990
A;Title: Glue protein genes in Drosophila virilis: their organization, developmental con-A;Reference number: A60095; MUID:90276249; PMID:23351069
 Cross-references: UNIPROT:Q27423; GB:X76203; NID:g433481; PIDN:CAA53796.1; PID:g433482; Lanio, W.; Swida, U.; Kress, H.
Libanio, W.; Swida, U.; Kress, H.
Lichim. Blophys. Acta 1219, S76-580, 1950; Arilis larval glue protein gene Lgp-3 and Title: Molecular cloning of the Drosophila virilis larval glue protein gene Lgp-3 and Reference number: S50125; MUID:95002181; PMID:7918662
 Cross-references: EMBL:229565; NID:9450901, PIDN:CAA82672.1, PID:9450903
Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994
 Accession: S50126; Status: preliminary; nucleic acid sequence not shown; translation not shown; Molecule type: DNA
 C;Keywords: glycoprotein; salivary gland; tandem repeat
F;1-23/Domain: signal sequence #status predicted <SIG>
F;43-86,94-104/Region: 11-residue repeats (T-T-T-T-P-C-P-T-T-T)
 2.4%; Score 10; DB 2; Length 127;
100.0%; Pred. No. 0.13;
 2.4%; Score 10; DB 2; Length 232;
100.0%; Pred. No. 0.22;
 0; Indels
 Indels
 A;Cross-references: UNIPROT:Q9LF22; EMBL:AL391143
A;Experimental source: cultivar Columbia; BAC clone T20K14
 F;105-160/Region: 8-residue repeats (T-T-T-T-T-T-T-T-T-P)
 nitrilase associated protein-like - Arabidopsis thaliana
 0; Mismatches
 llarity 100.0%; Pred. No. 0.2
Conservative 0; Mismatches
 A;Gene: FlyBase:Dvir/Lgp1
A;Cross-references: FlyBase:FBgn0010305
 C; Superfamily: salivary glue protein
 100.08;
 10; Conservative
 323 TITITITIT 332
 322 PTTTTTTT 331
 Triririri 48
 69
 Best Local Similarity
Matches 10; Conserv
 ;Molecule type: DNA
;Residues: 1-232 <SWI>
 Local Similarity
tes 10; Conserv
 A, Accession: T51538
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-127 <SAT>
 ;Residues: 1-232 <LA2>
 A; Map position: X16A
 Accession: A60095
 A; Note: T20K14 210
 A; Map position: 5
 A; Introns: 97/3
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 C;Genetics:
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 A;Residues: 1-1271 <TIGR>
A;Cross-references: UNIPROT:P47580; GB:U39716; GB:L43967; NID:g1046037; PID:g1046042; TJ
C;Genetics:
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-7962 <RES>
A;Residues: 1-7962 <RES>
Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g101C)
 CiSpecies: Mycoplasma genitalium
CiSpecies: Mycoplasma genitalium
CiDate: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
CiAccession: D64237
RiFraser, C.M.: Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J. C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
 Cispedies: Homo saminary from the cispedies: Homo saminary from the cispedies: Homo saminary from the cispedies: Homo saminary from the cispedies: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004 Cispedies: 23-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004 Cispedies: A; Kolmerer, B. Science 270, 293-296, 1995 A; Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity. A; Reference number: A57430; MUID:96026330; PMID:7569978
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 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-1271 <TIGR>
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 2.6%; Score 11; DB 2; Length 1093; 100.0%; Pred. No. 0.092; Live 0; Mismatches 0; Indels
 2.6%; Score 11; DB 2; Length 1271;
100.0%; Pred. No. 0.1;
ive 0; Mismatches 0; Indels
 2.6%; Score 11; DB 2; Length 7962;
100.0%; Pred. No. 0.49;
ive 0; Mismatches 0; Indels
 RESULT 71
D64237
hypothetical protein MG338 - Mycoplasma genitalium
 A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2q31-2q31
 elastic titin - human (fragment)
 C; Keywords: phosphotransferase
 Best Local Similarity 100.
Matches 11; Conservative
 Local Similarity 100.
10s 11; Conservative
 11; Conservative
 323 TTTTTTTT 333
 775 TTTTTTTT 785
 158 TIRWFKGNKEL 168
 901 TIRWFKGNKEL 911
 323 TTTTTTTT 333
 Best Local Similarity
Matches 11; Conserva
 A, Genetic code: SGC3
 A; Accession: I38346
 Query Match
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A; Note: PIK4
 Best Loca
Matches
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GSFF3
calivary glue protein agg-3 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 28-May-1986 #sequencer
C;Date: 28-May-1986 #sequencer
C;Date: 28-May-1986 #sequencer
C;Accession: A03329
R;Garfinkel, M. D.; Pruitt, R.E.; Meyerowitz, E.M.
J. Mol. Biol. 168, 765-789, 1983
A;Title: DNA sequences, gene regulation and modular protein evolution in the Drosophila
A;Reference number: A92904; MUID:83294545; PMID:6411930
A;Reference number: A92904; MUID:83294545; PMID:6411930
A;Residues: 1-307 cGAR>
A;Residues: 1-307 cGAR>
A;Cross-references: UNIPROT:P02840; GB:X01918; NID:g8581; PIDN:CAA25994.1; PID:g603989
C;Comment: This protein is produced by third-instar larvae.
C;Genetics:
A;Gene: sgg-3
A;Cross-references: FlyBase:FBgn0003373
A;Gross-references: FlyBase:FBgn0003373
A;Gross-references: In/1
C;Superfamily: sallvary glue protein
C;Superfamily: sallvary gland; tandem repeat
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2.4%; Score 10; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 10; Conservative 0; Mismatches 0; Indels
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Search completed: June 28, 2005, 10:21:29 Job time : 28.4289 secs

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| DR EMBL; AF434663; AAL86736.1;  DR MGD; MGT1.889272; Igsf4a.  DR GO; GO:0016021; C:integral to membrane; TAS.  DR GO; GO:0045202; C:synapse; IDA.  DR GO; GO:000812; C:synaptic vesicle; IDA.  DR GO; GO:000515; F:prorein binding; IPI.  DR GO; GO:000715; F:prorein binding; IPI.  DR GO; GO:000715; P:calcium-independent cell-cell adhesion; IDA.  DR GO; GO:000715; P:calcium-independent cell-cell adhesion; IDA.  DR GO; GO:000715; P:calcium-independent cell-cell adhesion; IDA.  DR GO; GO:000715; P:calcium-independent cell-cell adhesion; IDA.  DR GO; GO:000716; P:synaptogenesis; IDA.  DR InterPro; IPR003598; Neurexin-like.  DR InterPro; IPR003598; Neurexin-like.  DR SMART; SM00294; 4.1m; 1.  DR SMART; SM00408; IGC.21; 1.  DR SMART; SM00408; IGC.21; 1.  DR SEQUENCE 445 AA; 48664 WW; CSDSA070DAF70ESS CRC64; | 100.0%; Sest Local Similarity 100.0%; Feat Local Similarity 100.0%; Featches 423; Conservative 0; 1 AAPPGIRILILILISAAALIP                                                                                                                                                  | OY   61 PURQTIYFRDERPLKUSRFQLLNFSSSELKVSLTNVSISDEGRYPCQLYTDPPQESYTTI 120   1                                                                                                                                                                                          | QY         241 BGDAFELTCEAIGKPQPWWVTWVRVDDEMPQHAVLSGFNLFINNLNKTDNGTYRCEASNI         300           L                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 382 GVVAVVVFAMLCLLILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEEKK 421 EVF 423 | SUL                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ONO ZWOT                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
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MEDLINE-22841094; PubMed=12826663; DOI=10.1074/jbc.M305387200;
MEDLINE-22841094; PubMed=12826663; DOI=10.1074/jbc.M305387200;
Shingai T., Ikeda W., Kakunaga S., Morimoto K., Takekuni K., Itoh S., Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
"Implications of nectin-like molecule-
2/IGSF4/RAI75/SgIGSF/TSLC1/SynCAM1 in cell-cell adhesion and transmembrane protein localization in epithelial cells.";
J. Biol. Chem. 278:35421-35427(2003).
 Gaps
 Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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 (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
25-0cT-2004 (TrEMBLrel. 28, Last annotation update)
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100.0%; Pred. No. 2.4e-313;
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 301 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTT 334
 417 AA.
 Query Match
Best Local Similarity 100.
Matches 334; Conservative
 PRELIMINARY;
 Mus musculus (Mouse)
 SEQUENCE FROM N.A.
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 61 PNRÖTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTT1 120
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Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,
 1 AAPPGLRILLILLISAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLIN
 "SynCAM, a Synaptic Adhesion Molecule That Drives Synapse Assembly.";
Science 297:1525-1531(2002).
 Gaps
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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NCBI_TaxID=10090;
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Synaptic cell adhesion molecule 1 (RAITS isoform c)
Mame-1g8f4a; Synonyms-RAITS;
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100.0%; Pred. No. c,
... 0; Mismatches
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Fujita E., Aikawa K., Momoi T.;
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 01-UTM-2003 (TrEMBLrel. 24, Created)
01-UTM-2003 (TrEMBLrel. 24, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
A secretion form of SqIGSF/TSLC1 (RA175 isoform e).
Name=Igsf4a; Synonyms=RA175, sSgIGSF/sTSLC1;
Wans musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 Fujita E., Aikawa K., Momoi T.,
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR007110; IG-like.
InterPro; IPR005999; IG_2.
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SMART; SM00409; IGc; 3.
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SROATE; SM050935; IGC2; 3.
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 Gaps
 Fujica E., Alkawa K., Momoi T.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; A7351388; AAQ02381.1;
EMBL; A351388; AAQ02381.1;
EMBL; ABL83401 : BAD302020.1;

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016220; C:synapse; IDA.

GO; GO:0008021; C:synapse; IDA.

GO; GO:0008021; C:synapse; IDA.

GO; GO:0015339; P:calcium-independent cell-cell adhesion; IDA.

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GO; GO:000715; P:call adhesion; IDA.

GO; GO:000715; P:call adhesion; IDA.

GO; GO:000716; P:synapscogenesis; IDA.

R InterPro; IPR003598; Ig_c2.

R InterPro; IPR003598; Ig_c2.

R InterPro; IPR003598; Neurexin-like.
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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 Query Match

74.2%; Score 314; DB 2; Length 417;
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Last sequence update)
Last annotation update)
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 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
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 81
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STRAIN=C57BL/6J; TISSUE=Hippocampus;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The Manalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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 STRAIN=C57BL/67; TISSUE=Hippocampus; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
 ol-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male 15, Last annotation update)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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 Length 336;
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
 Score 313; DB 2; Le
Pred. No. 3.6e-293;
 100.0%; Pred. w..
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InterPro, IPR003598, Ig_c2
 VGKAHSDYMLYVY 313
 ||||||||||||||||||||||||||||||||||VGKAHSDYMLYVY 334
 Matches 313; Conservative
 PRELIMINARY;
 Local Similarity
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Q9D6E7;
01-JUN-2001 (
 Name=Igsf4a;
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 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
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 TVLVPPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 201
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STRAIN=C57BL/6J; TISSUE=Hippocampus; MEDLLHB=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLHB=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; prepare inditation and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 AAPPGLRLRLLLLLLSAAALIPTGDGONLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
 Degrate From M. A. Akahira S., Akimura T., Arai A., Aono H., Arakana T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishii K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshido K., Yoshino M., Muramatsu M., Hayashizaki Y., F.,
 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
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MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Riski Nincegrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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 EMBL; AKO1375; BASE3988.1; -...
MGD; MG1:1889272; Igsfa...
GO; GO:0016021; C:integral to membrane; TAS...
GO; GO:0045202; C:synaptic vesicle; IDA...
GO; GO:000521; C:synaptic vesicle; IDA...
GO; GO:000521; E:protein binding; IPI...
GO; GO:00155; F:protein binding; IPI...
GO; GO:00155; P:cell adhesion; IDA...
GO; GO:0007155; P:cell adhesion; IDA...
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PROSITE; PS50835; IG LIKE; 3.
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ive 0; Mismatches 0;
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Where 12477932; DOI=10.1073/pnas.242603899;

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B. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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Richards S., Worlley K.C., Hale S., Garcia A.M., Gabb R.A.,

Raha S., Worlley K.C., Hale S., Garcia A.M., Gibbs R.A.,

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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

A Jones S.J., Marra M.A.;

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 61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
 121 TVLVPPRNIMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
 22 AAPPGLRIALLILLIASAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLIN 81
 82 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDBGRYFCQLYTDFPQBSYTTI
 1 AAPPGLRLLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
 Rāttus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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 Query Match 53.7%; Score 227; DB 2; Length 476; Best Local Similarity 100.0%; Pred. No. 5.2e-210; Matches 227; Conservative 0; Mismatches 0; Indels
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
 333 AA
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25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, Hypothetical protein.
 PRELIMINARY;
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 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTC 249
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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 MGD; MGI:1889272; 19854a.

GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:004520; C:synappe; IDA.
GO; GO:00515; C:synappe; IDA.
GO; GO:00515; F:protein binding; IPI.
GO; GO:001515; P:calcium-independent cell-cell adhesion; IDA.
GO; GO:0007155; P:call adhesion; IDA.
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InterPro; IPR003589; Ig c2.
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Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF061260; AAC67243.1; -.
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 VGKAHSDYMLYVY 313
 VGKAHSDYMLYVY 334
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 PRELIMINARY;
 Pfam; PF00047; ig; 2.
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Best Local Similarity
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Pujita E., Soyama A., Momoi T.;
Fujita E., Soyama A., Momoi T.;
Fujita, Which is the mouse ortholog of TSLC1, a tumor suppressor gene in human lung cancer, is a cell adhesion molecule.";
Exp. Cell Res. 287:57-66(2003).
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Zhou Y., Du G., Chen J., Yuan J., Qiang B.;

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AR132811, AR469029.1;

InterPro; IRR007110; Ig-like.

InterPro; IRR003589; Ig_C2.

InterPro; IRR003589; Neurexin-like.

Pfam; PF00047; ig; 2.

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01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
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 PRELIMINARY;
 PRELIMINARY;
 Homo sapiens (Human)
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 94 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 16 SAAALIPTGDGQNLPTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 0; Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 SEQUENCE FROM N.A.

TISSUB-Whole embryo;
Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii
Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
Nagahari K., Sugano S., Isogai T.;
Submitted (WAR-2002) to the EMBL; GenBank/DDBJ databases.

EMBL; AK075502; BAC11657.1;
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 35.5%; Score 150; DB 2; Length 443; 100.0%; Pred. No. 1.1e-135; ive 0; Mismatches 0; Indels
 Score 150; DB 2; Length 333;
; Pred. No. 8.3e-136;
0; Mismatches 0; Indels
 Ito A., Koma Y., Nagano T.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB094146; BAC661791.;
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Ffam; PP00047; ig; 2.
SWART; SM00408; Ig_c2.
PROSITE; PS50835; IG_LIKE; 3.
SEQUENCE 333 AA; 36915 MW; D7C1102F46D08492 CRC64;
 SMART; SM00294; 4.1m; 1.
SMART; SM0408; IGc2; 1.
PROSITE; PS5085; IG LIKE; 3.
SEQUENCE 443 AA; 48648 MW; 046B43AA1S6F6F64 CRC64;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
101-JUAR-2004 (TrEMBLrel. 26, Last annotation update)
Secretory isoform of TSLC-1.
 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PSEC0200.
Homo sapiens (Human).
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 443 AA
 100.0%; Pred. no.
 PRT;
 Interpro; IPR007110; Ig-11ke.
Interpro; IPR003598; Ig c2.
Interpro; IPR003585; Neurexin-like.
 35.5%;
 Best Local Similarity 100.
Matches 150; Conservative
 Matches 150; Conservative
 Genew; HGNC:5951; IGSF4.
 PRELIMINARY;
 Pfam; PF00047; 19; 2.
 Homo sapiens (Human)
 Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 NCBI_TaxID=9606;
 TISSUE=Lung;
 92
 136
 154
 Query Match
 Query Match
 Q8N2F4
 RESULT 11
Q8N2F4
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130 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML 189
 130 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML 189
 1 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML 60
 1 MIDIQXDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML
 0; Gaps
 190 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDA 244
 61 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDA 115
 190 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDA 244
 Name=Igsf4a; Synonyms=ra175c;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; NCBI_TaxID=10090;
 Eukaryota; Metraa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
 Length 295;
 Query Match 27.2%; Score 115; DB 2; Length 29 Best Local Similarity 100.0%; Pred. No. 4.6e-102; Matches 115; Conservative 0; Mismatches 0; Indels
 01-MXY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Adhesion protein RA175C.
 295 AA
 PRT;
 PRT;
 Adhesion protein RA175A.
Name=Igsf4a; Synonyms=ra175a;
Mus musculus (Mouse).
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
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 090YL6
 RESULT 15
Q9QYL6
 RESULT 16
 Q9QYL4
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 MEDLINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8; MEDLINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8; Publida E., Soyama A., Momoi T.; Publida E., Soyama A., Momoi T.; Publida E., Soyama A., Momoi T.; In human lung cancer, is a cell adhesion molecule."; Exp. Cell Res. 287:57-66(22003).

In human lung cancer, is a cell adhesion molecule."; Exp. Cell Res. 287:57-66(2003).

Rembl. AB021965; BAA87915.1; -.. RGD; GO:0006219; C:integral to membrane; TAS.

GO; GO:000621; C:integral to membrane; TAS.

GO; GO:000515; F:protein binding; IPI.

GO; GO:0016318; P:cell adhesion; IDA.

GO; GO:001416; P:synaptogenesis; IDA.

GO; GO:001416; P:synaptogenesis; IDA.

RO; GO:001416; P:synaptogenesis; IDA.

RO; GO:001416; P:synaptogenesis; IDA.

RITHERPO; IPR003189; Ig-2.

RITHERPO; IPR003189; Neurexin-like.
 130 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML 189
 9
 1 MIDIQKOTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML
 Gaps
 Gaps
 190 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDA 244
 61 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDA 115
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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 MGD; MGI:1889272; Integral to membrane; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0004520; C:synappe; IDA.
GO; GO:000515; C:protein binding; IPI.
GO; GO:001515; P:protein binding; IPI.
GO; GO:001515; P:callau-independent cell-cell adhesion; IDA.
GO; GO:0007155; P:call adhesion; IDA.
GO; GO:0007155; P:synaptogenesis; IDA.
InterPro; IPR003589; Ig c2.
InterPro; IPR003589; Neurexin-like.
 27.2%; Score 115; DB 2; Length 278; 100.0%; Pred. No. 4.4e-102; ive 0; Mismatches 0; Indels
 27.2%; Score 115; DB 2; Length 289; 100.0%; Pred. No. 4.5e-102; Live 0; Mismatches 0; Indels
 Pfam; PF00047; 1g; 1.
SWART; SM00294; 4.1m; 1.
SWART; SM04081; 1Gc2; 1.
PROSITE; PS0835; 1Gc2; 1.
SEQUENCE 278 AA; 30636 MW; A295F4DEA2724B04 CRC64;
 PEAM; PF00047; 1g; 1.
SMART; SM00294; 4.1m; 1.
SMART; SM0408; IGc2; 1.
PROSITE; PS50835; IG LIKE; 2.
SEQUENCE 289 AA; 31811 MW; 8D1B836D0565AEA4 CRC64;
 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Adhesion protein RA175B.
Name=Igsf4a; Synonyms=ra175b;
Mus musculus (Mouse).
 289 AA
 01-MAY-2000 (TrEMBLrel. 13, Created)
 PRT;
EMBL; AB021967; BAA87917.1; -.
 Best Local Similarity 100.0
Matches 115; Conservative
 Query Match 27.2°
Best Local Similarity 100.
Matches 115; Conservative
 PRELIMINARY;
 NCBI_TaxID=10090;
 Query Match
 Q9QYL5
 RESULT 14
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Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
 Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 MEDLINE-98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843; MEDLINE-98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843; Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.; "The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions."; J. Biol. Chem. 273:10843-10850(1998). EMBL; AF036411; AAC14222.1; -... InterPro; IRF000458; Tryp_mucin. Pfam; PF01456; Mucin; 1.
 STRAIN-C1-Brenner;
MEDLINE-98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.;
Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.;
The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions.";
J. Biol. Chem. 273.10843-10850(1998).
EMBL; AF036436; AAC14240.1; -.
DinterPro; IPR000458; Tryp_mucin.
Pfam; PF01456; Mucin; 1.
 3.5%; Score 15; DB 2; Length 74; 100.0%; Pred. No. 4.9e-06; tive 0; Mismatches 0; Indels
 Length 86;
 Indels
 74 AA; 7743 MW; 734CC37663E21401 CRC64;
 86 AA; 8963 MW; 7AD26B22604E36A9 CRC64;
 Last sequence update)
Last annotation update)
 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
 3.5%; Score 15; DB 2; Le
100.0%; Pred. No. 5.6e-06;
iive 0; Mismatches 0;
 74 AA.
 Created)
 PRT;
 PRT,
 Mucin-like protein (Fragment).
Name=EMUCe-4;
 Mucin-like protein (Fragment)
 321 PPTTTTTTTTT 335
 321 PPTTTTTTTTT 335
 01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-MAR-2004 (TrEMBLrel. 26,
 71 PPTTTTTTTTT 85
 Matches 15; Conservative
 Conservative
 PRELIMINARY;
 PRELIMINARY;
QNNSEEKKEYF
 Query Match
Best Local Similarity
Matches 15; Conserv
 Best Local Similarity
 SEQUENCE FROM N.A. STRAIN=C1-Brenner;
 SEQUENCE FROM N.A.
 NCBI_TaxID=5693;
 Name=EMUCe-12;
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SEQUENCE
 SEQUENCE
 Query Match
 061023
 Q9TVF2
 RESULT 19
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 353 AVDHAVIGGVVAVVVEAMLCLLIILGRYFARHKGTYFTHRAKGADDAADADTAIINAEGG 412
 130 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML 189
 1 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML 60
 13 AVDHAVIGGVVAVVVPAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGG 72
 MEDLINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8; Pujíta E., Soyama A., Momoi T.; "RA175, which is the mouse ortholog of TSLC1, a tumor suppressor gene in human lung cancer, is a cell adhesion molecule."; Exp. Cell Res. 287:57-66(2003).
 Gaps
 190 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDA 244
 EMBL, AB021966; BAA8716.1;

R MGD, MGI.1889272; Igsf4a.

R GO, GO:0016021; C:integral to membrane; TAS.

R GO; GO:0005621; C:synaptic vesicle; IDA.

R GO; GO:000512; F:pyrotein binding; IPI.

R GO; GO:000515; P:cell adhesion; IDA.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:000716; P:synaptogenesis; IDA.

R InterPro; IRR003598; Neurexin-like.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Koehrer K., Beyer A., Mewes H.W., Well B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BX641042; CAE46024.1; -.
 ;
0
 Score 115; DB 2; Length 306;
Pred. No. 4.7e-102;
 16.8%; Score 71; DB 2; Length 84; llarity 100.0%; Pred. No. 4.7e-60; Conservative 0; Mismatches 0; Indels
 0; Indels
 SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 2.
SEQUENCE 306 AA; 33522 MW; A4CE37B0F23554D5 CRC64;
 84 AA; 8986 MW; D50A20AD25854087 CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 Hypothetical protein DKFZp686F1789 (Fragment) Name=DKFZp686F1789;
 84 AA.
 100.0%; Pred. NC.
 PRT;
 TISSUE=Human retina;
The German Human cDNA Consortium;
 27.28;
 Matches 115; Conservative
 ONNSEEKKEYF 423
 PRELIMINARY;
 Hypothetical protein.
 Homo sapiens (Human)
 Local Similarity
nes 71; Conserv
 Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 SEQUENCE
 413
 Query Match
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 Q6MZK6
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Matches
 RESULT 17
06MZK6
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AC 06MZK7
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 24, Last sequence update)
Hypothetical process of the sequence
 Trypanosoma cruzi.
Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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STRAIN=C1-Brenner;
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MINIORIAN: D'ONEO I., Aslund L., Sanchez D.O., Frasch A.C.;
"The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions.";
J. Biol. Chem. 2773:10843-10850(1998).
BIOL. Chem. 2773:10843-10850(1998).
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Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, ALO32637; CAA21621.1;
PIR; T26880; T26880.
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Science 282:2012-2018(1998)
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Di Noia J.M., D'Oreno I., Aslund L., Sanchez D.O., Frasch A.C.;
Di Moia J.M. D'Oreno I., Aslund L., Sanchez D.O., Frasch A.C.;
Genes having hypervariable regions.";
J. Blol. Chem. 273.10843-10850(1998).
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 MEDINE 9825151; pubMed=9556557; DOI=10.1074/jbc.273.18.10843; Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.; The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions."; J. Biol. Chem. 273:10843-10850(1998).

EMBL. AR03421, AAC14232.1; --
EMBL. PRO0458; Tryp_mucin.

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 Freitas-Junior L.H., Briones M.R., Schenkman S.;
"Two distinct groups of mucin-like genes are differentially expressed in the developmental stages of Trypanosoma cruzi.";
Mol. Biochem. Parasitol. 93:101-114(1998).
EMBL. AF027872; AAC48350.1; -.
Interpro, IPR000468; Tryp_mucin.
Pfam; PP01456; Mucin; 1.
 Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
 PubMed=14668015; DOI=10.1016/j.molbiopara.2003.09.006; Campo V., Di Noia J.M., Buscaglia C.A., Aguero F., Sanchez D.O., Frasch A.C.C.; Uli Moia J.M., Buscaglia C.A., Aguero F., Sanchez D.O., Prasch A.C.C.; Carrential accumulation of mutations localized in particular domains of the mucin genes expressed in the vertebrate host stage of Trypanosoma cruzi.";
 Trypanosoma cruzi.
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 MOI. Biochem. Parasitol. 133:81-91(2004).
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Di Noia J.M., D'Oroso I., Aslund L., Sanchez D.O., Frasch A.C.;
Di Noia J.M., D'Oroso I., Aslund L., Sanchez D.O., Frasch A.C.;
Green Having hypervariable regions.";
J. Biol. Chem. 273:10843-10850(1998).

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MEDLINE=97113006; PubMed=8943259; DOI=10.1074/jbc.271.50.32078;
Di Noia J.M., Pollevick G.D., Kavier M.T., Previato J.O.,
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"High diversity in mucin genes and mucin molecules in Trypanosoma cruzi.";
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Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.;
"The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions";
J. Biol. Chem. 273:10843-10850(1998).
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 Trypanosoma cruzi.
Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5693;
 Pubmed=14668015; DOI=10.1016/j.molbiopara.2003.09.006; Pubmed=14668015; DOI=10.1016/j.molbiopara.2003.09.006; Pubmed=14668015; DOI=10.1016/j.molbiopara.2003.09.006; Pussch A.C.C.; Prasch A.C.C.; Pubfferential accumulation of mutations localized in particular domains of the mucin genes expressed in the vertebrate host stage of
 Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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 MEDLINE=9711 005; PubMed=8943259; DOI=10.1074/jbc.271.50.32078; Di Noia J.M., Pollevick G.D., Xavier M.T., Previato J.O., Mendoca-Previato L., Sanchez D.O., Frasch A.C.; "High diversity in mucin genes and mucin molecules in Trypanosoma cruzi.";
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 3.5%; Score 15; DB 2; Length 139; 100.0%; Pred. No. 8.4e-06; ive 0; Mismatches 0; Indels
 Length 139;
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 STRAIN=C1-Brenner;
D1 Nois J.M., Frasch A.C.C.;
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF398552; AAK94015.1; -
 EMBL; U59482; AAC47399.1; -.
InterPro; IPR000458; Tryp_mucin.
Pfam; PF01456; Mucin; 1.
SEQUENCE 139 AA; 14395 MW; D7DCECEE2FF8A26B CRC64;
 139 AA; 14277 MW; 79A799908014DD21 CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Created)
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein MUC-locs.
 3.5%; Score 15; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 15; Conservative 0; Mismatches 0;
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 140 AA.
 Mol. Biochem. Parasitol. 133:81-91(2004).
EMBL; AY298908; AAQ74640.1; -.
 Biol. Chem. 271:32078-32083(1996).
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 InterPro; IPR000458; Tryp_mucin.
 321 PPTTTTTTTTTT 335
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 Pfam; PF01456; Mucin; 1
 Trypanosoma cruzi."; Mol. Biochem Darres
 Mucin-like protein.
 Best Local Similarity
Matches 15; Conserv
 SEQUENCE PROM N.A.
 NCBI_TaxID=5693;
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Freitas-Junior L.H., Briones M.R., Schenkman S.,
"Two distinct groups of mucin-like genes are differentially expressed
in the developmental stages of Trypanosoma cruzi.";
Mol. Biochem. Parasitol. 93:101-114(1998).
EMBL, AF027874; AAC48352.1;
InterPro: IPR000458; Tryp_mucin.
Pfam; PF01456; Mucin; 1.
NON TER 143 143 1443
SEQÜENCE 143 AA; 14610 MW; 6ABGE7B7FABSF58B CRC64;
 Trypanosoma cruzi.
Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5693;
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 Trypanosoma cruzi.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI TaxID=5693;
 STRAIN=Berkeley;
MEDLINE=98324409; PubMed=9662032; DOI=10,1016/S0166-6851(98)00025-5;
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 MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843; Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.; "The Trypanosoma cruzi mucin family is transcribed from hundreds genes having hypervariable regions."; J. Biol. Chem. 273:10843-10850(1998). BMBL; AF036407; AAC14218.1; -... Interpro; IPR00458; Tryp_mucin. Pfam; PF01456; Mucin, 1. SEQUENCE 148 AA; 15212 MW; ABF2E02CF13EA059 CRC64;
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 3.5%; Score 15; DB 2; Length 143; 100.0%; Pred. No. 8.6e-06; ive 0; Mismatches 0; Indels
 Length 148;
 3.5%; Score 15; DB 2; Length 140; 100.0%; Pred. No. 8.4e-06;
InterPro, IPR000458; Tryp_mucin.
Pfam; PF01456; Mucin; 1.
SEQUENCE 140 AA; 14343 MW; 5CC154418F2A58CA CRC64;
 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 Last sequence update)
Last annotation update)
 DB 2;
 143 AA.
 148 AA.
 100.0%; Prec. ...
 3.5%; Score 15;
 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
 PRT;
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 Mucin-like protein (Fragment).
 321 PPTTTTTTTTTT 335
 321 PPTTTTTTTTT 335
 PPTTTTTTTTTT 88
 PPTTTTTTTTT 86
 Query Match
Best Local Similarity 100.0
 Best Local Similarity 100.0
Matches 15; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Mucin-like protein.
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 STRAIN=C1-Brenner;
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 Gloeckner G., Bichinger L., Szafranski K., Pachebat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Plarzer M., Rosenthal A., Noegel A.A.;
"Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Mus musculus (Mouse). 12 days embryo head cDNA, RIKEN fulllength enriched library, clone:3000008H23 product:hypothetical Acyl-COA dehydrogenase/Glutamic acid-rich region containing protein, full
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 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostellum discoideum (Slime mold). Histidine kinase
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 MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
 MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
 3.5%; Score 15; DB 2; Length 648; 100.0%; Pred. No. 3.1e-05; Ive 0; Mismatches 0; Indels
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 Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC116986; AAOS1856.1; -.
 DiccyBase; DDB0168226; JC2V2_0_00892.
InterPro; IPR008654; IWS1_C.
Pfam, PF05909; IWS1_C; 1.
Hypothetical protein.
SEQUENCE 648 AA; 73372 WW; 2879FE40FCD76D3E CRC64;
 Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
 Dictyostelium discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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 Pred. No. 1.7e-05;
 648 AA.
 PRT; 1015 AA
 100.0%; Prea. ...
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 320 PPPTTTTTTTTT 334
 183 PPTTTTTTTTTT 197
 Best Local Similarity 100.
Matches 15; Conservative
Best Local Similarity 100.
Matches 15; Conservative
 321 PPTTTTTTTTTTT
 PRELIMINARY;
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 Nature 418:79-85(2002).
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 STRAIN=AX4;
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 Query Match
 Q86A81;
 Q86AG0
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 PubMed=14668015; DOI=10.1016/j.molbiopara.2003.09.006; PubMed=14668015; DOI=10.1016/j.molbiopara.2003.09.006; Campo V., Di Noia J.M., Buscaglia C.A., Aguero F., Sanchez D.O., Frasch A.C.C.;

"Differential accumulation of mutations localized in particular domains of the mucin genes expressed in the vertebrate host stage of Trypanosoma cruzi.";

Mol. Blochem. Parasitol. 133:81-91(2004).

EMBL; AY289908; AAQ74638.1; -.

InterPro; IPR000458; Tryp_mucin.

Pfam; PF01456; Mucin; 1.

SEQUENCE 148 AA; 15203 MW; C7F2E02CF13554E6 CRC64;
 Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
 Gaps
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 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
 Murray P.J., Spithill T.W.; "Variants of a Leishmania surface antigen derived from a multigenic
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 3.5%; Score 15; DB 2; Length 148; 100.0%; Pred. No. 8.8e-06; ive 0; Mismatches 0; Indels
 3.5%; Score 15; DB 2; Length 327;
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 327 AA; 34229 MW; 2571B35B6577E715 CRC64;
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 Last sequence update)
Last annotation update)
 100.0%; Pred. No. 8.8e-06;
 148 AA.
 327 AA.
 0; Mismatches
 family.",
7. Biol. Chem. 266:2447-24484 (1991).
EMBL; K57135; CAA40414.1;
PIR; S20074; S20074.
InterPro; IPR0003030; Grow fac_recept.
InterPro; IPR006210; IEGF.
InterPro; IPR001611; IRR.
Pfam; PF00560; IRR_Plant.
Pfam; PF00560; IRR_Plant.
SMART; SM00181; EGF; 1.
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MEDLINE=92105105; PubMed=1761547;
 Surface antigen P2 (Fragment)
 321 PPTTTTTTTTT 335
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 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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les 15; Conservative
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 Leishmania major.
 05-JUL-2004
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 Irypanosoma cruzi.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 "Genome sequence of the nematode C. elegans: a platform for
 3.3%; Score 14; DB 2; Length 216; 100.0%; Pred. No. 0.00011; ive 0; Mismatches 0; Indels
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hypothetical protein EEED8.11 in chromosome II precursor.
ORFNANNES-EEED8.11;
 Di Noia J.M., Frasch A.C.C.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 87398551, AAK94014.1;
InterPro; IPROMO458; Tryp_mucin.
Pfam; PF01456; Mucin; 1.
SEQUENCE 216 AA; 21815 MW; 01C85738541BB6C6 CRC64;
 investigating biology.";
Science 282:2012-2018(1998).
-!- SIMILARITY: Some, to C.elegans R13F6.2 and R13F6.8.
 10986 MW; 26E2947FD6EB06D2 CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein MUC-loc2.
 DB 2; Le
 216 AA.
 304 AA
 3.3%; Score 14; DB 100.0%; Pred. No. 6.2 tive 0; Mismatches
 Rhabditidae, Peloderinae, Caenorhabditis.
 The C. elegans sequencing consortium;
 PRT;
 PRT;
 STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
 322 PTTTTTTTTTT 335
 321 PPTTTTTTTT 334
 Query Match
Best Local Similarity 100.0
Matches 14; Conservative
 Best Local Similarity 100.
Matches 14; Conservative
 PRELIMINARY;
 STANDARD;
 Caenorhabditis elegans.
 107 AA;
 STRAIN=Cl-Brenner;
 SEQUENCE FROM N.A.
 NCBI_TaxID=5693;
 NCBI_TaxID=6239;
101
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SEQUENCE
 158
 SEQUENCE
 Query Match
 Q962W6
 RESULT 44
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 RESULT 43
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 STRAIN-Sprague-Dawley;

Xu C.S., Chang C.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,

Yang K.J., Zhao L.F., Ma H., Wang L., Wang S.F., Xing X.K., Shen G.M.,

Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;

Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY387047; AAQ91017.1;

SEQUENCE 58 AA; 6466 MW; DEA36599EB327F47 CRC64;
 Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 STRAIN=C1=Brenner;
MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.;
"The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions.";
J. Biol. Chem. 273:10843.10843.10850(1998).
EMBL; AF036454; AAC14251.1;
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 3.5%; Score 15; DB 2; Length 1015; 100.0%; Pred. No. 4.6e-05; ive 0; Mismatches 0; Indels
 3.3%; Score 14; DB 2; Length 58;
100.0%; Pred. No. 3.7e-05;
 0; Indels
 1015 AA; 116816 MW; 58CF6693543381A8 CRC64;
 Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC115594; AAO51537.1; -.
GO; GO:0016301; F:kinase activity; IEA.
 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 Last sequence update)
 107 AA
 100.0%; Pred. ...
 Created)
 PRT;
 InterPro, IPR000458; Tryp_mucin.
Pfam; PF01456; Mucin; 1.
 Mucin-like protein (Fragment).
 320 PPPTTTTTTTTT 334
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 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
 TTTTTTTTTT 336
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 15; Conservative
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 PRELIMINARY;
 PRELIMINARY;
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 SEQUENCE FROM N.A.
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 LRRGT00061.
 SEQUENCE
 323
 552
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 MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science_287.5461.2185; REDLINE=20196006; PubMed=10731132; DOI=10.1126/science_287.5461.2185; Adama M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gorere R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Brutcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Abarder S.E., Helf G., Nelson C.R., Gabor G.L., Rander A. D., Holl J.F., Agbayani A., An H.J., Andrews-Pfennkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley B.M., Bellew R.W., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Bother M.R., Dudkov D., C., Busam D.A., Bulle H., Caddeu B., Center A., Chandra I., Buckova J.M., Cawley S., Dahlke C., Davemport L.B., Center A., Chandra I., Ratis K.C., Busam D.A., Bulle H., Caddeu B., Center A., Chandra I., Bachon K., Doup L.E., Downes M., Dugal-Rocha S., Dunkov B.C., Dunn P., Robon K., Doup L.E., Downes M., Dugal-Rocha S., Dunkov B.C., Dunn P., Ratis M.J., Bardelian A.E., Garg N.S., Gelbart W.M., Gasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Kennison J.A., Ketchum K.A., Harris N.L., Harris N.L., Harris N.L., Harris N.L., Harris N.L., Harris N.L., Harris N.L., Houston K.A., Houston K.A., Houston K.A., Houston M., Willen W., Mather B., McInton D. T., Markel B., McInton D. T., Markel B., McInton N.V., Mobarry C., Morris J., Moshrefi A., Mulliam S., Mollar J., Murphy B., Murphy L., Murny D., Palazolo M., Puti V., Rese M., Reinert K., Remington K.A., Nakon K., Wangsen D., Puti V., Rese M., Sylen B., Sylen B., Sylen B., Sylen B., Sylen B., Sylen B., Sylen B., Shue B.C., Siden-Kamos I. Simpson M., Strong R., Sund S., Pala S., Pollar G., Strableton M., Strong R., Sund S., Zhen G., Zheng L., Stand R., Shen B., Solieba F., Saha M., Strong K., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zheng S., Zhen
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 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neopera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroida; Drosophilidae; Drosophila.
 Hypothetical protein EEED8.11.
Poly-Thr.
 3.3%; Score 14; DB 1; Length 304; 100.0%; Pred. No. 0.00015; ive 0; Mismatches 0; Indels
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 Last sequence update)
Last annotation update)
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EMBL, U23484; AAC46771.1; -.
PIR, T15922, T15922,
WormBase; WBGene00017139; EEED8.11.
WormPep; EEED8.11; CE01884,
InterPro; IPR001304; Lectin_C,
SMART; SM0034; CLECT; 1.
Hypothetical protein; Signal.
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304 AA; 32982 MW;
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23.
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
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 14; Conservative
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 Best Local Similarity
 ORFNames=CG31439;
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 OBIMS9;
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 RESULT 45
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 SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
 SEQUENCE FROM N.A.

MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Maceler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Celniker S.E., Maceler D.A., Lowerty T., Frise E., Hodgson A.,
Batel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
Svirskas R., Tabor P.E., Wan K., Stapleron M., Sutron G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
 Gaps
 MEDLINE=22426069; PubMed=12537572; Matthews B.B., Campbell K.S., Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Misra B., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.C., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 Annotation of the Drosophila melanogaster euchromatic genome: a
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 3.3%; Score 14; DB 2; Length 341;
100.0%; Pred. No. 0.00017;
.ive 0; Mismatches 0; Indels
 FlyBase; FBgn0051439; CG31439.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005061; F:chitin binding; IEA.

GO; GO:0006001; F:chitin bind PerA.

InterPro; IPR002557; Chitin bind PerA.

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InterPro; IPR002125; dCMP/cyt_deam.

Pfam; PF01607; CBM 14; 1.

SMART; SM00494; ChEBD2; 1.

PROSITE; PS09049; CHIT_BIND_II; 1.

PROSITE; PS09049; CTHIT_BIND_II; 1.

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SEQUENCE 341 AA; 38627 \(\text{MW} \) A935A06377885A1\(\text{CC64}; \)
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
 01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
 systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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 350
 EMBL; AE003751; AAN14054.1;
 a genomics perspective.";
 Conservative
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 Local Similarity
tes 14; Conserv
 SEQUENCE FROM N.A.
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 Lewis S.E.;
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 Query Match
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Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Blins T., Engels R., Mang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nielsen M., Washburne M., Schulte U., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Roche G., Jedg G., Mawes W., Staben C., Marcotte B., Greenberg D., Ramal M., Kamwysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Kamal M., Kamwysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Arstoffova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catchenide D., Ii W., Perkins D.D., Kroken S., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Parden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Nathen D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nubbaum C., Birren B., The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
 MEDLINE-22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A., Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
 -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostellium discoideum (Slime mold). Histidine
 3.3%; Score 14; DB 2; Length 364;
100.0%; Pred. No. 0.00018;
iive 0; Mismatches 0; Indels
 Baumgart C.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 Hypothetical protein.
SEQUENCE 364 AA; 40946 MW; ECIDF588FE543738 CRC64;
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Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 365 AA.
 EMBL; AC116957; AAO52509.1; -.
GO; GO:0016301; F:Kinase activity; IEA.
 PRT;
 EMBL; AABX01000420; EAA29686.1; -.
InterPro; IPR008547; DUF829.
Pfam; PF05705; DUF829; 1.
 322 PITITITITITI 335
 Conservative
 PRELIMINARY;
 Hypothetical protein.
 preliminary data.
 Local Similarity
nes 14; Conserv
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SEQUENCE FROM N.A.
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 STRAIN=OR74A;
 STRAIN=AX4;
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 Gaps
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
 Anopheles gambiae str. PEST.
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
 Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
 Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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 3.3%; Score 14; DB 2; Length 350;
100.0%; Pred. No. 0.00017;
ive 0; Mismatches 0; Indels
 Score 14; DB 2; Length 356;
Pred. No. 0.00017;
 0; Indels
 NON_TER 1 1 = SEQUENCE 350 AA; 37565 MW; P4765CEF710FA9A0 CRC64;
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356 356 386 MW; CS1B095A700DEC22 CRC64;
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 Created)
Last sequence update)
 AgCP8129 (Fragment).
Name-agCG53199; ORFNames=ENSANGG0000007781;
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EMBL; AAAB01008986; EAA00798.1; -.
 AAAB01008980; EAA14126.1;
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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 322 PTTTTTTTTTT 335
 316 PTTTTTTTTTT 329
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 Query Match
Best Local Similarity 100.v
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 SEQUENCE FROM N.A.
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 01-MAR-2004
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RESULT 47
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Q7S2P4

RESULT 48 Q7S2P4 ID Q7S2P AC Q7S2P DT 01-MAI

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Gaps

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[1]
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI TaxID=3570;
 1A1C DIACA
 thaliana."
 DNA_BIND
 SEQUENCE
 Query Match
 P27486;
 RESULT 52
 Best Loca
Matches
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 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 44, Last sequence update)
10-OCT-2003 (Rel. 44, Last sequence update)
10-OCT-2003 (Rel. 44, Last annotation update)
10-OCT-2003 (Rel. 44, Last annotation factor 33 (WRX)
10-2004 (Rel. 44, Last annotation factor 33 (WRX)
10-2004 (WRXY)
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10-2004 (Worse-car cress)
10-2005 (Wridiplantae; Streptophyta; Embryophyta; Tracheophyta;
10-2005 (Wridiplantae; Streptophyta; Embryophyta; Tracheophyta;
10-2006 (Wridiplantae; Streptophyta; Embryophyta; Tracheophyta;
10-2006 (Wridiplantae; Streptophyta; Embryophyta; Tracheophyta;
10-2006 (Wridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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10-2006 (Wridiplantae; Streptophyta; Embryophyta; Tracheophyta;
10-2006 (Wridiplantae; Streptophyta; Embryophyta; Gaps
 Name-agGS0324; ORFNames=ENSANGG0000010153;
Anopheles gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
 Gaps
 Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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 Length 365;
 3.3%; Score 14; DB 2; Length 445; 100.0%; Pred. No. 0.00021; ive 0; Mismatches 0; Indels
 0; Indels
 EMBL, AAABO1008905; EAA09700.1; -.
HSSP; P08709; JJBU.
GO; GO:0004295; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006293; F:trypsin activity; IEA.
GO; GO:0006298; F:trypsin activity; IEA.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009093; Pept_Ser_Cys.
 365 AA; 39409 MW; 132DEB0383959196 CRC64;
 445 AA; 48897 MW; 48A34474F5414364 CRC64;
 01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 Query Match
3.3%; Score 14; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 0;
 512 AA.
 PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOMN_1.
 Hydrolase; Protease; Serine protease.
 PRT;
 322 PITITITITIT 335
 266 Piriririririri 279
 PTTTTTTTTTT 335
 Local Similarity 100.
18 14; Conservative
 PRELIMINARY;
 STANDARD;
 SEQUENCE FROM N.A.
 AgCP4397 (Fragment)
 STRAIN=PEST
 WR33 ARATH
Q8S8P5;
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SEQUENCE
 322
SEQUENCE
 Query Match
 070956
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WR33_ARATH
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 -!- FUNCTION: Transcription factor. Interacts specifically with the W box (5'-(T)TGAC(C/T)-3'), a frequently occurring elicitor-responsive cis-acting element (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Belongs to the WRKY group I family.
-!- SIMILARITY: Contains 2 WRKY domains.
 STRAIN=CV. Columbia,
MEDLINE=20083487; PubMed=10617197; DOI=10.1038/45471;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.B., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 Gaps
 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (ACC synthase) (S-adenosyl-1-methionine methylthioadenosine-lyase).
Name-ACS2; Synonyms-CARACC;
Name-ACS2; Synonyms-CARACC;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllaceae; Dianthus.
 InterPro; IPR003657; WRKY.
Pfam; PF03106; WRKY; 2.
PROSITE; PS50811; WRKY; 2.
DNA-binding; Molicy Protein; Repeat; Transcription regulation.
Thr-rich.
 'Sequence and analysis of chromosome 2 of the plant Arabidopsis
 ö
 3.3%; Score 14; DB 1; Length 512;
100.0%; Pred. No. 0.00024;
 0; Indels
 "Arabidopsis thaliana transcription factor WRKY33.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 512 AA; 56457 MW; 8F19CBE41BC18662 CRC64;
 517 AA.
 100.0%; Preα. ...
ive 0; Mismatches
 Asn-rich
 WRKY 1.
WRKY 2.
STRAIN=cv. Columbia; TISSUE=Flower;
Lippok B., Somssich I.E.;
 PRT;
 EMBL; AF509499; AAM34736.1; -.
EMBL; AC004683; AAM14994.1; -.
PIR; T02498; T02498.
 322 PITITITITIT 335
 Local Similarity 100.
nes 14; Conservative
 Nature 402:761-768(1999)
 STANDARD;
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GO, GO:0008483; F:transaminase activity, IEA
GO, GO:0009058; P:biosynthesis, IEA.
 Pfam; PF00155; Aminotran 1 2; 1.
PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
 InterPro; IPR001176; ACC_synthase.
InterPro; IPR004839; Aminotrans I/II.
InterPro; IPR004838; NHtransf 1_BS.
Pfam; PP00155; Aminotran 1_2; I.
 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein. ORFNames=1MB.826;
 01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
 322 PITITITITI 335
 323 TTTTTTTTTI 336
 541 Piriririririr 554
 Best Local Similarity 100.0
Matches 14; Conservative
 Best Local Similarity 100.0
Matches 14; Conservative
 OrderedLocusNames=PF1233;
 PRELIMINARY;
 PRELIMINARY;
 Cryptosporidium parvum.
 Pyrococcus furiosus
 518 AA;
 Putative chitinase
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=2261;
 SEQUENCE
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 RESULT 54
Q7YYY0
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 ö
 Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.

EMBL; Z18952; CAA7947.1; -.

PIR; S31442; S31442.

HSSP; P18445; J1AX.

GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.

GO; GO:0016829; F:1yase activity; IEA.
 Park K.Y., Drory A., Woodson W.R.;
"Molecular cloning of an 1-aminocyclopropane-1-carboxylate synthase
from sensecing carnation flower petals.";
Plant Mol. Biol. 18:377-386(1992).
-!- FUNCTION: Catalyzes the formation of 1-aminocyclopropane-1-
carboxylate, a direct precursor of ethylene in higher plants.
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-aminocyclopropane-
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-aminocyclopropane-
-!- COFACTOR: Pyridoxal phosphate.
 Gaps
 -!- PATHWAY: Ethylene biosynthesis; first (rate-limiting) step.
-!- SUBUNIT: Homodimer.
-!- SIMILARITY: Belongs to the class-I pyridoxal-phosphate-dependent
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1-aninocyclopropane 1-carboxylate synthase (EC 4.4.1.14).
Dianthus caryophyllus (Carnation) (Clove pink).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
 Pyridoxal phosphate (By similarity)
 PROSITE; PS00105; AA TRANSFER CLASS 1; 1.
Ethylene biosynthesis; Fruit ripening; Lyase; Multigene family;
Pyridoxal phosphate.
 ö
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllaceae; Dianthus.
 3.3%; Score 14; DB 1; Length 517;
100.0%; Pred. No. 0.00024;
 0; Indels
 Poly-Thr.
C31BA10732E940AE CRC64;
 518 AA.
 100.0%; Preq. ...
 or send an email to license@isb-sib.ch)
 HSSP; P18485; 11AX.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR004839; Aminotrans_I/II.
InterPro; IPR004839; NHtransf_1_BS.
Pfam; PF00155; Aminotran 1_2; I.
PRINTS; PR00753; ACCSYNTHASE.
 PRT;
 MEDLINE=92119258; PubMed=1731995;
 453 470 P
 aminotransferase family.
 EMBL; M66619; AAA33275.1; -.
 323 TTTTTTTTTTI 336
 14; Conservative
 PRELIMINARY;
 ; S19252; S19252.
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=3570;
 TISSUE=Petal;
 Michael M.Z.;
 SEQUENCE
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 Archaea, Buryarchaeota, Thermococci; Thermococcales, Thermococcaceae,
Pyrococcus.
 Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M., Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
"Integrated mapping, chromosomal sequencing and sequence analysis of Cryptosporidium parvum.";
Genome Res. 0:0-0(2003).
EMBL; BX538353; CAD98350.1;
InterPro; IPR000458; Tryp_mucin.
Fram, PF01456; Mucin; 1.
Hypothetical protein.
SEQUENCE 667 AA; 73337 MW; 92F583112C839992 CRC64;
 Gaps
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 STRAIN=Vol / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
 3.3%; Score 14; DB.2; Length 667;
100.0%; Pred. No. 0.0003;
ive 0; Mismatches 0; Indels
 3.3%; Score 14; DB 2; Length 518; 100.0%; Pred. No. 0.00024;
 Bukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
Cryptosporidiidae, Cryptosporidium.
NCBI_TaxID=5807;
58003 MW; BF8B8BC8F03A493E CRC64;
 Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 717 AA.
 667 AA
 100.0%; Prec. ...
 Created)
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 PRT;
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Lewis S.E.;
 Query Match
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 023916
 Matches
 RESULT 57
Q23916
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 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E. Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Brandton G.G., Wortenan J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abrill J.F., Agbayani A., An H.J., Andrews-Fefannokoch C., Baldwin D., Ballew R.M., Basu A., Baxendla G., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Buckhan M.R., Bouck J., Brokestein P., Eorther P., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Posler C., Gabriellan A.B., Garg N.S., Gelbart W.M., Glasser K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harvey D., Hadiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Hostin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Howland T.J., Weinly M.H., Ibeyam C., Mallin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Howland T.J., Weinly M., Moherren D., Merkulov G., Milshina N.V., Nobarry C., Morris J., Moshreti A., Molon K., Sulder Kanen G.S., Sulder K., Sunder E., Shadling A.C., Staplecton M., Strong K., Sun E., Shradling A.C., Staplecton M., Strong K., Sun E., Shradling A.C., Staplecton M., Strong K., Sun E., Shradling A.C., Staplecton M., Strong K., Wang S.M., Wong Z., Yun S., Shapaki M., Wang Z.Y., Wassarman D.A., Weinley G., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhan G., Zhan G., Zhan G., Zhan G., Zhan G., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhan G., Zhan G., Zhan G., Zh
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 GO; GO:0016787; F.hydrolase activity; IEA.
GO; GO:0004553; F.hydrolase activity, hydrolyzing O-glycosyl . .; IEA.
GO; GO:0008152; F.carbohydrate metabolism; IEA.
GO; GO:0008152; F.metabolism; IEA.
PFam; PF00553; CBM 2; 1.
SMART; SM0653; CBD_II; 1.
COMPLETE proteome.
 Gaps
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 ORFNāmes=CG8181;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
 3.3%; Score 14; DB 2; Length 717;
100.0%; Pred. No. 0.00032;
ive 0; Mismatches 0; Indels
 (FEB-2002) to the EMBL/GenBank/DDBJ databases
 717 AA; 78635 MW; FBCB55B9C850E38B CRC64;
 Last sequence update)
Last annotation update)
 746 AA
 Created)
 PRT;
 EMBL; AE010230; AAL81357.1;
HSSP; Q13231; 1LG2.
 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
 322 PTTTTTTTTTT 335
 235 PTTTTTTTTTTT 248
 Best Local Similarity 100. Matches 14; Conservative
 PRELIMINARY;
 SEQUENCE FROM N.A.
 Submitted
 CG8181-PA.
 SEQUENCE
 Query Match
 09V515
 RESULT 56
1099515
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AC 099511
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MEDLINE-22426065; PubMed=12537568;

Gelniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

Patel S., Adams M., Champe M., Dugan S.P., Prise E., Hodgson A.,

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 Gaps
 MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 Annotation of the Drosophila melanogaster euchromatic genome:
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 3.3%; Score 14; DB 2; Length 746;
100.0%; Pred. No. 0.00033;
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 to the EMBL/GenBank/DDBJ databases.
 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
 FlyBase;
Submitted (MAR-2004) to the EWBL/GenBank/DDBJ database:
EMBL, AE003135; AAF59007.1; -.
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Last annotation update)
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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 STRAIN-DG61, MEDLINE=99189343; PubMed=10087212; DOI=10.1006/plas.1998.1385; Gonzales C.M., Spencer T.D., Pendley S.S., Welker D.L.; "Dgp1 and Dfp1 are closely related plasmids in the Dictyostelium Ddp2 plasmid family.";
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"Dictyostelium giganteum plasmid Dgpl is a member of the Ddp2 plasmid
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 Broc. Natl. Acad. Sci. U.S.A. 93:15260-15265 (1996).

R MSD; Vallad. Sci. U.S.A. 93:15260-15265 (1996).

R HSSP; Q1131-31, IR3M.

R DictyBase; DDB0191179; mkcA.

GO; GO:0005524; F:ATP binding; IEA.

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GO; GO:0006464; P:protein amino acid phosphorylation; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

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R InterPro; IRR00109; Kinase like.

R InterPro; IRR002290; Ser thr pkinase.

R InterPro; IRR002151; Ser thr pkinase.

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R Pfam; PF00069; Pkinase: 1.
MEDLINE=97140317; PubMed=8986798; DOI=10.1073/pnas.93.26.15260; Shaulsky G., Escalante R., Loomis W.F.; "Developmental signal transduction pathways uncovered by genetic
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 Length 860;
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 ProDom; PD000001; Prot_Kinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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ATP-binding; Hypothetical Protein; Kinase; Transferase.
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 STRAIN=WS380B;
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Slade M.B., Chang A.C.M., Williams K.L.;
Slade m.B., Chang A.C.M., Williams K.L.;
The sequence and organisation of Ddp2, a high copy number plasmid of Dictyostelium discoideum.";
Plasmid 24:195-207(1990).
 MEDLINE=99189343; PubMed=10087212; DOI=10.1006/plas.1998.1385;
Gonzalas C.M., Spencer T.D., Pendley S.S., Welker D.L.;
"Dgpl and Dfpl are closely related plasmids in the Dictyostelium Ddp2
plasmid family.";
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NCBI_TaxID=79012;
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Plasmid 28:37-45(1992).
EMBL; U94491; AAC33153.1; -.
PIR; P00444; P00444.
InterPro; IPR007778; Dict_REP.
Pfam; PF05086; Dicty_REP; I.
Plasmid.
 Plasmid 41:99-96(1999).

EMBL; AF076279; AAC33156.1; -.

InterPro; IPR007778; Dict_REP.

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Similar to Arabidopsis thaliana (Mouse-ear cress). Hypothetical 79.2
 STRAIN=WS380B;
MEDLINE=90287164; PubMed=2192261;
Leiting B., Lindner I.J., Noegle A.A.;
"The extrachromosomal replication of Dictyostelium plasmid Ddp2
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requires a cis-acting element and a plasmid-encoded trans-acting
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 Chang A.C.M., Slade M.B., Williams K.L.,
"Identification of the origin of replication of the eukaryote
Dictyostellum discoideum nuclear plasmid Ddp2.";
 3.3%; Score 14; DB 2; Length 887;
100.0%; Pred. No. 0.00038;
tive 0; Mismatches 0; Indels
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 Discription 24:008-217(1990).

EMBL; X51478; CAA35843.1; -.

Bictyasae; DDB0001833; Ddp2-rep.

InterPro; IFR007778; Dict_REP.

Ffam; PF05086; Dicty_REP; I.

SEQUENCE 887 AA; 100809 MW; 478B68C4E500F470 CRC64;
 MOI. Celi. Biol. 10:3727-3736(1990).

EMBL, M55298; AAA33191.1; -.

PIR; A35679; A35679.

DictyBase; DDB0001833; Ddp2-rep.

InterPro; IFR007778; Dict REP.

Pfam; PF05086; Dicty REP; I.

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Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
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MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
 STRAIN=AX4;
MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
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Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and analysis of chromosome 2 of Dictyostellum discoideum.";
Nature 418:79-85(2002).
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ive 0; Mismatches 0; Indels
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 Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 SMART; SM00382; AAA; 1.
ATP-binding; Hypothetical protein.
SEQUENCE 937 AA; 106088 MW; 0AFD6F0123CE2967 CRC64;
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 01-JUN-2003 (TrEMBLrel. 24, Created)
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Shirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.Y., Wassaraman D.A., Weilbing G., Zhoo Q., Zhon G., Shence S., Shirth H.O.,
R. Ferner E., Spradling A.C., Stapleton M., Strong R., Shirk, Spracel J. Shon S.,
R. The genom
 MEDLINE=2245065; PubMed=12537568; MEDLINE=2245065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome spotumn Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
CG32972-PB (RE16941p).
Mame=BG:BC051523.2, ORFNames=CG32972;
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Haxapoda, Insecta, Pterygota, Mooptera; Endopterygota, Diptera, Brachycera; Muscomorpha, Ephydroidea, Drosophilae, Drosophila.
NCBI_TaxID=7227;
 PRT; 1166 AA
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 Science 287:2185-2195(2000).
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MEDLINE=22426070; PubMed=12537573;
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";
 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostelium discoideum (Slime mold). Nucleotide exchange
 Gaps
 MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 STRAIN=Berkeley; Stapleton D., Agbayani A., Carlson J., Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 ;
 Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome:
 Length 1166;
 1166 AA; 128893 MW; DD25F816E75F7CF9 CRC64;
 FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
 Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases EMBL; AE003642; AAN10874.1; -- EMBL; BT010014; AAQ22483.1; --
 Dictyostelium discoideum (Slime mold).
Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium
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 Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
 Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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 Score 14;
Pred. No.
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InterPro; IPR000782; B1gH3_FAS1.
Pfam; PF02469; Fasciclin; Z.
SMART; SM00554; FAS1; Z.
PROSITE; PS50213; FAS1; Z.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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 ORFNames=CG32972;
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 MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Gilgo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
 Gaps
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MEDILINE=99066915; PubMed=8851610; DOI=10.1016/S0166-6851(88)00119-4;
Barnes D.A., Bonnin A., Huang J.X., Gousset L., Wu J., Gut J.,
Barnes D.A., bubremetz J.F., Ward H., Petersen C.;
"A novel multi-domain mucin-like glycoprotein of Cryptosporidium
 Gaps
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 Score 14; DB 2; Length 1832;
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 Score 14; DB 2; Length 1728; Pred. No. 0.00067;
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SEQUENCE 1728 AA; 192334 WW; D8B4425042FF48EA CRC64;
 0; Indels
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Mol. Biochem. Parasitol. 96:93-110(1998).
EMBL; AF068065; AAC98153.1; -.
PIR; T31113; T31113.
SEQUENCE 1832 AA; 192653 MW; 590E6ACB16BBE0D2 CRC64;
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 Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC116956; AAL92600.1; -.
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 Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
Cryptosporidiidae, Cryptosporidium.
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Last sequence update)
Last annotation update)
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Last sequence update)
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InterPro; IPR001547; Glyco hydro_5.
InterPro; IPR001936; RasGAP.
InterPro; IPR008936; Rho_GAP.
 3.3%;
 01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2003 (TrEMBLrel. 24,
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
 PITITITITITI 335
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 322 PTTTTTTTTTTT 335
 151 PTTTTTTTTTT 164
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 Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., F., The transposable elements of the Drosophila melanogaster euchromatin:
 SEQUENCE FROM N.A.
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe W., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Paters B.D., Richards S., Sodergren E.J., Wenter C., Weinstcok G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila
Drosophila melanogaster (Fruit fly).

Bukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
 melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
 SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
 MEDLINE=22426069; PubMed=12537572;
 genomics perspective."
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Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Sethi H., Snir B., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
Ziezan L.L., Rubin G.M.;
 Gaps
 MEDLINE=99403001; PubMed=10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris N., Hartzell G., Harrvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K
Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region.";
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 Annotation of the Drosophila melanogaster euchromatic genome: a
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 Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
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 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein BG:DS01523.2.
Name-BG:DS01523.2; ORFNames-CG32972;
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 3.3%; Scc.
larity 100.0%; Pr
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 01-OCT-2000 (TrEMBLrel. 15,
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 MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A. Nsequence and analysis of chromosome 2 of Dictyostelium discoideum." Nature 418:79-85(2002).
 -1- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family. EMBL; AC116957; AAO52538.1; -.
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 GO; GO: 00004840; Fubiquitin conjugating enzyme activity; IBA. GO; GO: 00004840; Fubiquitin cycle; IEA. GO; GO: 0006512; Pubiquitin cycle; IEA. InterPro; IPR008083; MATH.
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InterPro; IPR008974; Traf_like.
Fam; PF00179; WO_Con; UO_Co
 3.3%; Score 14; DB 2; Length 1893;
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SEQUENCE 2208 AA; 250169 WW; CF247BA99B0E2205C CRC64;
 2C3152610B858A4D CRC64;
 Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 Volume 2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
101-MAP-Doublin and an antique and a sequence update)
Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyostelium.
 Score 14; DB 2; Le
Pred. No. 0.00083;
0; Mismatches 0;
 100.0%; Prec. ...
FlyBase; FBG0028905; CG32972.

GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR0100782; BIGH3-FAS1.
InterPro; IPR011009; Kinase_like.
Pfam; PF02469; Fasciclin; 2.
PROSITE; PS50213; FAS1; 2.
Hypothetical protein.
SEQUENCE 1893 AA; 206483 MW; 2C3152
 3.35,
100.0%; Pre
 447 PTTTTTTTTT 460
 322 PTITITITITI 335
 334
 Local Similarity 100.
 Conservative
 PRELIMINARY;
 HSSP; P51966; 1C4Z.
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hes 14; Conserv
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 SEQUENCE FROM N.A.
 NCBI TaxID=44689
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 Query Match 3.1
Best Local Similarity 100.
Matches 13; Conservative
 PRELIMINARY;
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 Nature 418:79-85(2002).
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI TaxID=10116;
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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 Culp D.J. Latchney L.R., Fallon M.A., Denny P.C.,
Culp D.J. Latchney L.R., Fallon M.A., Denny P.C.,
Cuwenhoven R.I., Chuang S.;
The Gene Brodding Mouse Muc19: cDNA, Genomic Organization and
T Relationship to SMGC.";
Physiol. Genomics (Online) 0:0-0(2004).
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STRAIN=BN/SNHsdMcW;
Culp D.J., Latchney L.R., Fallon M.A., Denny P.A., Denny P.C.,
Couwenhoven R.I., Chuang S.;
"The Gene Encoding Mouse Muc19: cDNA, Genomic Organization and
Relationship to SMCC."
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 3.3%; Score 14; DB 2; Length 3295; 100.0%; Pred. No. 0.0012; ve 0: Mismatches 0; Indels
 3295 AA; 317336 MW; 322D0CF90BF9F292 CRC64;
 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Last annotation update)
 PRT; 3295 AA.
 PRT; 3550 AA.
 100.0%; Pred. ...
 Physiol. Genomics (Online) 0:0-0(2004).

EMBL; BK005556; DAA05596.1; -.

InterPro; IPR006207; Cys knot C.

InterPro; IPR001007; PMP_SGCI.

InterPro; IPR001007; VWF_C.

SMART; SM00041; CT; 1.
 Mucin apoprotein precursor (Fragment)
Name=Muc19;
 PROSITE; PS01185; CTCK 1; UNKNOWN 1. PROSITE; PS01225; CTCK 2; 1. PROSITE; PS01208; VWFC 1; UNKNOWN 1. PROSITE; PS50184; VWFC 2; 1.
 Created)
 Mucin apoprotein (Fragment). Name=Muc19;
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 Q6GT4;
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
 066GT3;
25-OCT-2004 (TrEMBLrel. 28,
 323 TITITITITITI 336
 Local Similarity 100.
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 PRELIMINARY;
 Rattus norvegicus (Rat)
 Rattus norvegicus (Rat)
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STRAIN=BN/SBNHBdMCW;
 NCBI_TaxID=10116;
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SEQUENCE
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266GT4
AC Q66GT4
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 MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
 Bukaryota; Pungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
Pneumocystis.
 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAINE-prototype form 1;
MEDLINE-95107908; PubMed-7808998;
Linke M.J., Smulian A.G., Stringer J.R., Walzer P.D.;
Linke M.J., Smulian of multiple unique cDNAs encoding the major surface glycoprotein of rat-derived Pneumocystis carinii.";
Parasitol. Res. 80:478-486(1994).
EMBL; U07057; AAA74069.1; -.
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 Score 14; DB 2; Length 3550;
Pred. No. 0.0012;
0; Mismatches 0; Indels
 Length 56;
3550 AA; 354982 MW; 108149CC5F35DBFC CRC64;
 0; Indels
 Baumgart C.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC116551; AAOS2164.1; -
 56 AA; 5825 MW; AEIF4EA7718D7DF7 CRC64;
 Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Major surface glycoprotein (Fragment).
Preumocystis carinii.
 01-JUN 2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
 3.1%; Score 13; DB 2; L. 100.0%; Pred. No. 0.00033; tive 0; Mismatches 0;
 56 AA.
 56 AA
 Query Match 3.3%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 14; Conservative 0; Mismatches
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Search completed: June 28, 2005, 10:20:31 Job time : 112.051 secs
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 STRAIN=V333;
Hoffmann E.H., Silveira L.A., Tonhosolo R., Pereira F.J.,
Ribeiro W.L., Tonon A.P., Marrelli M.T., Kawamoto F., Ferreira M.U.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AX008396; AAG330717.1;
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 Hoffmann E.H., Silveira L.A., Tonhosolo R., Pereira F.J., Ribeiro W.L., Tonon A.P., Marrelli M.T., Kawamoto F., Ferreira M.U.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2002 (TrEMBLrel. 22, Last annotation update)
Morozoite surface protein 2 (Fragment).
Plasmodium falciparum.
Enkaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL TaxID=5833;
 Merozoite surface protein 2 (Fragment).
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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67 AA, 5732 MW; 6B2B3F43575D87C7 CRC64;
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67 AA; 5706 MW; 6C5E8980203990C4 CRC64;
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 67 AA
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 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2002 (TrEMBLrel. 22,
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|--------------------------------------------------------------------------------------|---------------------------------|----------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------|--------------------------------------|-----------------------------------------------------------------|----------------|---------------------------------|------------------------------------------------------------|--------------------------------|----------------|---------------------------------------------------------------|--------|-------------------------|----------------|--------------------------------------|-------------------------------------------------------------|-----------|----------------|------------------|-------------------------------|--------------------------|----------------|----------------------------------------|----------------------------------------------------|--------------------|----------------------------------------|-------------------------|-------------------|-------------------------------|-------------------------|-------------------------|-------------------------|-------------------------|---------------------------------------|
| 0000                                                                                 | , o o                           |                                                                                              | ••••                                                                            | , , , ,                              | 9 9 9                                                           | 999            | 99                              |                                                            |                                |                | 900                                                           | 9 40 6 | 2 4 4<br>5 0 4<br>5 0 4 |                | 0 0                                  |                                                             | 9 9 9     | 40 6           | 40<br>40<br>6    | 9 9                           | φ u                      | 40 6           | 40 6                                   | ω ω<br>0 0                                         | 9                  | 40<br>40<br>60                         |                         | 0.40              | . w                           | 40 6                    | 40 6                    | 40 6                    | 9                       | 40<br>00<br>9                         |
| 35.                                                                                  | 35.                             | 335.                                                                                         | m m m m n                                                                       |                                      | 35.                                                             | 35.            | 35.                             | 35.                                                        | 35.                            | 35.            | 30.0                                                          | 9 2    | <br>                    |                | 32.                                  | 35.                                                         | 30.0      | 32.            | 35.              | 35.                           | 35.                      | 32.            | 35.                                    | 35.                                                | 35.                | 35.                                    | 35.                     |                   | 9 0                           | 35.                     | 35.                     | 35.                     | 35.                     | 35.                                   |
| 26 150<br>27 150<br>28 150<br>29 150                                                 |                                 |                                                                                              |                                                                                 |                                      |                                                                 | 444            |                                 | יההי                                                       |                                |                | 1                                                             |        |                         |                |                                      |                                                             |           | н.             |                  |                               | П.                       | 17             |                                        |                                                    |                    |                                        | -                       | 1 <del>-1</del> - |                               |                         |                         |                         |                         |                                       |
| GenCore version 5.1.6<br>(c) 1993 - 2005 Compugen Ltd.                               | using sw model                  | 09:54:53 ; Search time 114.43 Seconds (without alignments) 1429.691 Million cell updates/sec | 4<br>LLLSAAALTAIINAEGGQNNSEEKKEYF 423                                           | Gapext 60.0                          | 386760381 residues                                              |                | g chosen parameters: 2105692    | 000                                                        | 150 summaries                  | ec04:*         | * * * * * O O O                                               | 0.00   | 025:*<br>0358:*<br>     | 048:*          | esults predicted by chance to have a | of the t                                                    | SUMMARIES |                | B ID Description | AAY45093 ABO84563 Abo8456     | AAB25586 Aab25586 Protei | ADE86588 Novel | ADR41469 Adr41469 Human AAM23691 Human | AAY53028 Aay53028 Human<br>ABO84564 Abo84564 Human | AAY17830 Human     | AABU1321 AUMAN AAU29040 Human AAU29040 | ABU58416 Abu58416 Human | 133               | ABR65543 Human Abr65543 Human | ABU99483 Abu99483 Human | ABU82722 Abu82722 Human | ABU89843 Abu89843 Novel | ABU96145 Abu96145 Novel | ABU92576 Abu9257<br>ABO08653. Abo0865 |
| Ge.<br>Copyright (c)                                                                 | OM protein - protein search, us | Run on: June 28, 2005,                                                                       | Title: US-10-622-237-4<br>Perfect score: 423<br>Sequence: 1 AAPPGLRLLLLLLLSAAAL | Scoring table: OLIGO Gapop 60.0 , Ga | Searched: 2105692 segs, 3                                       | Word size : 0  | Total number of hits satisfying | Minimum DB seq length: 0 Maximum DB seq length: 2000000000 | Post-processing: Listing first | ۰ 'که          | 1: geneseduliyada:<br>2: geneseduliyada:<br>3: geneseduliyada |        |                         | ກ ຫ<br>        | No. is the number                    | score greater than or equa<br>and is derived by analysis    | ,         | c Query        | Length D         | 423 100.0 423<br>396 93.6 397 | 150 35.5 364             | 150 35.5 364   | 150 35.5 370<br>150 35.5 402           | 150 35.5 414<br>150 35.5 425                       | 150 35.5 440       | 150 35.5 440                           | 150 35.5 440            |                   | 150 35.5 440                  | 150 35.5 440            | 150 35.5 440            | 150 35.5 440            | 150 35.5 440            | 150 35.5 440<br>150 35.5 440          |

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|---------------------------------------|-------------|-----------|-------|--------|---------|----------------------|-------|----------|----------|--------|------------|----------|-----------------|------------------|----------|----------|----------|----------------|--------|----------|----------|----------|----------|-----------|-----------|-------------|---------|---------|---------|----------|----------|---------|----------|-------------|---------|---------|----------|--------|--------|---------|---------|---------|----------|----------|---------|--------------|
|                                       |             |           |       |        |         |                      |       |          |          |        |            |          |                 |                  |          |          |          |                |        |          |          |          |          |           |           |             |         |         |         |          |          |         |          |             |         |         |          |        |        |         |         |         |          |          |         |              |
| mnų.                                  | hum         | Sec<br>Ti | hum   | sec    |         | PRO                  | Sec   | hum      | PRO      | PRO    | sec        | PRO      | 2 0             | ם<br>מ<br>מ<br>מ | Bec      | PRO      | hum      | hum            | sec    | sec      | sec      | PRO      | PRO      | sec       | Sec       | 200         | 2 4 6   | sec     | sec     | pro      | PRO      | PRO.    | mnd<br>G | ָ<br>ה<br>ה | Bec     | sec     | sec      | sec    | sec    | sec     | sec     | sec     | sec      | Sec      | Sec     | 9<br>8       |
| Novel                                 | Novel       | Movel     | Novel | Human  | Human   | Human                | Human | Novel    | Human    | Human  | Human      | Human    | numan.          | הבתול            | Human    | Human    | Novel    | Novel          | Human  | Human    | Human    | Human    | Human    | Human     | Human     | Human       | Human   | Human   | Human   | Human    | Human    | Human   | Novel    | Nove 1      | Human   | Human   | Human    | Human  | Human  | Human   | Human   | Human   | Human    | Human    | нишал   | нишап        |
| 4.0                                   | <b>co</b> 1 | ٠.        | 984   | 8458   | ۰ و     | و<br>م م             | 5514  | 5819     | 8091     | 35     | 84         | o 0      | יים             | 0 0              | 18       |          |          |                |        |          |          |          |          | ٠.        | <b>.</b>  | 4 0         | ,       |         | 9       |          |          | s.      | 40       |             | 0       | 'n      |          | 36     | 6      | 8       | 4       | _       |          |          | ٠.      | 50           |
| Abu817                                | Abu6591     | Ab1193974 | Abu9  | Abr6   | Abr9087 | Abu943               | Abu8  | Abu86    | Abu94    | Abo04  | Abr 702    | Abu9844  | ADIBO           | Ab1.794          | Abu928   | Abu95840 | Abu91060 | Abu90153       | Abo095 | Abo10840 | Abr70894 | Abu87502 | Abu91370 | ADU84     | Abresse 7 | Abue 332    | Abo0987 | Abougg  | Abu1052 | Abu11312 | Abu67131 | Abu9553 | Abu9674  | About 4     | Abo0834 | Abo0555 | Abr73944 | Abr95  | Abr808 | Abr8113 | Abm0083 | Abr8843 | Abm77257 | Abo28741 | AD03148 | ADIIIO / 9   |
|                                       |             |           |       |        |         |                      |       |          |          |        |            |          |                 |                  |          |          |          |                |        |          |          |          |          |           |           |             |         |         |         |          |          |         |          |             |         |         |          |        |        |         |         |         |          |          |         |              |
|                                       |             |           |       |        |         |                      |       |          |          |        |            |          |                 |                  |          |          |          |                |        |          |          |          |          |           |           |             |         |         |         |          |          |         |          |             |         |         |          |        |        |         |         |         |          |          |         |              |
|                                       |             |           |       |        |         |                      |       |          |          |        |            |          |                 |                  |          |          |          |                |        |          |          |          |          |           |           |             |         |         |         |          |          |         |          |             |         |         |          |        |        |         |         |         |          |          |         |              |
| 54                                    | 813         | 2.5       | 88    | 58     | 176     | 20.5                 | 514   | 119      | 80       | 535    | 84         | 2, 2     | 0 10            | 490              | 181      | 04       | 09       | 53             | 268    | 40       | 94       | 07       | 20       | ים<br>מני | 4 5       | 10          | 22      | 28      | 56      | 12       | 31       | 32      | 4.0      | 0 4         | 8       | 555     | 944      | 536    | 33     | 38      | m       | 436     | 57       | 14.      | 9 0     | <del>ا</del> |
| ABU817                                | ABU6591     | ABR33/4/  | BU997 | ABR664 | ABR9087 | ABU94303<br>ABU79185 | ABU86 | ABU8681  | ABU94608 | AB0045 | ABR7028    | ABUS844  | ADKOJC<br>PORCA | ARIT794          | ABU92881 | ABU9584  | ABU91060 | <b>ABU9015</b> | ABO095 | ABO1084  | ABR70894 | ABU87502 | ABU9137  | ABU84     | ABK69674  | ARITG332    | ABO0987 | AB00895 | ABU1052 | ABU1131  | ABU6713  | ABU9553 | ABU9674  | ABO04 94    | ABO0834 | AB0055  | ABR739   | ABR955 | ABR808 | ABR8113 | ABM008  | ABR884  | ABM772   | AB02874  | ABO3148 | ABMU / 90    |
| 9 (                                   |             |           |       |        |         | •                    |       | ·        | •        |        | ·          |          |                 |                  |          | •        |          |                |        | ·        | •        | ·        |          | •         |           |             |         |         |         | •        | •        | •       | •        |             |         |         | •        | •      | •      |         | ·       | •       | •        | •        | •       | •            |
|                                       | 440         | * 4       | 4     | 4      | ₹,      | 440                  | 4     | 440      | 4        | 4      | 4.         | 9440     | * <             | 7 4              | 4        | 4        | 440      | 440            | 440    | 4        | 4        | 4        | 0 4 4    | 4 -       | 244       | 44          | 440     | 440     | 440     | 440      | 440      | 440     | 440      | 4 4         | マヤ      |         | 440      | 4      | 4      | 4       | マ       | 4.      | 4        | 440      | 4.      | ○<br>**      |
| ıvi r                                 | Ų r         | i ri      | 5.    | ινί    | ıηι     | ú rú                 | 'n    | 7.       | ri.      | 5.     | ų.         | ΰп       | ם יי            | יי               | Ś        | Ŋ        | ĸ.       | r.             | ī.     | ı.       | r.       | νi       | ύr       | ų.        | υ'n       | ייו         | · w     | S       | 5       |          |          |         |          | י ער        | ı ın    |         |          |        |        |         |         |         |          |          |         | n            |
| 35.                                   | υ.<br>υ.    | 3 0       | 35.   | 35.    |         | 3 5                  | 35.   | 35.      | 35.      | 35.    | 35         | קיני     | . ה             | . ה              | 35.      | 35.      | 35.      | 35.            | 35.    | 35.      | 35       | 9.0      |          | , r       |           | י<br>י<br>י | n e     | 35      | 35.     | 35.      | 35.      | 35.     |          |             |         | 35.     | 35.      | 35.    | 35.    | 35.     | 35.     | 32      | 35       |          | , i     | ,<br>n       |
| 150                                   | 150         | 150       | 150   | 150    | 150     | 150                  | 150   | 150      | 150      | 150    | 150        | 150      | 1 1             | 150              | 150      | 150      | 150      | 150            | 150    | 150      | 150      | 150      | 150      | 100       | 150       | 100         | 150     | 150     | 150     | 150      | 150      | 150     | 150      | 1 1 2 0     | 150     | 150     | 150      | 150    | 150    | 150     | 150     | 150     | 150      | 150      | 001     | 120          |
| 0.1                                   | <b>.</b>    |           | ~     | -u ·   | ٠.      | ۰.                   | ~     | •        | _        | . س    | <b>~</b> 1 | • -      |                 |                  |          | ~        | •        | _              | _      | ~        | ~        |          | ٠.       |           | ۰. ۳      | . ~         | . ~     |         | ٥.      | ~        |          | ٠.      | ۰.       | . ~         |         | _       | _,       | ۵,     | _      | _       |         | ٠.      |          | <b>.</b> |         | _            |
| 99                                    | 3 5         | 107       | 103   | 104    | 101     | 107                  | 108   | 105      | 11(      | 11     | 11;        | 113      | 1 -             | 116              | 11       | 118      | 115      | 12(            | 12     | 15       | 15.      | 124      | 12.      | 7 7       | 120       | 1 7         | 130     | 131     | 132     | 133      | 134      | 135     | 136      | 13.5        | 135     | 140     | 141      | 4      | 143    | 144     | 145     | 146     | 147      | 146      | 1 4 V   |              |
|                                       |             |           |       |        |         |                      |       |          |          |        |            |          |                 |                  |          |          |          |                |        |          |          |          |          |           |           |             |         |         |         |          |          |         |          |             |         |         |          |        |        |         |         |         |          |          |         |              |

ALIGNMENTS

Mouse lymphoid derived dendritic cell adhesion molecule. AAY45093 standard; protein; 423 AA (first entry) 31-MAY-2000 AAY45093; 

Lymphoid derived dendritic cell adhesion molecule; LDCAM; mouse; B7-1; B7-L1; T cell proliferation; natural killer cell; NK; tumour cell; biological activity; quality control reagent; treatment; inflammation; immune system disorder; autoimmune; viral infection; infectious disease; organ transplant rejection; bone marrow; modulator; immune response.

Novel molecules designated LDCAM are capable of altering or modulating T .85 te= "N-Glycosylation site" /note= "N-Glycosylation site" 286. .288 286. .288 /note= "N-Glycosylation site" 290. .292 note= "N-Glycosylation site" "N-Glycosylation site" 357. .377 /label= Transmembrane\_domain /label= Extracellular domain 378. .423 /label= Cytoplasmic\_domain "N-Glycosylation Location/Qualifiers 99WO-US017905. 98US-0095672P 147. .149 /note= /note= /note= Baum PR, Fanslow WC; (IMMV) IMMUNEX CORP. 2000-205712/18. WPI; 2000-205712/ N-PSDB; AAZ50883 WO200008158-A2 cell function. Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site 05-AUG-1999; 07-AUG-1998; 17-FEB-2000 Domain Domain Domain 

cells and displays homology to adhesion molecules, B7-1 and cytoplasmic region of B7-11. Mouse LDCAM. Is found on lymphoid derived dendrificated in and displays homology to adhesion molecules, B7-1 and cytoplasmic region of B7-11. Mouse LDCAM is found on whole embryo, testes, triple negative cells murine splenic and lymph node CD8+, S49.1 and dendrification. BCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM binding protein and increases natural killer (MK) cell populations. It may be used to measure the biological activity and a quality control reagents of LDCAM binding proteins. LDCAM may be used for treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for prevention or reducing the effect of corgan and bone marrow transplant rejection and for modulating T cell immune responses. LDCAM polypoptides may also be used as carriers for delivering agents attached to T cells or present amino acid sequence is the mouse lymphoid derived dendrtitic Claim 7; Page 46-47; 44pp; English.

Sequence 423 AA;

cells bearing B7L-1

ö 9 1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN 0; Gaps 100.0%; Score 423; DB 3; Length 423; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 423; Conservative Query Match Best Local Similarity

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comprising at least 10 contiguous nucleotides of any of the above-
comprising at least 10 contiguous nucleotides of any of the above-
comprising at least 10 contiguous nucleotides of any of the above-
complement), an isolated antibody, or its antigen binding fragment) that
complement), an isolated antibody, (or its antigen binding fragment) that
complement), an isolated antibody, (or its antigen binding fragment) that
complement), an isolated antibody, or its antigen binding fragment) that
complement), an isolated antibody or its antigen binding fragment) that
complement, an antibody or pharmaceutical composition comprising the above
antibody and a pharmaceutical excipient, a kit for detecting cancer
colls (comprising the antibody cited above, methods for detecting the presence or absence of cancer cells in an
individual, a method for inhibiting growth of cancer cells in an
individual, an electronic library comprising the above
individual, an electronic library comprising the above
contained anticancer activity or for a bioactive agent capable of modulating
the activity of a CA protein (CAP), methods for detecting cancer
associated with expression of a polypeptide in a test cell sample, a
method for treating cancers and a method for inhibiting the expression of
conferent in a cell. The composition and methods are useful for detecting,
cancer. The present sequence is a mouse CAP protein sequence. Note: The
sequence data for this patent did not form part of the printed
concer. The present sequence is a mouse CAP protein sequence. The
sequence data for this patent did not form part of the printed
concer. The present sequence is a mouse CAP protein sequence. The
sequence data for this patent did not form part of the printed
concer. The present sequence is a mouse CAP protein sequence. The
 ELKVSLINVSISDEGRYFCQLYTDPPQESYTTIIVLVPPRNLMIDIQKDTAVEGEEIEVN 120
 EMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTT 300
 301 TTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGT 360
 121 CTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHP 180
 Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
 1 NLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSS
 ELKVSLTNVSISDEGRYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVN
 28 NLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSS
 CTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHP
 AVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDD
 EMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPTTTTT
 Score 396; DB 8; Length 397;
 Indels
 Protein encoded by human secreted protein gene #11.
 YFTHEAKGADDAADADTAIINAEGGONNSEEKKEYF 396
 ;
0
 YFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYF
 ftp.wipo.int/pub/published_pct_sequences
 Query Match
93.6%; Score 396; DE
Best Local Similarity 100.0%; Pred. No. 0;
Matches 396; Conservative 0; Mismatches
 Š
 standard; protein; 364
 (first entry)
 Sequence 397 AA;
 21-NOV-2000
 88
 61
 148
 268
 241
 328
 388
 AAB25586
 AAB25586;
 208
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 The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancerassociated proteins. Also included are an expression vector comprising the isolated nucleic acid cited above, a host cell comprising the above
 240
 240
 300
 300
 360
 420
 recombinant nucleic acid or expression vector, a microarray for detecting
 180
 New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
 TVLVPPRNLMIDIOKOTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
 EGDAFELTCEAIGKPQPVMVTWTVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
 TTTILTITDSRAGEEGTIGAVDHAVIG
 TVLVPPRNLMIDIOKDTAVEGEE1EVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
 GVVAVVVFAMLCLLIILGRYPARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK
 cancer-associated protein; cytostatic; cancer; leukaemia;
 Mouse cancer-associated protein MP16-039.1.
 English
 Malandro MS;
 ABO84563 standard; protein; 397 AA.
 ; 2003US-00388838.
; 2003US-00417375.
; 2003US-00461862.
; 2003US-00663431.
 disclosure; segid 419; 310pp;
 15-APR-2003; 2003US-00417375.
13-UM-2003; 2003US-00461862.
15-SEP-2003; 2003US-00663431.
15-DEC-2003; 2003US-00663431.
 17-FEB-2004; 2004WO-US004730
 SAGRES DISCOVERY INC
 (first entry)
 Morris DW, Morris DW,
 WPI; 2004-652914/63.
 N-PSDB; ABD32790.
 EYF 423
 EYF 423
 WO2004074320-A2
 lymphoma; CAP
 Mus musculus
 14-FEB-2003;
 14-MAR-2003;
 18-NOV-2004
 02-SEP-2004
 361
 181
 241
 301
 121
 121
 181
 241
 301
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 421
 421
 AB084563
 (SAGR-)
 AB084563
 RESULT
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ADA27058 standard; protein; 364

4DA27058

(first entry)

20-NOV-2003

ADA27058;

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The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAA806061-480623 encode the 12 secreted protein sequences given in AAA806061-480623 encode the 12 secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the cativities of the proteins include: immunosuppressant, anti-inflammatory; antiarthritic; antirheumatic, dermaclogical; antiproliferative; antiarthritic; antirheumatic, dermaclogical; antibroliferative; antiarthrity. The proteins, polypeptides, agonists and antiproliferative; antagonists may be used to treat prevent and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. clasoris disease, the unatoid arthritis, dermatitis, and multiple clerosis; inflammatory disorders e.g. inflammatory bowel disease, crohn's disease and nephritis; hyperproliferative disorders such as paraproteinaemias and purpuras; cancer e.g. melanoma and lymphoma. The proteins and polymucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene
 Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases.
 anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; Crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer; melanoma; lymphoma; wound healing; human.
 antirheumatic, dermatological; antiproliferative; antiarteriosclerotic;
 #11 and protein sequences are represented in sequences AAA80616 and AAB25586. Sequences AAA80677-A80682 represent genes related to the
 Wei
 Young PE, Kenny JJ, Moore PA,
 Claim 1; Fig 28A-B; 803pp; English.
 99WO-US025031.
 98US-0105971P.
 (HUMA-) HUMAN GENOME SCI INC.
 Ruben SM, Olsen HS,
 protein gene#11
 2000-387742/33.
 N-PSDB; AAA80616.
 WO200029435-A1
 Homo sapiens.
 27-OCT-1999;
 28-OCT-1998;
 25-MAY-2000.
 Greene JM;
 secreted
 J,
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DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 153
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 DSRFQLLNFSSSELKVSLTUVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK
 SAAALI PTGDGQNLFTKDVTVI EGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 ö
 35.5%; Score 150; DB 3; Length 364;
 0; Indels
 6.5e-135;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 100.0%; Prec. nc.
 Conservative
 Local Similarity
Sequence 364 AA;
 Matches 150;
 16
 92
 94
 154
 Query Match
 136
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The invention relates to an isolated nucleic molecule that is at least of a fidentical to 18 human cDNA sequences representing 12 novel genes according secreted proteins or a polynucleotide fragment of the cDNA sequence contained in American Type Culture Collection (TCC) deposit No. defined in the specification, its species homologue, a variant or allelic variant of the polynucleotide having a polynucleotide capable of hybridising under conditions the polynucleotide capable of having a nucleotide sequence of only A or T residues. Also included are recombinant vectors, host cells (for producing the polypeptide), the secreted polypeptide (Comprising a sequence that is at least 95% identical to a polypeptide fragment, domain, epitope, full-length secreted polypeptide (Comprising a sequence that is at least 95% identical to a polypeptide fragment, domain, epitope, full-length concentrating to the polypeptides, diagnosing, treating, preventing or ameliorating a medical condition by administering the polynucleotide or the polypeptide, the gene corresponding to the cDNA sequence and identifying an activity in a biological assay (by expressing the cDNA sequence in a cell, isolating the supernatant, and detecting an activity in a biological assay and identifying the protein in the supernatant
 New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
 Greene JM;
 cytostatic, antiinflammatory; immunomodulator; neuroprotective; hemostatic; gene therapy; cancer; inflammation; immune disorder; neurological disorder; blood clotting disorder; food additive;
 Wei Y,
 Human novel secreted protein from cDNA HOUDJ81 #1.
 Olsen HS, Moore PA,
 preservative; human; secreted protein.
 Claim 11; Fig 28; 454pp; English.
 Kenny JJ, O]
Crocker PR;
 27-OCT-1999; 99WO-US025031.
19-APR-2000; 2000US-0198407P.
20CCT-2000; 2000US-023792P.
18-APR-2001; 2001US-00836353.
 29-OCT-2001; 2001US-00984130
 WPI; 2003-567103/53.
N-PSDB; ADA27040.
 YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
WEI Y.
GREENE J M.
 CROCKER P R
 ng PE, K
Liu D,
 RUBEN S M.
 US2003055231-A1.
 Homo sapiens.
 Young
 28-OCT-1998;
 20-MAR-2003
 Ruben SM,
 disorders.
 (RUBE/)
(LIUD/)
(CROC/)
 (/CCIN)
 KENN/)
 OLSE/)
 (MEIY/)
 (GREE/)
 (MOOR/
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having the activity). The polypeptides, nucleic acids and antibodies are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation and other immune disorders, neurological and blood clotting disorders (many examples are given in the specification). The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. The polypeptide, polynucleotide, agonist or antagonist may also be used as a food additive or preservative to increase or decrease storage capabilities, fat content or other nutritional components. The present is a secreted protein of the
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 75
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Greene JM;
 0; Gaps
 35.5%; Score 150; DB 6; Length 364; 100.0%; Pred. No. 6.5e-135; Live 0; Mismatches 0; Indels
 secreted protein; cancer; liver disorder; hepatitis;
 Wei Y,
 Olsen HS, Moore PA,
 DTAVEGEELEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 disorder; Alzheimer's disease.
 ADE86588 standard; protein; 364 AA
 Novel human secreted protein #11.
 27-OCT-1999; 99WO-US025031.
19-APR-2000; 2000US-0198407P.
 98US-0105971P
 18-APR-2001; 2001US-00836353
 Kenny JJ,
 29-JAN-2004 (first entry)
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 NI J.
YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
WRI Y.
GREENE J M.
RUBEN S M.
 WPI; 2004-020335/02
 Young PE,
 N-PSDB; ADE86570
 Sequence 364 AA;
 US2003129685-A1
 28-OCT-1998;
 Homo sapiens
 10-JUL-2003.
 invention.
 Ruben SM:
 ADE86588;
 34
 92
 94
 136
 154
 (WEIY/)
(GREE/)
(RUBE/)
 (/ffIN)
 (KENN/)
 (VOUN)
 human;
 neural
 (OLSE/)
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The invention relates to an isolated nucleic acid sequence, or its altalic variant, a fragment of the cDNA sequence, or its fragment domain, epitope or species homologue. The nucleic acid is useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, liver disorders such as hepatitis or neural disorders such as Alzheimer's disease. The present sequence represents the amino acid sequence of a novel human secreted protein.
 ö
 antipsoriatic; immunosuppressive; vasotropic; nootropic; neuroprotective; antithyroid; thyromimetic; gynaecological; virucide; hepatotropic; antibacterial; dermatological; chromosome 11q23.2.
 94 DSRPQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 prevention; immune disorder; immunodeficiency; autoimmune disorder; blood-related disorder; haematological disorder; haemostatic disorder; thrombolytic disorder; hyperproliferative disorder; cancer; tumour; apoptocic disorder; ardiovascular disorder; respiratory disorder; angiogenic disorder; neovascularisation; neurological disorder; eproductive system disorder; infectious disease; gastrointedinal disorder; drug sercening; tissue regeneration; chemoteaxis; gene therapy; antibody therapy; drug targeting; chromosome mapping; forensic analysis; immunophenotyping; cytostatic; haemostatic; tranquiliser; vulnerary; antififiammatory; hephrotropic, cardiant; antiallergic; anti-HIV; antirheumatic; antiathritic;
 SAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLLNPNRQTI Y FRDFRPLK
 New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g. cancer, liver disorders or neural disorders.
 0; Gaps
 CD-like molecule; cluster of differentiation; diagnosis;
 Length 364;
 Indels
 35.5%; Score 150; DB 8; Lv
100.0%; Pred. No. 6.5e-135;
iive 0; Mismatches 0;
 Human CD-like molecule HATCZ07, SEQ ID NO:268.
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 Claim 11; SEQ ID NO 39; 380pp; English
 Ź
 ADR41469 standard; protein; 370
 25-SEP-2001; 2001WO-US029838
 26-SEP-2000; 2000US-0235484P
 (HUMA-) HUMAN GENOME SCI INC
 07-OCT-2004 (first entry)
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 Birse CE
 Sequence 364 AA;
 WO200226930-A2
 Homo sapiens.
 04-APR-2002
 Rosen CA,
 16
 94
 136
 ADR41469;
 ADR41469
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DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 94 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 Human; secreted protein, nutritional; cytokine; cell proliferation; differentiation; immune stimulating; vaccine; suppression; haematopoiesis regulation; tissue growth, activin; inhibin; chemotactic; chemotatic; thrombolytic; receptor; ligand; anti-inflammatory; cadherin; tumour invasion suppressor; tumour inhibition; gene therapy.
 New polynucleotides encoding secreted human proteins, derived from adult placenta, adult retina, fetal brain, fetal.
The present invention provides the protein and coding sequences of nove proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (EST from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 34 SAAALIPTGGGOLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
 Human secreted protein clone cw1000_2 protein sequence SEQ ID NO:62.
 Collins-Racie LA, Evans C;
Steininger RJ, Bowman MR;
 ..
 Length 402;
 Indels
 35.5%; Score 150; DB 4; Le 100.0%; Pred. No. 7.1e-135; live 0; Mismatches 0;
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 Lavallie ER,
Agostino MJ,
 Ŕ
 AAY53028 standard; protein; 414
 98US-0084564P.
98US-0087645P.
98US-0093712P.
98US-0094935P.
 99WO-US009970
 98US-0095880P
 99US-00306111
 Treacy M, Agos
th E, Widom A;
 (GEMY) GENETICS INST INC.
 (first entry)
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 protein of the invention
 Mccoy JM,
 WPI; 2000-052937/04.
 Merberg D, Treacy
Diblasio-Smith E,
 N-PSDB; AAZ33346
 Sequence 402 AA;
 WO9957132-A1.
 07-MAY-1999;
 06-MAY-1999;
 07-MAY-1998;
 29-FEB-2000
 02-JUN-1998
 22-JUL-1998,
 10-AUG-1998
 11-NOV-1999
 31-JUL-1998
 Jacobs K,
Merberg D.
 94
 136
 AAY53028;
 RESULT 8
AAY53028
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 Novel polynucleotides and polypeptides useful for treating, preventing or ameliorating cardiovascular, renal, neurovascular, and autoimmune disorders.
 Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
 The invention relates to 167 novel human CD (cluster of differentiation) - like molecules (ADR41388-ADR41563) and to CDNAs encoding them (segid:11}-
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 101
 75
 SAAALIPIGDGONLFTKDVTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
 Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
 ;
>
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 Asundi
 Length 370;
 Indels
 ď,
 Chen
 Score 150; DB 5; Le
Pred. No. 6.6e-135;
 ö
 Zhou P, Qian XB, Wang Z,
 35.5%; Scor.
100.0%; Pred. No. e...
0; Mismatches
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 191
 Human EST encoded protein SEQ ID NO: 1216.
 Claim 11; SEQ ID NO 268; 1243pp; English
 Claim 20; Page 877-878; 1275pp; English
 Ŕ
 25-JAN-2000; 2000US-00491404.
17-JUL-2000; 2000US-00617746.
03-AUG-2000; 2000US-00631451.
 25-JAN-2001; 2001WO-US002687
 15-SEP-2000; 2000US-00663870
 AAM23691 standard; protein;
 (first entry)
 Conservative
 gene therapy; nutrition.
 Tang YT, Liu C, Zh
Cao Y, Drmanac RA,
 WPI; 2001-476164/51
N-PSDB; AAH98350.
 WPI; 2002-405050/43
 Query Match
Best Local Similarity
 (HYSE-) HYSEQ INC.
 N-PSDB; ADR41293
 Sequence 370 AA;
 WO200154477-A2
 Homo sapiens
 12-OCT-2001
 02-AUG-2001.
 150;
 AAM23691;
 42
 9/
 102
 136
 162
 Matches
 AAM2369
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The present invention describes new human secreted proteins which were isolated from adult placenta, adult retina, foetal brain, foetal kidney, adult blood, adult brain, adult thyroid, adult blood adult brain, adult thyroid, adult blood adult hereis.

I sissue, adult testes, and adult lymph node cDNA libraries. The human secreted proteins, and the polynucleotides encoding them, are predicted treating, preventing or ameliorating make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and call proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, issue growth activity, activin/inhibin activity, cadherin/tumour ceptor/ligand activity, anti-inflammatory activity, cadherin/tumour function activity. The polynucleotides are also stated to be useful for gene therapy. AAX3316 to AAX3373 encode human secreted proteins, and AAX52998 to AAX5360 crepresent human secreted proteins, given in the present invention
 ö
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 SAAALIPHININITTEEVATISCOVNKSDDSVIQLENPNRQTIYFRDFRPLK 93
 Gaps
 cancer-associated protein; cytostatic; cancer; leukaemia;
 Query Match 35.5%; Score 150; DB 3; Length 414; Best Local Similarity 100.0%; Pred. No. 7.3e-135; Matches 150; Conservative 0; Mismatches 0; Indels
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 Human cancer-associated protein HP16-039.1
Claim 71; Page 416-417; 492pp; English
 Malandro MS;
 ABO84564 standard; protein; 425 AA
 2003US-00388838.
2003US-00417375.
2003US-00461862.
2003US-00663431.
 (SAGR-) SAGRES DISCOVERY INC
 17-FEB-2004; 2004WO-US004730
 2003US-00737318
 (first entry)
 Morris DW, Morris DW,
 WPI; 2004-652914/63.
N-PSDB; ABD32792.
 Sequence 414 AA;
 WO2004074320-A2
 lymphoma; CAP
 Homo sapiens.
 13-JUN-2003;
15-SEP-2003;
 LS-APR-2003;
 15-DEC-2003;
 18-NOV-2004
 14-MAR-2003;
 02-SEP-2004.
 34
 92
 94
 ABO84564;
 136
 Human;
 RESULT 9
 AB08456
 8 X C C C C C C C C C C C C C C C C X 8
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The invertion relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancerassociated (cretion and or expression vector, a microarray for detecting the isolated nucleic acid or expression vector, a microarray for detecting a cancerassociated (CA) nucleic acid comprising at least one probe comprising at least one probe comprising at least one probe comprising at least to contiguous nucleotides of any of the above.

Comprising at least 10 contiguous nucleotides of any of the above comprising frame of a CA sequence selected from any of the 95 complement), an isolated antibody, (or its antigen binding fragment) that complement), an isolated antibody, (or its antigen binding fragment) that complement), an isolated antibody, (or its antigen binding fragment) to binds to the above polypeptide, a hybridoma that produces the above monoclonal antibody, a pharmaceutical composition comprising the above monoclonal antibody, a pharmaceutical composition comprising the above calls (comprising the antibody cited above, methods for diagnosing cancer or for detecting the presence or above, methods of cancer cells in an individual, a method for inhibiting growth of cancer cells in an individual, an electronic library comprising the above polynucleotide or polypeptide (or their fragments), methods of screening context associated with expression of a polypeptide in a test cell sample, a setting cancer activity or fa CA protein (CAP), methods for diagnosing the activity of a CA protein (CAP), methods for detecting the expression of a polypeptide in a test cell sample, and and and and and and method for inhibitate general and method for trademental modulate contexting and treating cancers, especially lymphoma and electronic library compensation and method for trademental and presented and method for trademental and presented and presented in a cell. The composition and method for electring can
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLINFSSSELKVSLINVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK 93
 relates to an isolated nucleic acid comprising at least 10
 cancer. The present sequence is a human CAP protein sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
 New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
 SAAALIPTGDGQNLFTKDVTV1EGEVAT1SCQVNKSDDSV1QLLNPNRQT1YFRDFRPLK
 Gaps
 Human, PRO protein; tumour necrosis factor family; TNF; cytokine; secreted protein; transmembrane protein; inflammation disorder.
 ;
 Length 425;
 Indels
 35.5%; Score 150; DB 8; Le
100.0%; Pred. No. 7.5e-135;
:ive 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 at ftp.wipo.int/pub/published_pct_sequences
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 claim 18; seqid 422; 310pp; English.
 AAY17830 standard; protein; 440
 Human PRO355 protein sequence.
 12-AUG-1999 (first entry)
 Conservative
 Local Similarity
les 150; Conserv
 Seguence 425 AA;
 Homo sapiens
 92
 94
 136
 154
 AAY17830;
 Query Match
 Best Loca
Matches
 RESULT 10
 AAY17830
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New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical and diagnostic
PRO715; PRO241; PRO323; PRO2299; PRO233; PRO344; PRO347; PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human.
 ton DL, Ferrara N, Filvaroff E;
Godowski PJ, Grimaldi CJ, Gurney AL;
apier MA, Roy MA, Tumas D, Wood WI;
 "Tyrosine kinase phosphorylation site"
 "Tyrosine kinase phosphorylation site"
 /note= "N-myristoylation site"
430. .434
 "N-myristoylation site"
 "N-myristoylation site"
 "N-myristoylation site"
 /note= "N-myristoylation site"
233. .240
 "N-myristoylation site"
 /note= "N-myristoylation site"
 "N-myristoylation site"
 /note= "N-glycosylation site" 227. .233
 /note= "N-glycosylation site"
 "N-glycosylation site"
 'note= "N-glycosylation site"
 'note= "N-glycosylation site"
 306. .310
/note= "N-glycosylation site"
 172. .393
'label= Transmembrane domain
 302. .306
/note= "N-glycosylation
 1. .36
/label= Signal peptide
 Location/Qualifiers
 Baker KP, Botstein D, Eaton DL,
Gerritsen ME, Goddard A, Godowski
Hillan KJ, Kljavin IJ, Napier MA,
 Claim 12; Fig 24; 187pp; English
 98WO-US025108.
98US-0112850P.
98US-0113296P.
 99WO-US028301
 , 433
/note= "N
 , 371
/note= "W
 411. .417
/note= "N-
 .408
 . 233
 111. .115
 . .328
 69
 note=
 9. .15
/note=
 /note=
 note=
 'note=
 (GETH) GENENTECH INC.
 WPI; 2000-412324/35.
 N-PSDB; AAA49563
 WO200032776-A2
 Modified-site
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 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Modified-site
 Homo sapiens,
 01-DEC-1999;
 01-DEC-1998;
 22-DEC-1998;
 08-JUN-2000
 Peptide
 Domain
 ö
 transmembrane proteins used therapeutically. The PRO proteins have everytestatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynuclectides can be used in therapy, identification of homologues, raising antibodies and design of probes and priners. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 91
 present invention describes nucleic acids encoding PRO secreted and
 PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243;
 Gaps
 ö
 Nucleic acids encoding PRO secreted and transmembrane proteins
 Chen J;
 35.5%; Score 150; DB 2; Length 440; 100.0%; Pred. No. 7.7e-135; Live 0; Mismatches 0; Indels
 Baker KP,
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Yuan J,
 AAB01321 standard; protein; 440 AA
 Gurney AL,
 Claim 12; Fig 27; 123pp; English.
 97US-0069696P.
97US-0069702P.
97US-0069870P.
97US-0069873P.
 97US-0068017P.
98US-0070440P.
98US-0074086P.
98US-0074092P.
 97US-0067411P.
97US-0069278P.
97US-0069334P.
 97US-0069335P.
97US-0069425P.
97US-0069694P.
 98WO-US025108
 98US-0075945P
 (first entry)
 Best Local Similarity 100.
Matches 150; Conservative
 Human PRO355 polypeptide
 (GETH) GENENTECH INC
 Wood WI, Goddard A,
 WPI; 1999-371118/31
 N-PSDB; AAX80055
 Sequence 440 AA;
 12-DEC-1997;
16-DEC-1997;
16-DEC-1997;
16-DEC-1997;
 01-DEC-1998;
 25-FEB-1998;
 25-SEP-2000
 10-JUN-1999
 17-DEC-1997
17-DEC-1997
 11-DEC-1997
 11-DEC-1997
 18-DEC-1997
 16
 32
 96
 Query Match
 136
 152
 AAB01321
 RESULT 11
 AAB0132
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ABU58416;
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 RESULT 13
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New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources
 PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabblt; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 Gaps
 ö
 Length 440;
 0; Indels
 35.5%; Score 150; DB 3; Le
100.0%; Pred. No. 7.7e-135;
tive 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Human PRO polypeptide sequence #17.
 AAU29040 standard; protein; 440
 2000US-0189320P.
2000US-0189328P.
2000WO-US006884.
 2000US-0194647P.
2000US-0195975P.
2000US-0196000P.
 2000US-0187202P.
2000US-0186968P.
 2000US-0191007P.
 2000US-0196690P.
 2000US-0190828P
 2000US-0192655P
 2000US-0193032P
 000WO-US008439
 2000US-0194449P
 2000US-0196187P
 28-FEB-2001; 2001WO-US006520
 (first entry)
 150; Conservative
 Similarity
 Sequence 440 AA;
 WO200168848-A2.
 21-MAR-2000;
21-MAR-2000;
 04-APR-2000;
11-APR-2000;
 15-MAR-2000;
21-MAR-2000;
 MAR-2000;
 29-MAR-2000;
 04-APR-2000;
 11-APR-2000;
11-APR-2000;
 28-MAR-2000;
 11-APR-2000;
 Homo sapiens
 18-DEC-2001
 20-SEP-2001
 16
 92
 92
 136
 152
 AAU29040;
 Query Match
 Local
 Matches
 AAU29040
 888888888888
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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of detect the presence of a tumour in a mammal by comparing the level of and a control sample of normal cells, whereby a higher level of expression of a PRO polypeptide in a test sample of cells from the animal mammal. Mammals include dogs, cats, catle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, creast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
 Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and to screen for modulators of the compounds.
 DSRFOLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
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 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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Smith V, Watanabe CK, Wood WI, Zhang Z;
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
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2000WO-US020710.
2000US-00644848.
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2000WO-US014941.
2000WO-US015264.
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2000WO-US032678
 20-DEC-2000; 2000WO-US034956
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Matches 150; Conservative
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01-DEC-2000;
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ABU87964 standard; protein; 440 AA

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| % % % % % % % % % % % % % % % % % % %                                                                                                                                         | X X X X X X X X X X X X X X X X X X X                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |

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RESULT 15 ABU84279 ID ABU84279 standard; protein; 440 AA.

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17-AUG-1998
 and transmembrane protein; PRO; TNP-alpha; factor alpha; chondrocyte cell; tumour; gene therapy;
 Human secreted/transmembrane protein (PRO) #17.
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98US-008463P.
 2002US-00176756
 02-AUG-2003 (first entry)
 Human, secreted a tumour necrosis fi tissue typing.
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 Homo sapiens.
 21-JUN-2002;
 -DEC-1997;
 13-FEB-2003
 ABU84279;
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catracellular domain; tumour. necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
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 Human secreted polypeptide PR0355, SEQ ID NO:34
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28 - AUG - 1998

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01-OCT-1998;
02-OCT-1998;
 07-OCT-1998
 32
 92
 92
 136
 16
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ABR66153
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|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|------------------------------------------------|-----------|
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Score 150; DB 6; Length 440;<br>Pred. No. 7.7e-115;<br>0; Mismatches 0; Indels 0; Gaps | VTVIEGEVATISCOVNKSDDSVIQLANDNRQTIYFRDFRPLK<br> |           |
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| 17-AUG-1998, 17-AUG-1998, 17-AUG-1998, 17-AUG-1998, 17-AUG-1998, 18-AUG-1998, 18-AUG-1998, 18-AUG-1998, 26-AUG-1998,  Match<br>Best Local Simil<br>Matches 150; C                                      | 16 SAAALI<br>      <br> 32 SAAALI              | 76 DSRFQ1 |
| ************************************                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Óm̈Σ̈                                                                                  | <b>상</b> 셤                                     | ර් සිටුර් |

136 152

셤

RESULT

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98US-0084640P
98US-0084643P
98US-0085582P
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 04-AUG-1998;
10-AUG-1998;
 Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; civit; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
 Human secreted polypeptide PRO355, SEQ ID NO:34,
 ABR65543 standard; protein; 440 AA
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 2002US-00188773
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 US2003036159-A1
 18-SEP-1997

24-OCT-1997

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28-OCT-1997

28-OCT-1997

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31-ARR-1998

32-ARR-1998

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38-ARR-1998

 Homo sapiens
 02-JUL-2002;
 05-AUG-2003
 20-FEB-2003
 ABR65543;
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Human; secreted and transmembrane protein; PRO; TNF-alpha;
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
tissue typing.
 Human secreted/transmembrane protein (PRO) #17.
 ABU99483 standard; protein; 440 AA
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 152
 Query Mat
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Matches
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| BUS-0085580<br>BUS-0085582<br>BUS-0086720<br>BUS-008632<br>BUS-0087486<br>BUS-0087208<br>BUS-0087208<br>BUS-008728<br>BUS-0087609<br>BUS-0087609<br>BUS-0088025<br>BUS-0088025                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | BUS-0088326<br>BUS-0088126<br>BUS-00881212<br>BUS-0088217<br>BUS-0088621<br>BUS-0088621<br>BUS-0088626<br>BUS-008826<br>BUS-008826<br>BUS-008826<br>BUS-008826<br>BUS-0088818<br>BUS-0088818<br>BUS-0088818<br>BUS-0088818<br>BUS-0088618<br>BUS-0089105<br>BUS-0089538<br>BUS-0089538<br>BUS-0089538<br>BUS-0089538<br>BUS-0089538<br>BUS-0089538<br>BUS-0089538<br>BUS-0089638<br>BUS-0089538<br>BUS-0089538<br>BUS-0089538<br>BUS-0089538 | 98US-0090435P. 98US-0090444P. 98US-0090444P. 98US-0090531P. 98US-0090678P. 98US-0090678P. 98US-009069P. 98US-009069P. 98US-009069P. 98US-009069P. 98US-009069P. 98US-009069P. 98US-009069P. 98US-009069P. 98US-009069P. 98US-009163P. 98US-009163P. 98US-009163P. 98US-009163P. 98US-009163P. 98US-009163P. 98US-009163P. 98US-009163P. 98US-009163P. 98US-009163P. 98US-009163P. 98US-009163P. 98US-009163P. |
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| 5-MAY-1998<br>8-MAY-1998<br>8-MAY-1998<br>2-MAY-1998<br>2-MAY-1998<br>8-MAY-1998<br>8-MAY-1998<br>8-MAY-1998<br>8-MAY-1998<br>8-JUN-1998<br>4-JUN-1998<br>4-JUN-1998<br>4-JUN-1998                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 4 - CUN-199 5 - CUN-199 5 - CUN-199 6 - CUN-199 9 - CUN-199 0 - CUN-199 0 - CUN-199 0 - CUN-199 0 - CUN-199 1 - CUN-199 1 - CUN-199 1 - CUN-199 1 - CUN-199 1 - CUN-199 1 - CUN-199 1 - CUN-199 2 - CUN-199 4 - CUN-199 8 - CUN-199 8 - CUN-199 8 - CUN-199 8 - CUN-199 8 - CUN-199 8 - CUN-199 8 - CUN-199 8 - CUN-199                                                                                                                      | 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                        |
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| 8US-0096867<br>8US-0096891<br>8US-0096949<br>8US-0096959<br>8US-0097052<br>8US-0097952<br>8US-0097954<br>8US-0097954 | 98US-009873P. 98US-009803P. 98US-009803P. 98US-009803P. 98US-0099602P. 98US-0099741P. 98US-0099741P. 98US-0099763P. 98US-010068P. 98US-0100664P. 98US-0100664P. 98US-0100648P. 98US-010093P. | 8US-0101471<br>8US-0101472<br>8US-0101475<br>8US-0101739<br>8US-0101739<br>8US-0101743<br>8US-0101743<br>8US-0101743<br>8US-0102207<br>8US-0102340<br>8US-0102340<br>8US-0102340<br>8US-0102540<br>8US-0102571<br>8US-0102684<br>8US-0102684<br>8US-0102684<br>8US-0102684<br>8US-0102684<br>8US-0102684<br>8US-0102684<br>8US-0102684<br>8US-0102684<br>8US-0102684 |
|----------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 7-AUG-199<br>7-AUG-199<br>8-AUG-199<br>8-AUG-199<br>8-AUG-199<br>6-AUG-199<br>6-AUG-199<br>6-AUG-199                 |                                                                                                                                                                                              | 3SEP-199 3SEP-199 3SEP-199 3SEP-199 4SEP-199 4SEP-199 6SEP-199                                                                                                                                                                                  |
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0; Gaps

Query Match 35.5%; Score 150; DB 6; Length 440; Best Local Similarity 100.0%; Pred. No. 7.7e-135; Matches 150; Conservative 0; Mismatches 0; Indels

8 6 8 6

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The invention relates to an isolated PRO polypeptide (a secreted or transmembrane protein) comprising: (a) at least 80% sequence identity or positives when compared to any of 15 sequences, fully defined in the specification, lacking or with itse associated signal peptide; or (b) at least 80% sequence of any defined in the American Type Culture coding sequence of a DNA deposited in the American Type Culture Collection (ATCC). Also included are: (l) an isolated mucleic acid comprising: (a) at least 80% sequence identity to a nucleotide sequence in the amorphism of the any of 15 fully defined sequence or full-length coding sequence with any of 15 fully defined sequences of 957-3441 base pairs, given in the specification; or (c) at least 80% sequence identity to a full-length coding sequence of a nucleotide sequence of 40% sequence identity to a full-length coding sequence of a collection of a collect
 New isolated PRO polypeptide and encoding nucleic acid, useful for the diagnosis and treatment of disorders associated with the PRO polypeptide, such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.
 Human; PRO; secreted protein; transmembrane protein; anti-HIV; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; cardiant; AIDS; acquired immunodeficiency syndrome; cancer; atherosclerosis; inflammatory disease; diabetic complication; cardiac injury; organ failure.
 Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 Human secreted/transmembrane protein PR0355.
 ABUS5930 standard; protein; 440 AA
 Claim 12; Fig 24; 178pp; English
 15-500-1599; 99W0-USC11203.
30-NOV-1999; 99W0-USC12030.
30-NOV-1999; 99W0-USC28313.
30-NOV-1999; 99W0-USC28301.
16-DEC-1999; 99W0-USC38301.
16-DEC-1999; 99W0-USC38301.
22-FEB-2000; 2000W0-USC0955.
22-FEB-2000; 2000W0-USC08414.
30-MAR-2000; 2000W0-USC08413.
31-MAR-2000; 2000W0-USC08439.
32-MAR-2000; 2000W0-USC08439.
32-MAR-2000; 2000W0-USC08439.
32-MAR-2000; 2000W0-USC08439.
 98WO-US025108.
99WO-US012252.
99WO-US021090.
 28-FEB-2001; 2001WO-US006520
25-MAY-2001; 2001US-00866028
 31-AUG-2001; 2001US-00944654
 (first entry)
 (GETH) GENENTECH INC.
 WPI; 2003-174141/17.
N-PSDB; ABX75486.
 US2002142959-A1
 Homo sapiens
 26-MAR-2003
 03-OCT-2002
 ABU55930;
ASSOCIATION NOTICE OF THE SECOND SECO
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135
 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 75
 91
cell comprising the vector which, when cultured under conditions suitabl for expression of the PRO polypeptide, produces the PRO protein; (4) a chimeric molecule comprising PRO fused to a heterologous amino acid sequence; and (5) an anti-PRO antibody. The methods and compositions of the present invention are useful for the diagnosis and treatment of disorders associated with the PRO polypeptide, such as AIDS (acquired immunodeficiency syndrome), cancer, atheroscierosis, inflammatory disease, diabetic complications, cancer, autheroscierosis, inflammatory antibodies can also be used in the different screening, therapeutic and biological assays. The present sequence represents a PRO protein
 32 SAAALIPTGDGQNLFTKDVTVIBGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
 Human, PRO polypeptide; secreted and transmembrane protein; tumour; chromosome mapping; gene mapping; cytostatic.
 ;
 Length 440;
 Indels
 35.5%; Score 150; DB 6; Le
100.0%; Pred. No. 7.7e-135;
Live 0; Mismatches 0;
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 ABU82722 standard; protein; 440
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97US-0059266P.
97US-0063280P.
97US-0063120P.
97US-0063121P.
97US-006314P.
97US-0063541P.
97US-0063734P.
97US-0063734P.
97US-0063734P.
97US-0063734P.
 97US-0069425P.
97US-0069870P.
97US-0068017P.
98US-0077450P.
 20-JUN-2002; 2002US-00176911
 (first entry)
 Human PRO polypeptide #17.
 Conservative
 Best Local Similarity
Matches 150; Conserv
 Sequence 440 AA;
 US2003032113-A1.
 24-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
29-0CT-1997;
31-0CT-1997;
 27-JUN-2003
 18-DEC-1997;
10-MAR-1998;
 18-SEP-1997
 13-FEB-2003
 ABU82722;
 16
 96
 92
 136
 152
 24-NOV-19
11-DEC-19
 Query Match
 21-OCT-1
 31-OCT-1
13-NOV-1
 21-NOV-1
 2-DEC-1
 24-NOV-1
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| 98US - 00904414P<br>98US - 00904414P<br>98US - 00904414P<br>98US - 00906516P<br>98US - 00906516P<br>98US - 0090663P<br>98US - 0090663P<br>98US - 0090663P<br>98US - 0090663P<br>98US - 0090663P<br>98US - 0090663P<br>98US - 0091359P<br>98US - 0091359P<br>98US - 0091486P<br>98US - 0091486P<br>98US - 0091486P<br>98US - 0091486P<br>98US - 0091622P<br>98US - 0091622P<br>98US - 0091632P<br>98US - 0091754P<br>98US - 0091754P<br>98US - 0091754P<br>98US - 0091775P<br>98US - 0091754P<br>98US - 009174P<br>98US - 009174P<br>98US - 0009174P<br>98US - 0100684P<br>98US - 0100684P                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 98US-0101475F.<br>98US-0101477P.<br>98US-0101739P.<br>98US-0101739P.<br>98US-0101732P.<br>98US-0101786P. |
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100.0%; Pred. No. ...
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The invention relates to a human secreted and transmembrane polypeptide (PRO) and the polynucleotide encoding it. The PRO polypeptide or polynucleotide is useful in pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating cancers, inflammatory diseases, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS) and diabetic complications in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are also useful in biotechnological and medical research and in various polypeptides of the invention
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 New secreted and transmembrane polypeptides (e.g. PRO241, for use in pharmaceuticals, diagnostics or bioreactors, particularly for detecting or treating e.g. cancers, infertility or acquired immunodeficiency syndrome in mammals.
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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apier MA, Roy MA, Tumas D, Wood WI;
 Filvaroff E;
 Length 440;
 Indels
 35.5%; Score 150; DB 6; L6
100.0%; Pred. No. 7.7e-135;
iive 0; Mismatches 0;
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 d A, Godomo...
d. Napier MA, F
 Eaton DL,
 Claim 1; Fig 24; 173pp; English.
 2000WO-US008439.
2000WO-US014042.
2000WO-US020710.
2000WO-US032678.
2001WO-US006520.
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98US-0074092P-
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 2000WO-US005841
 99WO-US028301
 99WO-US030095
 2000WO-US004414
 2001US-00866028
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Best Local Similarity 100.
Matches 150; Conservative
 Hillan KJ, Kljavin IJ,
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ME, Goddard
 (GETH) GENENTECH INC.
 WPI; 2003-174088/17.
 N-PSDB; ABX89477
 Sequence 440 AA;
 16-DEC-1999;
11-FEB-2000;
22-FEB-2000;
 30-MAR-2000;
22-MAY-2000;
28-JUL-2000;
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25-FEB-1998;
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 30-NOV-1999;
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 02-MAR-2000;
 01-DEC-2000;
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 Gerritsen ME,
 28-JUL-1999;
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22-JUN-1999
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 Human; PRO; secreted polypeptide; transmembrane polypeptide; cancer; inflammatory disease; atherosclerosis; cardiac injury; AIDS; infertility; birth defect; premature aging; diabetes; dog; cat; horse; acquired immunodeficiency, syndrome; cow, sheep; pig; goat; rabbit; industry; cytostatic; antiinflammatory; cardiant; antiinfertility; anti-HIV; antiarteriosclerotic; antidiabetic.
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
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Pred. No. 7.7e-135;
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 35.5%; bcc. 100.0%; Pred. No. ... 0; Mismatches
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98US-0101773B.
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 18-8EP-1998
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11-DEC-1997;
11-DEC-1997;
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12-DEC-1997;
 29-SEP-1998
 19-SEP-2002
 01-OCT-1998
 16-DEC-1997
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01-JUN-2001;
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 15-JAN-2002;
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 Baker KP,
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 ABU98754;
 Pan J,
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 PRO; secreted polypeptide; transmembrane polypeptide;
necrosis factor alpha; TNF-alpha; chondrocyte cell; tumour;
ABU85594 standard; protein; 440 AA
 99WO-US021090.
99US-00403297.
99US-00423844.
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 2000WO-US005601.
 2000WO-US034956.
2001WO-US006520.
 98US-00202054,
 99WO-US005028.
 99WO-US010733.
 99US-00380137.
 99WO-US028551
 99WO-US031274
2000WO-US000219
 2000WO-US004341
 2000WO-US005841
 2000WO-US008439
 2000WO-US014941
 2000WO-US015264
 2000US-00644848
 2000WO-US023328
 2000US-00664610
 99WO-US020111
 2000WO-US004414
 2000WO-US005004
 2000WO-US014042
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 2000WO-US004342
 98US-00187368
 98WO-US025108
 2000WO-US006884
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 92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITULVPPRNLMIDIQK 151
 transmembrane polypeptides) and the PRO polymucleotides encoding them. The invention also relates to a method for stimulating the release of two invention also relates to a method for stimulating the release of two invention also relates to a method for stimulating the release of the blood with a sequence of the invention, a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO polypeptide and a method for detecting the presence of a tumour in a mammal. The polypeptides and polymucleotides are useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. Sequences ABUBSSPR represent human PRO polypeptides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html
 32 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK 91
 Desnoyers L, Goddard A, Godowski PJ, Gurney AL; stanabe CK, Wood WI, Zhang Z;
 Three hundred and five nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating tumor.
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 The invention relates to human PRO polypeptides (secreted and
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2001WG - US019692
2001WG - US021066
2001WG - US021066
2001WG - US0210135
2001US - 00918585
2001US - 00924419
2001US - 00924419
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2001US-00854280.
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 2001US-00946374
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26-JUN-1998;
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 0-JUN-1998
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 Human; gene therapy; chromosome identification; tissue typing.
 Novel human secreted and transmembrane protein PRO355.
 970S-0059263P.
970S-0053266P.
970S-00634286P.
970S-0063121P.
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 2002US-00176985
 US2003027277-A1
 21-JUN-2002;
 11. MAR. 1998

11. MAR. 1998

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27. MAR. 1998

27. MAR. 1998

31. MAR. 1998

01. APR. 1998

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115-MAY-1998

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 01-JUL-2002; 2002US-00187597
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 Human PRO polypeptide #17.
 US2003036141-A1.
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 21-NOV-1997;
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 Score 150; DB 6; Le
Pred. No. 7.7e-135;
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 136
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AC ABU8
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98US-0086023P.
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02 JUN 1998

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Gaps

ABU86209 standard; protein; 440 AA

RESULT 35
ABU86209
ID ABU86
XX
AC ABU86

ABU86209,

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Human, immunogen, secreted protein, transmembrane protein; PRO; tumour, proliferation; differentiation; chondrocyte cells; tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
 Human secreted/transmembrane protein (PRO) #17
 28-FEB-2001; 2000WO-US034956,
28-FEB-2001; 2001WO-US006520,
22-MAR-2001; 2001US-000520
 98WO-US019330
98US-00168978
 98US-00202054
99US-00254311
 98WO-US025108
 99WO-US005028
 99US-00380139
 2002US-00187603
 98US-00187368
 99WO-US010733
 99WO-US012252
 99US-00403297
 99WO-US031274
 2000WO-US005841
 2001WO-US021735
 01-JUL-2003 (first entry)
 99WO-US
 SU-OW66
 99WO-US
 US2003036146-A1.
 01-MAR-2000;
02-MAR-2000;
15-MAR-2000;
30-MAR-2000;
17-MAY-2000;
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 32-JUL-2002;
 09-JUL-2001;
 20-FEB-2003
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 07-OCT-1998
 JUN-1999
 OCT-1999
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The invention relates to three hundred and five nucleic acids encoding CC PRO polypeptides (secreted and transmembrane), sequences 80% identical to them, or encoding a PRO polypeptide lacking its associated signal peptide.

Or an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide. Also included are the encoded PRO proteins, CRO produce PRO proteins, a chimaraic molecule comprising the PRO proteins), a chimaraic molecule comprising the PRO proteins), a chimaraic molecule comprising the PRO proteins), a chimaraic molecule comprising the PRO proteins), a chimaraic molecule comprising the PRO proteins), a chimaraic molecule comprising the PRO proteins), a method for stimmlating the release of tumor necrosis factor alpha (TNR-alpha) from human blood (by contacting the blood with PRO1079, PRO4313), a method for stimmlating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO6029 polypeptide, or anti-PRO antibody is useful for preparing a method for detecting the presence of tumour in a mammal and an oppose. The PRO polypeptide or anti-PRO antibody is useful for preparing a medicament for treating a condition that is responsive to the PRO as hybridisation probes in chromosome and gene mapping, or in generating action and cell and gene mapping, or in generating action and gene mapping, or in generating actions to generate transgenic animals or knockout contaction, to generate transgenic animals or knockout contacting the presence of atumour in a mammal, and cell the presence of atumour in a mammal, and cell the presence of atumour in a mammal, and cell ferrentiation of chodrocyte cells, in gene therapy. The PRO polypeptides and nucleic acid molecules are also useful for detecting the presence of atumour in a mammal, and cell ferrentiation of chodrocyte cells, in gene therapy, or as molecular markers for protein evidenting the cells in prepared the presence of a tumour necrosis factor-alpha from human blood, in gene cells in purposes. The an
 Three hundred and five nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, and for detecting the presence of tumor in a mammal.
 76 DSRPQLLNPSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
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 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
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 Smith V, Watanabe CK,
 2001US-00924419.
2001US-00929404.
2001US-00931836.
2001US-00941992.
2001US-00946374.
 2002US-00052586
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05-JAN-2000; 2000W0-US000219.

18-FEB-2000; 2000W0-US004341.

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22-FEB-2000; 2000W0-US005414.

24-FEB-2000; 2000W0-US005604.

01-MAR-2000; 2000W0-US005601.

02-MAR-2000; 2000W0-US005681.

15-MAR-2000; 2000W0-US006884.

30-MAR-2000; 2000W0-US006884.
 99WO-US021090.
99US-00403297.
99US-00423844.
 98US-00202054.
99US-00254311.
99WO-US005028.
 99US-00380137.
99US-00380138.
99US-00380139.
99US-00380142.
99WO-US020111.
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 99WO-US028301
 2000WO-US014042
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 2000WO-US014941
 2000WO-US023328
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 18-SEP-2000; 2
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The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides. Also disclosed is an antibody that tensmembrane (PRO) polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO polypeptide, a method for detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the PRO nucleotide sequences. The nucleotide sequences are useful as probes, no chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoreals purposes, for chromosome identification, as chromosome markers, as therapeutic agents, for stimulating the release of TNF-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes and detecting the proliferation or differentiation of chondrocytes and detecting the presence of a tumour. The PRO polypeptides and nucleic acids may also be used diagnostically for tissue typing. The sequences presented in ABU67406-ABU67710 are the PRO polypeptides of the invention
 nucleic acids, useful chromosome markers,
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPHTGGGGNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 Godowski PJ, Gurney AL;
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 0; Gaps
 Query Match 35.5%; Score 150; DB 6; Length 440; Best Local Similarity 100.0%; Pred. No. 7.7e-135; Matches 150; Conservative 0; Mismatches 0; Indels
 New secreted and transmembrane PRO polypeptides and in gene therapy, in chromosome and gene mapping, as in tissue typing, and in chromosome identification.
 , Desnoyers L, Goddard A, Godo
Watanabe CK, Wood WI, Zhang Z;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 181
 Claim 11; Fig 34; 706pp; English.
 10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-0086628.
01-UNN-2001; 2001WS-00874503.
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20-JUN-2001; 2001WS-00874503.
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13-MUG-2001; 2001US-00924419.
14-AUG-2001; 2001US-00931836.
28-AUG-2001; 2001US-00931836.
28-AUG-2001; 2001US-00941992.
29-AUG-2001; 2001US-00941992.
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 (GETH) GENENTECH INC.
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N-PSDB; ACA05716.
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10-MAY-2001;
10-MAY-2001;
25-MAY-2001;
 15-JAN-2002;
 16
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 Pan J,
 Baker
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75

RESULT 37 ABU80450

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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTITTVLVPPRNLMIDIQK 151
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 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 KW Human, PRO, secreted protein, transmembrane protein,
extracellular domain; tumour necrosis factor-alpha, TNR-alpha;
chondrocyte; proliferation; differentiation; cartilage disorder;
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
adrenal tumour; lung; colon; breast; prostate; kidney, rectum; cervix;
liver; drug screening; transgenic animal; genetic analysis;
 Human secreted polypeptide PRO355, SEQ ID NO:34.
 100.0%; Pred.
 DIAVEGERIEVNCTAMASKPATTIRWFKGN 165
 ABR99368 standard; protein; 440 AA
 18-SEP-2003 (first entry)
 Best Local Similarity 100.
Matches 150; Conservative
 WPI; 2003-342038/32.
N-PSDB; ACA66550.
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Smith V, W
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16-AUG-2001;
 28-AUG-2001;
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 Baker KP,
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 92
 ABR99368;
 Query Match
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 Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
liver; PRO; gene therapy.
ABU80450 standard; protein; 440 AA
 98WO-US021141.
98US-00187368.
98WO-US025108.
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99WO-US005028.
99US-00311832.
 99WO-US012252.
99US-00380137.
99US-00380138.
99US-00380139.
 99US-00403297.
99US-00423844.
99WO-US028301.
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 2000WO-US004342
 2000WO-US005601
 2000WO-US005841
 2000WO-US013705,
 2000US-00665350,
 2002US-00184640
 98WO-US019330
98US-00168978
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 99WO-US010733
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 2000WO-US020710
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 2001WO-US019692
 2001WO-US006520
 2001US-00874503
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 JS2003036137-A1.
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 15-SEP-1999
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Gaps ;

0; Indels

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The invention relates to three hundred and five nucleic acids encoding PRO polypeptides (secreted and transmembrane). Methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of tumours, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumours. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human CDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence represents a human PRO polypeptide of the invention
 transmembrane
 Three hundred and five nucleic acids encoding secreted and transmembrane PRO polypeptides, useful for the diagnosis, prevention and/or treatment of tumors, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumors.
 Gurney AL;
 35.5%; Score 150; DB 6; Length 440; 100.0%; Pred. No. 7.7e-135;
 Godowski PJ,
 Goddard A, Goαυν
cod WI, Zhang Z;
 Wood WI,
 Claim 11; Fig 34; 708pp; English.
 Desnoyers L,
 Watanabe CK,
2001MO-US021066.
2001MS-0090827.
2001US-00918827.
2001US-00924419.
2001US-00929404.
2001US-00931836.
 ; 2001WO-US027099.
; 2001US-00946374.
; 2002US-00052586.
 (GETH) GENENTECH INC
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 Human; PRO; secreted protein, transmembrane protein, extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
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28-OCT-1997

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21-NOV-1997

21-NOV-1997

22-NOV-1997

23-OCT-1997

24-NOV-1997

24-NOV-1997

25-OCT-1997

26-OCT-1997

27-NOV-1997

27-NOV-1998

27-MAR-1998

27-MAR-1998

27-MAR-1998

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28-APR-1998

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 25-JUN-2002;
 06-MAR-2003
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DSRFQLLNPSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
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 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 Length 440;
 Indels
 Human; PRO; secreted protein; transmembrane protein;
 35.5%; Score 150; .c., 100.0%; Pred. No. 7.7e-135; rive 0; Mismatches 0;
 Human secreted polypeptide PRO355, SEQ ID NO:34.
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 ABR78243 standard; protein; 440 AA
 98US-0098716P.
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98US-0098803P.
98US-0098821P.
98US-0098843P.
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9803-0099754P.
9803-0099763P.
9803-0099812P.
9803-0100388P.
 9805-0101751P.
98WO-US019330.
98US-0100683P.
98US-0100619P.
98US-0100919P.
98US-0100849P.
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 98US-01
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 18-SEP-1998
 SEP-1998
 -SEP-1998
 06-OCT-1998
 ABR78243;
 32
 92
 136
 16
 92
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extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy. Gurney AL; Godowski PJ, Chen J, Desnoyers L, Goddard A, Godo th V, Watanabe CK, Wood WI, Zhang Z; Smith V, Watanabe CK, 99WO-US012252. 99US-00380137. 22-JUL-2002; 2002US-00201530. 28-FEB-2001; 2001WO-US006520 15-JAN-2002; 2002US-00052586 (GETH ) GENENTECH INC WPI; 2003-503631/47. N-PSDB; ACF00116 JS2003054474-A1. Homo sapiens. 22-JUN-1998; 02-JUN-1999; 5-AUG-1999; 20-MAR-2003 Baker KP, Pan J,

New secreted and transmembrane PRO polypeptides and nucleic acids, usefuin gene therapy, or for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody.

Claim 11; Fig 34; 700pp; English.

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N-PSDB, ABX96814.
 Sequence 440 AA;
 a PRO protein
30-MAR-2000;
 ABU84979;
 RESULT 45
ABU84979
ID ABU849
XX
AC ABU849
DT 30-JUN
XX
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 ö
 Human; PRO; secreted protein; transmembrane protein;
Cornelia de Lange syndrome; gene therapy; immune disorder;
inflammatory disease; organ failure; atherosclerosis; cardiac injury;
infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 91
 SAAALI PTGDGQNLFTKDVTVI EGEVATISCQVNKSDDSVI QLLNPNRQTI YFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
 ö
 Score 150; DB 6; Length 440;
Pred. No. 7.7e-135;
 0; Indels
 35.5%; Sco...
100.0%; Pred. No. ...
... 0; Mismatches
 Human secreted/transmembrane protein PRO355.
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97US-0069694P.
 97US-0069696P.
97US-0069702P.
97US-0069870P.
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97US-0068017P.
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98US-0075945P.
98WO-US019330.
 98US-0112850P.
98US-0113296P.
 97US-0069334P.
 98WO-US025108
 99WO-US012252.
 99US-0146222P
 99WO-US028313
 99WO-US028409
 2000WO-US004414
2000WO-US005841
 2000WO-US003565
 31-AUG-2001; 2001US-00944944
 (first entry)
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22-FEB-2000;
02-MAR-2000;
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 15-MAY-2003
 21-NOV-2002.
 30-NOV-1999
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 16-DEC-1997
17-DEC-1997
 05-JAN-1998
09-FEB-1998
 16-DEC-1998
 22-DEC-1998
 02-JUN-1999
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 09-FEB-1998
 FEB-1998
 16-SEP-1998
 01-DEC-1998
 11-DEC-1997
 11-DEC-1997
 17-DEC-1997
 18-DEC-1997
 32
 92
 ABU64926;
 136
 152
 Query Match
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 ABU64926
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The invention relates to an isolated nucleic acid encoding a secreted/
transmembrane polypeptide (designated as PRO proteins). 15 PRO
CC polypeptides and their encoding polymuclectides are disclosed. Also
cincluded are a vector comprising the PRO nucleic acid, a host cell
comprising the vector, a process for producing a PRO polypeptide (by
CC culturing the host cell under conditions for the expression of the PRO
colypeptide, and recovering the PRO polypeptide (by
CC culturing the host cell under conditions for the expression of the PRO
polypeptide, and recovering the PRO polypeptide (by
CC the PRO polypeptides a chimaeric molecule comprising PRO fused to a
heterologous amino acid sequence and an antibody which specifically binds
CC the PRO polypeptides, a chimaeric molecule comprising PRO fused to a
heterologous amino acid sequence and an antibody which specifically binds
CC the PRO nucleotide sequences are useful as hybridisation probes,
in chromosome and gene mapping, in generating sense and antisense RNA or
DNA, in generating transgenic or knock-out animals which can be used in
the development and screening of therapeutically useful reagents, and in
CC gene therapy. The polypeptides may be used as molecular weight markers
CC for procein alectrophoresis purposes. The PRO polypeptides and nucleic
Cacids may also be used for chromosome identification, and tissue typing.
CC syndrome. Other PRO proteins are variously implicated in immune
CC syndrome. Other PRO proteins are variously implicated in immune
CC injury, infertility, birth defects, premature aging, cardiac injury,
ADD, cancer and diabetic complications. The present sequence represents
 92 DSRPQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 75
 91
 chromosome
 32 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 0; Gaps
 New transmembrane polypeptides and polynucleotides useful for chrome identification, tissue typing, gene therapy, in chromosome and gene mapping, or as molecular weight markers.
 Eaton DL, Ferrara N, Filvaroff E;
A, Godowski PJ, Grimaldi JC, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
 Length 440;
 0; Indels
 35.5%; Score 150; DB 6; Le 1100.0%; Pred. No. 7.7e-135; ive 0; Mismatches 0;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 ABU84979 standard; protein; 440 AA.
 Claim 12; Fig 24; 172pp; English.
 22-MAY-2000; 2000WO-US014042.
28-JUL-2000; 2000WO-US020710.
01-DEC-2000; 2000WO-US032678.
 28-FEB-2001; 2001WO-US006520.
25-MAY-2001; 2001US-00866028.
2000WO-US008439
 Baker KP, Botstein D, Ea
Gerritsen ME, Goddard A,
Hillan KJ, Kljavin IJ, N
 30-JUN-2003 (first entry)
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Best Local Similarity 100.
Matches 150; Conservative
 (GETH) GENENTECH INC.
 2003-311003/30.
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| 02-JUN-1998; 98US-0087609P. 03-JUN-1998; 98US-0087759P. 04-JUN-1998; 98US-0087759P. 04-JUN-1998; 98US-0088022P. 04-JUN-1998; 98US-0088023P. 04-JUN-1998; 98US-0088023P. 05-JUN-1998; 98US-0088124P. 10-JUN-1998; 98US-0088124P. 10-JUN-1998; 98US-0088124P. 10-JUN-1998; 98US-0088124P. 10-JUN-1998; 98US-0088124P. 11-JUN-1998; 98US-0089528P. 12-JUN-1998; 98US-0089528P. 12-JUN-1998; 98US-0089528P. 11-JUN-1998; 98US-0089528P. 12-JUN-1998; 98US-0089628P. 12-JUN-1998; 98US-0089628P. 12-JUN-1998; 98US-0089628P. 12-JUN-1998; 98US-0089628P. 12-JUN-1998; 98US-008963P. 12-JUN-1998; 98US-008963P. 12-JUN-1998; 98US-008963P. 12-JUN-1998; 98US-008963P. 12-JUN-1998; 98US-008963P. 12-JUN-1998; 98US-008963P. 12-JUN-1998; 98US-008963P. 13-JUN-1998; 98U |                                                                               |
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| ***************************************                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | X                                                                             |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | with                                                                          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                               |
| therapy;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                               |
| itic; gene                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                               |
| r cytostati                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                               |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                               |
| prote mapp 1; tu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                               |
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| 1: at c d a a a a a a a a a a a a a a a a a a                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 00-Sn8                                                                        |
| n hint                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                               |
| Novel human  Human, Exangencia e Chondrocyte Chondrocyte Chondrocyte Chondrocyte 13 - FEB - 2003.  13 - FEB - 2003.  14 - CT - 1997; 18 - SEP - 1997; 18 - SEP - 1997; 19 - CT - 1997; 24 - CT - 1997; 24 - CT - 1997; 25 - CT - 1997; 26 - CT - 1997; 27 - CT - 1997; 28 - CT - 1997; 29 - CT - 1997; 21 - CT - 1997; 22 - CT - 1997; 23 - CT - 1997; 24 - CT - 1997; 25 - CT - 1997; 26 - CT - 1997; 27 - CT - 1997; 28 - CT - 1997; 29 - CT - 1997; 21 - CT - 1997; 22 - CT - 1997; 23 - CT - 1998; 20 - MAR - 1998; 20 - MAR - 1998; 21 - MAR - 1998; 22 - MAR - 1998; 23 - MAR - 1998; 24 - MAR - 1998; 25 - MAR - 1998; 26 - MAR - 1998; 27 - MAR - 1998; 27 - MAR - 1998; 28 - APR - 1998; 29 - APR - 1998; 29 - APR - 1998; 29 - APR - 1998; 20 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998; 30 - MAY - 1998;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                               |
| 2 × 5 × 5 × 5 × 5 × 5 × 5 × 5 × 5 × 5 ×                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                               |

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tumour necrosis factor alpha; TNF-alpha;
 Novel human secreted and transmembrane protein PR0355
 Human, gene therapy, tumour necrosis factor all chondrocyte stimulation; tumour; tissue typing
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 22-MAY-1998;
28-MAY-1998;
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 21-0CT-1997;
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 5-APR-1998
 8-APR-1998
 29-APR-1998
 29-APR-1998
 07-MAY-1998
 07-MAY-1998
 LS-MAY-1998
 ö
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 SAAALIPTGGGONLFTKDVTVIEGEVATISCOVNKSDDSVIOLLNPNRQTIYFRDFRPLK 75
 Gaps
 ;
0
 Query Match
35.5%; Score 150; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 7.7e-135;
Matches 150; Conservative 0; Mismatches 0; Indels
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 ABO00118 standard; protein; 440 AA
98US-0097955P

98US-0097971P

98US-0098014P

98US-0098011E

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Best Loca Matches

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RESULT 48
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standard; protein; 440

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Human, antinflammatory, antiarteriosclerotic, cardiant, gynecological, anti-HIV, cytostatic, antidiabetic; BMP-agonist, BMP-Antagonist, cytokine-agonist, gene-Therapy; cytokine-antagonist, gene-Therapy; inflammatory disease; organ failure; atherosclerosis, cardiac injury; infertility, birth defect; premature aging; AIDS; cancer; diabetic complication.
 New isolated PRO polypeptide and encoding nucleic acids, useful for the diagnosis and treatment of disorders such as inflammatory disease, atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic complications.
 Eaton DL, Ferrara N, Filvaroff E;
,, Godowski PJ, Grimaldi JC, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
 Baker KP, Botstein D, Eaton DL, F
Gerritsen ME, Goddard A, Godowski
Hillan KJ, Kljavin IJ, Napier MA,
 Novel human secreted protein PR0355
 97US-0069378P
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97US-0069694P
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98US-0074092P.
98US-0075945P.
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2000WO-US005841.
2000WO-US008439.
 2000WO-US032678.
2001WO-US006520.
 98WO-US019330
 99WO-US012252
 99WO-US021090
 99WO-US028313
 2000WO-US003565
 2000WO-US014042
 2001US-00866028
 2001US-00943851
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 WPI; 2003-198285/19.
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22-MAY-2000; 2
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 Human, gene therapy, chondrocyte stimulation, TNF-alpha release, chondrocyte proliferation; chondrocyte differentiation; tumour detection;
 91
 The invention describes a novel isolated PRO polypeptide. The methods a compositions of the present invention are useful for the diagnosis and treatment of disorders such as inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diaberic complications and mutations in general. This is the amino acid sequence of a novel human secreted PRO protein
 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 SAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLLNPNRQTI YFRDFRPLK
 Gape
 ö
 Length 440;
 Indels
 Novel human secreted and transmembrane protein PR0355.
 35.5%; Score 150; DB 6; Le
ilarity 100.0%; Pred. No. 7.7e-135;
Conservative 0; Mismatches 0;
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 ABU88669 standard; protein; 440 AA.
 Claim 12; Fig 24; 171pp; English.
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 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYPRDFRPLK
 Gaps
 Human; secreted and transmembrane protein; PRO; chromosome mapping; gene mapping; transgenic animal; knockout animal; tissue typing; chromosome identification; tumour; chondrocyte prollieration; chondrocyte differentiation; tumour necrosis factor-alpha release;
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 Length 440;
 0; Indels
 Novel human secreted and transmembrane protein PRO355.
 tch
al Similarity 100.0%; Pred. No. 7.7e-135;
150; Conservative 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
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98US-010220P

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98US-0102687P

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98US-00168978.
98WO-US021141.
98US-00187368.
98WO-US025108.
 99WO-US012252.
99US-00380137.
99US-00380138.
99US-00380139.
 99WO-US005028
 99US-00311832
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 98US-00105413
 99US-00254311
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 20-FEB-2003
 AB019127;
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The invention describes a novel isolated PRO polypeptide. The PRO polypeptide or anti-PRO antibody is useful for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules involved in binding
 New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, chromosome identification, tissue typing, for detecting the presence of tumor in a mammal, or as hybridization probes in gene mapping.
 Gurney AL;
 Godowski PJ,
 Baker KP, Chen J, Desnoyers L, Goddard A, Godo
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 Claim 11; Fig 34; 707pp; English.
 2000US-00644848.
2000WO-US023328.
2000US-00664610.
 2000US-00709238.
2000WO-US030952.
2000WO-US032678.
2000US-00747259.
 2000WO-US034956.
2001WO-US006520.
2001US-00816744.
 2001US-00854208.
2001US-00854280.
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2001WO-US017800.
 2001US-00874503.
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2001WO-US021066.
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2001US-00924419.
 2001US-00929404.
2001US-00931836.
2001US-00941992.
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99WO-US028551.
99WO-US031274.
 99US-00403297
 2000WO-US014941.
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 2000WO-US005601
2000WO-US005841
 2000WO-US006884
 2000US-00665350
 2001WO-US021735
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 (GETH) GENENTECH INC.
 WPI; 2003-402071/38.
N-PSDB; ACD25374.
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 reaction, to generate transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful for detecting the presence of tumour in a mammal, stimulating proliferation or defection of chondrocyte cells, stimulating the release of tumour necrosis factor-alpha from human blood, in gene therapy, or as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
 DSRPQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
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 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
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 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
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 25-JUN-2002; 2002US-00180551
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 Human; PRO; secreted protein, transmembrane protein, extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
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100.0%; Pred. No. 7.7e-135;
tive 0; Mismatches 0;
 Human secreted polypeptide PRO355, SEQ ID NO:34.
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28-FEB-2001; 2001WO-US06520.
25-MAY-2001; 2001US-00866028.
 Ä
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 Sequence 440 AA;
 Homo sapiens
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 Human; antiinflammatory; antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic; antidiabetic; transmembrane; antiinflammatory; anti-HIV; antiarteriosclerotic; cardiant; infertility; anti-infertility; cytostatic; antidiabetic; gene therapy; birth defect; inflammatory disease; organ failure; atherosclerosis; cardiac injury; premature aging; AIDS; cancer; diabetic complication.
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98US-010268P.
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2000WO-US004414.
2000WO-US005841.
2000WO-US008439.
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98WO-US025108.
99WO-US012252.
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22-FEB-2000; 2
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This invention relates to a nucleotide sequence encoding an isolated secreted and/or transmembrane protein. The nucleotide sequences of the invention may have antiinflammatory, antiarteriosclerotic, cardiant, anti-infertility, anti-HIV, cytosetatic and antidiabetic activities and may be used in gene therapy. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, of diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA probes, in the polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. The present sequence represents a protein encoded by the nucleic acids of the
 Human, PRO; secreted protein; transmembrane protein; cytostatic; antiarthritic; ostoopathic; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cryical tumour; liver tumour; TNF-alpha release; arthritis; tumour necrosis factor alpha; chondrocyte cell; bone disorder; cartilage disorder; sports injury.
 New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or
 SAAALIPTGGGONLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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,, Godowski PJ, Grimaldi JC, Gurney AL;
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 35.5%; Score 150; DB 6; Length 440; 100.0%; Pred. No. 7.7e-135; cive 0; Mismatches 0; Indels
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 | DSRFQLINFSSSELKVSLINVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
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 Human secreted/transmembrane protein (PRO) #17.
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Homo sapiens

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 Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TRF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
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 27-AUG-2003
 23-SEP-1998
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 136
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 AB015671;
 152
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Matches
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 AB01567
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Pan J,

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Human; secreted protein; transmembrane protein; PRO; antiarthritic; vulnerary; tumour necrosis factor-alpha; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour; bone disorder; cartilage disorder;
 Human secreted/transmembrane protein, PRO355.
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 29-0CT-19
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 24 - NOV - 1
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 DEC-
The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides, with or without their associated signal CC transmembrane (PRO) polypeptides, with or without their associated signal CC peptide. Also disclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating the release of tumour necrosis differentiation of chodrocyte cells by contacting the blood with a CC differentiation of chodrocyte cells by contacting the cells with a PRO CC polypeptide, a method for detecting the presence of a tumour in a mammal an oligonucleotide probe derived from any of the PRO nucleotide cand an oligonucleotide probe derived from any of the PRO nucleotide and gene mapping, in generating antiense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as concented defective gene). The PRO polypeptides are useful as concented defective gene). The PRO polypeptides are useful as concented in the proliferation or differentiation of chondrocytes and concentrating the presence, prevention and/or treatment of a tumour, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumour. The PRO polypeptide and nucleic acids may also be used diagnostically concentration. Note: The sequence data for this patent can also be obtained concentrated by an encoded concentration or directly from USPTO at
 ö
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 Three hundred and five nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating tumor or for measuring or detecting expression of an associated gene.
 ', Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Smith V, Watanabe CK, Wood WI, Zhang Z;
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 Claim 11; Fig 34; 699pp; English
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15-JAN-2002; 2002US-00052586.
 26-JUL-2002; 2002US-00205907
 (GETH) GENENTECH INC
 WPI; 2003-479876/45.
 N-PSDB; ACD21185.
 Sequence 440 AA;
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 Homo sapiens.
 20-MAR-2003
 Baker KP,
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protein electrophoresis; tumour necrosis factor-alpha; TNF-alpha; blood;
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 ABO07738;
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136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165

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 2001WO-US006520
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(ABR69963-ABR70267) and nucleic acids encoding them (ACC90994-ACC91298).

The invention also relates to sequences at least 80% identical to the PRO nucleic acid and polypeptide sequences of the invention, recombinant vectors and host cells comprising a PRO nucleic acid, a method for the recombinant production of a PRO polypeptide, antibodies against a PRO polypeptide, and fusion proteins comprising a PRO polypeptide. Nucleic acids encoding PRO polypeptides of the invention were initially identified via homology screening using consensus sequences based on the extracellular domain sequences from known secreted proteins. Human cDNA libraries containing sequences from known secreted proteins. Human cDNA cligonucleotides based on the consensus sequences, and cDNA clones were significated and characterised. The PRO polypeptides are useful for stimulating release of tumour necrosis factor-alpha (TNF-alpha) from characterised which have used in the treatment of conditions in which enhanced TNF-alpha release would be beneficial. They are also useful for enhanced TNF-alpha is a man allowed and may thus be used in the treatment of conditions in which enhanced TNF-alpha is a man allowed and may thus be used in the treatment of conditions in which enhanced TNF-alpha is release would be beneficial. They are also useful for enhanced the proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins and proteins are also useful for enhanced the proteins and proteins
 therapeutically useful compounds. Sequences ABR69963-ABR70267 represent the human PRO secreted/transmembrane polypeptides of the invention. Note The sequence data for this patent is also available in electronic format from USPTO at sequate.uspto.gov/sequence.html
 invention relates to human PRO secreted/transmembrane polypeptides
 Gurney AL;
 PRO polypeptides, for genetic analysis of individuals with genetic disorders, and for generating either transgenic animals or knock-out animals which are useful in the development and screening of
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 New secreted and transmembrane PRO polypeptide useful in preparing medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody.
 Godowski PJ,
 KP, Chen J, Desnoyers L, Goddard A, Godor
Smith V, Watanabe CK, Wood WI, Zhang Z;
 Claim 11; Fig 34; 707pp; English.
 29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
29-AUG-2001; 2001WO-US027099.
1S-JAN-2002; 2002US-00052588.
2001WO-US017800
 GETH) GENENTECH INC.
 WPI; 2003-341977/32.
 N-PSDB; ACC91010
 20-JUN-2001;
29-JUN-2001;
09-JUL-2001;
01-JUN-2001;
 Pan J,
 Baker
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Sequence 440 AA;

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 DSRFQLINFSSSELKVSLINVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 75
 91
 16 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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35.5%; Score 150; DB 6; Length 440; 100.0%; Pred. No. 7.7e-135;
 Indels
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 Matches 150; Conservative
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 92
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26-JUN-1998;
 01-JUL-1998;
 6-JUN-1998
 24-JUN-1998
 16-JUN-1
 Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cliver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
 Human secreted polypeptide PRO355, SEQ ID NO:34.
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 2002US-00184629
 11-AUG-2003 (first entry)
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chondrocyte cell; colon; breast; prostate; rectum; cervix; liver.
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 21-JUN-2002; 2002US-00176758
 (first entry)
 Human PRO polypeptide #17.
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 27-MAR-1998;
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Matches 150
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transmembrane polypeptides and interactive secretaries the interactive control of the polymerlectides encoding them. The invention also relates to an antibody that specifically binds to a PRO polypeptide a method for stimulating the release of tumour necrosis factor alpha (TMF-alpha) from human blood by contacting the blood with a PRO polypeptide and a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO polypeptide. The polypeptides and polymucleotides are useful for detecting the presence of a tumour, such as an adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumour, and for treating such tumours. The polymucleotides are useful as phyridisation probes, in chromosome and gene mapping and in generating antisense RNA or DNA. The polypeptides are useful in tissue typing acceptable should be acceptable to the search human PRO polypeptides of the invention. Note: The sequence data for this patent is also available in electronic format from
 Three hundred and five nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO, useful for detecting the presence of, or treating tumor, e.g. adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumor.
 Godowski PJ, Gurney AL;
 The invention relates to human PRO polypeptides (secreted and
 P, Chen J, Desnoyers L, Goddard A, Godo
Smith V, Watanabe CK, Wood WI, Zhang Z;
 Claim 11; Fig 34; 707pp; English.
 17-MAY-2000; 2000MC-US013705.
22-MAY-2000; 2000WC-US013705.
30-MAY-2000; 2000WC-US014041.
02-JUN-2000; 2000WC-US012544.
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24-AUG-2000; 2000WC-US03328.
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 99WO-US028301.
 98WO-US021141
 98WO-US025108
 99WO-US005028
 99WO-US010733
 99WO-US012252
 2000WO-US004342
 29-AUG-2001; 2001WO-US027099
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Human; PRO; tumour necrosis factor-alpha; TNF-alpha; blood;
chondrocyte cell; tumour; adrenal; kidney; lung; colon; breast; prostate;
rectum; cervix; liver; cytostatic.
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Matches 150; Conservative
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 US2003017542-A1.
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 91
 Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; civer; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
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tive 0; Mismatches 0;
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; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; CURRENT FILING DATE: 1999-08-05
; PRIOR FILING DATE: 1999-08-05
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; WINDER OF SEQ ID NOS: 10
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FILE REPERENCE:
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PRIOR FILING DATE: 2001-02-06
PRIOR PILING DATE: 1099-08-05
PRIOR PILING DATE: 1999-08-05
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PRIOR PLING DATE: 2001-02-07
PRIOR PLING DATE: 1999-08-05
PRIOR PLING DATE: 1999-08-05
PRIOR PLING DATE: 1999-08-05
PRIOR PLING DATE: 1998-08-05
PRIOR PLING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
SEQ ID NO 22
 ; Sequence 22, Application US/10302041; Publication No. US20030144478A1; GENERAL INFORMATION:
 tcn
al Similarity 100.0%;
423; Conservative 0.
 SOFTWARE: PatentIn version 3.1
 423; Conservative
 ORGANISM: Mus musculus US-10-302-041-22
 musculus
 Similarity
 Query Match
Best Local Similarity
Matches 423; Conserv
 423
 EYF 423
 ; TYPE: PRT
; ORGANISM: mus
US-09-778-1878-4
 EYF
 RESULT 3
US-10-302-041-22
 LENGTH: 423
 241
 61
 19
 121
 SEQ ID NO 4
 181
 181
 241
 301
 361
 361
 421
 421
 Query Match
Best Local (
 Matches
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papelicant: Li, Li

APPLICANT: Edigaru, Muralidhara

TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of

TITLE OF INVENTION: Using the Same

TITLE OF INVENTION: Using the Same

FILE REPREBRES: 21402-11

CURRENT APPLICATION NUMBER: 60/249,153

FRICH FILING DATE: 2000-11-17

FRICH FILING DATE: 2000-11-17

FRICH FILING DATE: 2000-11-26

FRICH FILING DATE: 2001-01-26

FRICH FILING DATE: 2001-01-26

FRICH FILING DATE: 2001-02-26

FRICH FILING DATE: 2001-02-26

FRICH FILING DATE: 2001-02-16

FRICH FILING DATE: 2001-02-16

FRICH FILING DATE: 2001-02-16

FRICH FILING DATE: 2001-02-16

FRICH FILING DATE: 2001-07-10

FRICH FILING DATE: 2001-07-10

FRICH FILING DATE: 2001-07-10

FRICH FILING DATE: 2001-07-10

FRICH FILING DATE: 2001-07-10

FRICH FILING DATE: 2001-07-10

FRICH FILING DATE: 2001-08-17

FRICH FILING DATE: 2001-08-17

FRICH FILING DATE: 2001-08-17

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FRICH FILING DATE: 2001-08-17

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FRICH FILING DATE: 2001-08-17

FRICH FILING DATE: 2001-08-17

FRICH FILING DATE: 2001-08-17

FRICH FILING
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 121 TVLVPPRNIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
 240
 120
 141
 201
 261
 241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
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 81
 22 AAPPGLRLKLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
 61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
 142 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
 181 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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 82 PNRQTIYFRDFRFLKDSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTI
 Gaps
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 Length
 Indels
 Query Match 100.0%; Score 423; DB 15; Best Local Similarity 100.0%; Pred. No. 0; Matches 423; Conservative 0; Mismatches 0;
 Sequence 112, Application US/10015115
Publication No. US20030207800A1
GENERAL INFORMATION:
 Shenoy, Suresh G
Spytek, Kimberly A
Zerhusen, Bryan D
Patturajan, Meera
Guo, Xiaojla
Kekuda, Ramesha
Gangolli, Esha A
Shimkets, Richard A
Taupier, Raymond J
 APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
 ; ORGANISM: Mus musculus
US-10-015-115-112
 421 EYF 423
 US-10-015-115-112
 APPLICANT:
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 121 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
 240
 240
 GVVAVVVPAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKK 420
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 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK 420
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 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK 420
 361 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADAATAIINAEGGQNNSEEKK 420
 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
 9
 APPLICANT: YAN, Wei
TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
FILE REPERENCE: 3467-A
CURRENT APPLICATION NUMBER: US/10/898,408
CURRENT FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: 60/490,027
PRIOR FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
 1 AAPPGERIRLELLILIESAAALIPTGDGQNEFTKDVTVIEGEVATISCQVNKSDDSVIQLIN
 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
 1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
 Gaps
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 DB 17; Length 423;
 Indels
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 Query Match 100.0%; Score 423; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 423; Conservative 0; Mismatches
 Sequence 4, Application US/10898408; Publication No. US20050058642A1, GENERAL INFORMATION:
APPLICANT: GALIBERT, Laurent J. APPLICANT: YAN, Wei
 TYPE: PRT ORGANISM: mus musculus
 |||
EYF 423
 EYF 423
 LENGTH: 423
 RESULT 5
US-10-898-408-4
 US-10-898-408-4
 241
 181
 241
181
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 121
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 421
 SEQ ID NO 4
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239
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 241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
 300 EGDAFELICEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 359
 ELKVSLINVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVN 120
 CTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHP 207
 ELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVN 147
 9
 180 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
 240 YIVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
 1 NLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSS
 CTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHP
 181 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
 28 NLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSS
 Gaps
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 Indels
 in Cancer
 DB 16;
 Sequence 145, Application US/10417375
Publication No. US20040219528A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
ITILE OF INVENTION: Novel Therapeutic Targets in
FILE REFERENCE: 529452001600
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 145
LENGTH: 393
 Query Match
62.4%; Score 264; DB 16;
Best Local Similarity 100.0%; Pred. No. 6e-228;
Matches 264; Conservative 0; Mismatches C
 APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PF498P2
CURRENT APPLICATION NUMBER: US/09/984,130
PRIOR APPLICATION NUMBER: 60/243,792
 EMPQHAVLSGPNLFINNLNKTDNG 264
 ; Sequence 39, Application US/09984130; Publication No. US20030055231A1; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Mus musculus
US-10-417-375-145
 US-10-417-375-145
 US-09-984-130-39
 148
 121
 88
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 ### APPLICANT: iaupler, Kaymonu u

APPLICANT: iaupler, Kaymonu u

APPLICANT: Padigaru, Muralidhara

APPLICANT: Padigaru, Muralidhara

ITILE OF INVEXTION: Using the Same

FILE REPERENCE: 21402-21

CURRENT APPLICATION NUMBER: 06/249,153

PRIOR PELING DATE: 2000-11-13

PRIOR PELING DATE: 2000-11-13

PRIOR PELING DATE: 2001-01-02-05

PRIOR PELING DATE: 2001-01-02-05

PRIOR PELING DATE: 2001-02-06

PRIOR PELING DATE: 2001-02-06

PRIOR PELING DATE: 2001-02-06

PRIOR PELING DATE: 2001-02-16

PRIOR PELING DATE: 2001-02-16

PRIOR PELING DATE: 2001-02-16

PRIOR PELING DATE: 2001-07-10

PRIOR PELING DATE: 2001-07-10

PRIOR PELING DATE: 2001-07-10

PRIOR PELING DATE: 2001-07-11

PRIOR PELING DATE: 2001-07-11

PRIOR PELING DATE: 2001-07-11

PRIOR PELING DATE: 2001-07-11

PRIOR PELING DATE: 2001-07-11

PRIOR PELING DATE: 2001-07-11

PRIOR PELING DATE: 2001-07-11

PRIOR PELING DATE: 2001-07-11

PRIOR PELING DATE: 2001-07-11

PRIOR PELING DATE: 2001-07-11

PRIOR PELING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 205

SOGTWAREE: PALEANTIN VEV. 2.1
 ö
 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK 420
 GVVAVVVFAMLCLIIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK 441
 60 AAPPGLRIRLILLILLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN 119
 61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
 1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
 Gabs
 ö
 Length 494;
 0; Indels
 Score 342; DB 15; I Pred. No. 8.3e-298;
 80.9%; Score 342; DB
100.0%; Pred. No. 8.3
ive 0; Mismatches
 Sequence 113, Application US/10015115
Publication No. US20030207800A1
GENERAL INFORMATION:
 Shenoy, Suresh G
Spytek, Kimberly A
Zerhusen, Bryan D
Patturajan, Meera
Guo, Xiaojia
Kekuda, Ramesha
Gangoli, Esha A
Shimkets, Richard A
 Taupier, Raymond J
 Query Match 80.9
Best Local Similarity 100.
Matches 342; Conservative
 ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-015-115-113
 EYF 423
 EYF 444
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 361
 382
 421
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APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
 RESULT 12
US-10-417-375-148
 US-10-821-273-62
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 а
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQX 153
 DSRFOLLNFSSSELKVSLINVSISDEGRYFCQLYIDPPQESYTTITVLVPPRNLMIDIQK 153
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 ;
0
 35.5%; Score 150; DB 10; Length 364; 100.0%; Pred. No. 9.4e-126; ive 0; Mismatches 0; Indels
 Length 364;
 35.5%; Score 150; DB 10; I 100.0%; Pred. No. 9.4e-126; tive 0; Mismatches 0;
 APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REPERENCE: PF489P1
CURRENT APPLICATION NUMBER: US/09/836,353A
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-28
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION WUMBER: 09/836,353
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2000-04-19
PRIOR PLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
PRIOR PILING DATE: 1998-10-27
PRIOR PILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 149
 ; Sequence 39, Application US/09836353A; Publication No. US20030129685A1; GENERAL INFORMATION:
 NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.0
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 Matches 150; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
 US-09-836-353A-39
 US-09-836-353A-39
 US-09-984-130-39
 SEQ ID NO 39
LENGTH: 364
 SEO ID NO 39
LENGTH: 364
 92
 94
 136
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 94 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 34 SAAALIPITGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK 93
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Bowman, Michael R.
APPLICANT: DiBlasio-Smith, Blizabeth
APPLICANT: Widom, Angela
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
 0; Gaps
 Query Match 35.5%; Score 150; DB 16; Length 414; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 Sequence 148, Application US/10417375
Publication No. US20040219528A1
Publication No. US20040219528A1
REBERRY: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer FILE REPRENCE: 529452001600
CURRENT APPLICATION NUMBER: US/10/417,375
CURRENT FILING DATE: 2003-04-15
 136 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 154 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 FILE KEFEKEREL OVIGE. UCURENT APPLICATION NUMBER: US.
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: US 09/306,111
PRIOR PILING DATE: 1999-05-06
PRIOR PILING DATE: 1999-05-06
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-07-22
PRIOR PILING DATE: 1998-07-31
PRIOR PILING DATE: 1998-07-31
PRIOR PILING DATE: 1998-07-31
PRIOR FILING DATE: 1998-07-31
PRIOR PILING DATE: 1998-08-10
PRIOR PILING DATE: 1998-08-10
PRIOR PILING DATE: 1998-08-11
NUMBER OF SEQ ID NOS: 180
SEQ ID NO 62
LENGTHER 1414
Sequence 62, Application US/10821273
Publication No. US20040248256A1
GENERAL INFORMATION:
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152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181

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us-10-622-237-4.oligo.rapb

NUMBER OF SEQ ID NOS: 176 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 148

LENGTH

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P2548PICI CURRENT APPLICATION NUMBER: US/09/944,449

CURRENT APPLICATION NUMBER: US/09/966,028

PRIOR PLING DATE: 2001-09-26

PRIOR PLING DATE: 2001-05-25

PRIOR PLING DATE: December 13, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

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PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997
 APPLICATION NUMBER: PCT/US98/19330
 RELIGIO DATE: December 18, 1997
RAPPLICATION NUMBER: 60/070,440
RAPLICATION NUMBER: 60/070,408
RAPLICATION NUMBER: 60/074,086
RFILING DATE: PEDRUARY 9, 1998
RAPLICATION NUMBER: 60/074,092
RAPLICATION NUMBER: 60/074,092
RAPLICATION NUMBER: 60/074,993
RAPLICATION NUMBER: 60/075,945
 APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
 FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
 FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
 APPLICATION NUMBER: 60/113,290
 Sequence 61, Application US/0994449
Patent No. US20020102647A1
GENERAL INFORMATION:
 FILING DATE: December 1, 1998
 FILING DATE: December 11, 195
APPLICATION NUMBER: 60/069,4
FILING DATE: December 12, 195
APPLICATION NUMBER: 60/069,65
 FILING DATE: December 17, 199
APPLICATION NUMBER: 60/069,8°
FILING DATE: December 17, 199
APPLICATION NUMBER: 60/068,0
 FILING DATE: December 16, 19 APPLICATION NUMBER: 60/069,6
 FILING DATE: December 16, 1 APPLICATION NUMBER: 60/069,
 FILING DATE: December 16, 1 APPLICATION NUMBER: 60/069,
 Grimaldi,Christopher
 FILING DATE: July 28, 1999
 FILING DATE: December 16
 Ferrara, Napoleone
Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gerritsen,Mary
 Goddard, Audrey
 Gurney, Austin
Hillan, Kenneth
 Godowski, Paul
 Kljavin, Ivar
 Wood, William
 FILING DATE:
 PRIOR
PRIOR
PRIOR
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 94 DSRFQLINFSSSELKVSLINVSISDEGRYFCQLYTDPPQESYTTITVIVPPRNLMIDIQK 153
 92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2540P1C1
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 Query Match 35.5%; Score 150; DB 16; Length 421; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels (
 Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 120
 Query Match 35.5%; Score 150; DB 9; Length 440; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 154 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
 Sequence 61, Application US/09866028
Patent No. US20020058309A1
GENERAL INFORMATION:
 Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
 Gerritsen, Mary
Goddard, Audrey
 Gurney, Austin
Hillan, Kenneth
 Godowski, Paul
 Kljavin, Ivar
 Roy, Margaret
Tumas, Daniel
 Wood, William
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-375-148
 Napier, Mary
 CRGANISM: Homo Sapien
US-09-866-028-61
 US-09-866-028-61
 SEQ ID NO 61
 136
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 136
 APPLICANT:
APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: PASABPLCI CURRENT PAPLICATION NUMBER: US/09/944,457

CURRENT FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: December 3, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR FILING DATE: December 11, 1997

PRIOR PAPLICATION NUMBER: 60/069,335

PRIOR PILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,425

PRIOR PILING DATE: December 11, 1997

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PRIOR PLING DATE: December 12, 1997

PRIOR PLING DATE: December 16, 1997

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PRIOR PLING DATE: December 16, 1997
 PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION DATE: NO. US20020110859Alember 30, 1999
PRIOR PILING DATE: NO. US20020110859Alember 30, 1999
 APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: February 9, 1998
PRIOR PLING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR PILING DATE: February 25, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR PLING DATE: December 22, 1998
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PRIOR FILING DATE: December 16, 1998
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DR APPLICATION NUMBER: 09/216,021
DR FILING DATE: December 16, 1998
DR FILING DATE: December 22, 1998
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DR FILING DATE: December 22, 1998
DR APPLICATION NUMBER: 09/254,311
DR APPLICATION NUMBER: PCT/US99/12252
 APPLICATION NUMBER: PCT/USOO/03565
FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/USOO/04414
 PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR PELING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
 FILING DATE: February 22, 2000
 PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
 FILING DATE: December 16, 1999
 FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,870
FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/069,873
 APPLICATION NUMBER: 60/069,702
 FILING DATE: December1,
 Wood, William
 PRIOR
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
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 35.5%; Score 150; DB 9; Length 440;
 0; Indels
 FRIOR APPLICATION NUMBER: 09/254,311

PRIOR APPLICATION NUMBER: 09/254,311

PRIOR PILING DATE: March 3, 1999

PRIOR PILING DATE: March 3, 1999

PRIOR PILING DATE: June 22, 1999

PRIOR PELING DATE: June 22, 1999

PRIOR PILING DATE: September 15, 1999

PRIOR FILING DATE: NO. US20020102647Alember 30, 1999

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PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR APPLICATION NUMBER: PCT/US99/28310

PRIOR PILING DATE: NO. US20020102647Alember 30, 1999

PRIOR PILING DATE: NO. US20020102647Alember 30, 1999

PRIOR PILING DATE: December 1, 1999

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PRIOR PILING DATE: PEDRUARY 21, 2000

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PRIOR PILING DATE: March 2, 2000

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PRIOR PILING DATE: PEDRUARY 28, 2001
 Pred. No. 1.1e-125;
 100.0%; Pred. ...
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 APPLICATION NUMBER: 09/218,517
 Sequence 61, Application US/0994457
Patent No. US200201010859A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
 Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 Botstein, David
 NUMBER OF SEQ ID NOS: 120
 Kljavin, Ivar
 TYPE: PRT
ORGANISM: Homo Sapien
 JS-09-944-449-61
 US-09-944-457-61
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 SEQ ID NO 61
 92
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 152
 APPLICANT:
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FRIOR AFFLICATION NUMBER: 60/113.296

PRIOR PLINIG DATE: December 16, 1998

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PRIOR PLILING DATE: PEDITATY 11, 2000

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PRIOR PRILING DATE: PEDITATY 28, 2001
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OR APPLICATION NUMBER: 60/074,092
OR FILING DATE: February 9, 1998
OR APPLICATION NUMBER: 60/075,945
OR FILING DATE: February 25, 1998
OR FILING DATE: February 25, 1998
OR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: 60/112,296
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 60/146,222
OR FILING DATE: JULY 28, 1998
OR APPLICATION NUMBER: ECT/US98/19330
OR FILING DATE: SEPERMBER 16, 1998
OR APPLICATION NUMBER: PCT/US98/19330
OR APPLICATION NUMBER: PCT/US98/25108
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R APPLICATION NUMBER: 60/069,873
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R FILING DATE: December 18, 1997
R FILING DATE: December 18, 1997
R APPLICATION NUMBER: 60/070,440
 FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
 APPLICATION NUMBER: 60/069,694
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,702
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,870
 ORGANISM: Homo Sapien
 US-09-944-862-61
 Query Match
 APPLICANT: ROY, Wargaret
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,862
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: December 3, 1997
PRIOR PILING DATE: December 11, 1997
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 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
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 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 PRIOR APPLICATION NUMBER: PCT/USO0/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/08439
PRIOR APPLICATION NUMBER: PCT/USO0/14042
PRIOR PLICATION NUMBER: PCT/USO0/14042
PRIOR PELICATION NUMBER: PCT/USO0/20710
PRIOR PELING DATE: July 28, 2000
PRIOR PILING DATE: UNWBER: PCT/USO0/32678
PRIOR PLILNG DATE: December 1, 2000
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PRIOR PLILNG DATE: Pebruary 28, 2001
PRIOR PLILNG DATE: Pebruary 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
 Sequence 61, Application US/09944862
Patent No. US20020115145A1
GENERAL INFORMATION:
 Grimaldi, Christopher
Gurney, Austin
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Hillan, Kenneth
 Godowski, Paul
 Kljavin, Ivar
 ; ORGANISM: Homo Sapien
US-09-944-457-61
 Napier, Mary
 Eaton, Dan
 US-09-944-862-61
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 136
 TYPE: PRT
 APPLICANT:
APPLICANT:
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FILING DATE: February 25, 1998
 RESULT 18
US-09-945-015-61
 US-09-945-587-61
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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 0; Indels
 Pred. No. 1.1e-125;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 0; Mismatches
 TILE REFERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/945,587
CURRENT FILE DESTRUCTION NUMBER: US/09/945,587
CURRENT FILING DATE: 2001-09-26
PRIOR PELLING DATE: 2001-05-26
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 Sequence 61, Application US/09945587
Patent No. US20020127643A1
GENERAL INFORMATION:
 Ferrara Napoleone
Filvaroff, Ellen
Gerriteen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
100.08;
 Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
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 Roy, Margaret
 Tumas, Daniel
 Napier, Mary
 Best Local Similarity
 RESULT 17
US-09-945-587-61
 136
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 APPLICANT:
APPLICANT:
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
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 35.5%; Score 150; DB 9; Length 440; 100.0%; Pred. No. 1.1e-125; ive 0; Mismatches 0; Indels
 CR APPLICATION NUMBER: 60/146,222

(OR FILING DATE: December 22, 1998

(OR RELING DATE: Suptember 16, 1999

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(OR RILING DATE: December 16, 1998

(OR APPLICATION NUMBER: 09/216,021

(OR FILING DATE: December 22, 1998

(OR APPLICATION NUMBER: 09/218,517

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(OR FILING DATE: March 3, 1999

(OR APPLICATION NUMBER: PCT/US99/1252

(OR FILING DATE: Wow 12, 1999

(OR APPLICATION NUMBER: PCT/US99/28313

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(OR APPLICATION NUMBER: PCT/US99/28313

(OR FILING DATE: No. US20020127643Alember 30, 1999)

(OR FILING DATE: No. US20020127643Alember 30, 1999)

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(OR FILING DATE: DATE: PCT/US99/28313

(OR FILING DATE: PCT/US99/30095)
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
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PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: DECEMBER: 60/146,222
PRIOR PILING DATE: JULY 28, 1999
PRIOR FILING DATE: JULY 28, 1999
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PRIOR FILING DATE: DECEMBER: 1, 1998
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 ; Sequence 61, Application US/09945015; Patent No. US20020132768A1
 Matches 150; Conservative
 ORGANISM: Homo Sapien
 Query Match
Best Local Similarity
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 32 SAAALIPIGGGGULFIKDVIVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
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 OR FILING DATE: No. US20020137768Alember 30, 1999
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OR FILING DATE: No. US20020132768Alember 30, 1999
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OR FILING DATE: December1, 1999
OR FILING DATE: December 16, 1999
OR APPLICATION NUMBER: PCT/US00/03565
OR FILING DATE: Pebruary 11, 2000
OR APPLICATION NUMBER: PCT/US00/03465
 35.5%; Score 150; DB 9; L4
100.0%; Pred. No. 1.1e-125;
iive 0; Mismatches 0;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 PRIOR APPLICATION NUMBER: PCT/USO0/04414.
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: March 2, 2000
PRIOR PLING DATE: March 3, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PRIOR DAPLICATION NUMBER: PCT/USO0/14042
PRIOR PRIOR DATE: May 22, 2000
PRIOR PLING DATE: July 28, 2000
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PRIOR PLING DATE: December 1, 2000
PRIOR PLING DATE: Pebruary 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
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 Sequence 61, Application US/09944396
Patent No. US20020132981A1
 Godowski, Paul
Grimaldi, Christopher
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ilvaroff, Ellen
 Query Match
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Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Hillan, Kenneth
 Gerritsen, Mary
 Goddard, Audrey
 Gurney, Austin
 Kljavin, Ivar
 Roy,Margaret
Tumas,Danie]
 Napier, Mary
 ; ORGANISM: Homo Sapien
US-09-945-015-61
 -09-944-396-61
 152
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 APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
HITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
HITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P2548PICI
CURRENT APPLICATION NUMBER: US/09/945,015
CURRENT FILING.DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
 FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
 FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
 FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
 APPLICATION NUMBER: PCT/US99/12252
 OR FILING DATE: 2001-05-25
OR FILING DATE: 2001-05-25
OR APPLICATION NUMBER: 60/067,411
OR FILING DATE: December 3, 1997
OR FILING DATE: December 11, 1997
OR RILING DATE: December 11, 1997
OR APPLICATION NUMBER: 60/069335
OR APPLICATION NUMBER: 60/069,278
OR FILING DATE: December 11, 1997
OR APPLICATION NUMBER: 60/069,425
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OR APPLICATION NUMBER: 60/069,425
OR APPLICATION NUMBER: 60/069,425
OR PILING DATE: December 12, 1997
OR APPLICATION NUMBER: 60/069,696
 APPLICATION NUMBER: 60/075,945
 FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
 FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
 FILING DATE: December 1, 1998
APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
 APPLICATION NUMBER: 09/218,517
 APPLICATION NUMBER: 60/146,222
 FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
 FILING DATE: December 17, 199
APPLICATION NUMBER: 60/069,8
FILING DATE: December 17, 199
 APPLICATION NUMBER: 60/068,0
 FILING DATE: December 16, 19
APPLICATION NUMBER: 60/069,7
FILING DATE: December 16, 19
APPLICATION NUMBER: 60/069,8
 Godowski, Paul
Grimaldi, Christopher
 FILING DATE: January 5, 19
APPLICATION NUMBER: 60/074
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 FILING DATE: December 22
 FILING DATE: February 9
APPLICATION NUMBER: 60/
FILING DATE: February 9
 Botstein, David
 Gurney, Austin
 Kljavin, Ivar
 Roy, Margaret
 Napier, Mary
 APPLICANT:
APPLICANT:
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CURRENT PAILANTON WUNBER: US/09/944,336

CURRENT PAILANTON WUNBER: US/066,028

PRIOR PRILICATION WUNBER: 05/066,028

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CURRENT FILING DATE: 2001-09-26
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PRIOR FILING DATE: July 28, 2000
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PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: Pebruary 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LEMOTH: 440
TYPE: PRI
 FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,702
FILING DATE: December 16, 1997
 FILING DATE: December 16, 1997 APPLICATION NUMBER: 60/069,694
 Sequence 61, Application US/09944432 Patent No. US20020142419A1
 Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Gerritsen, Mary
 Goddard, Audrey
 Kljavin, Ivar
Napier, Mary
Roy, Margaret
Tumas, Daniel
 Godowski, Paul
 Wood, William
 ORGANISM: Homo Sapien
 Eaton, Dan
 GENERAL INFORMATION:
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 JS-09-944-432-61
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 PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
 FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
 FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/075,945
 Sequence 61, Application US/09943762
Patent No. US20020142958A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 FILING DATE: February 25, 1996 APPLICATION NUMBER: 60/112,850
 Godowski, Paul
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Hillan, Kenneth
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 Goddard, Audrey
 Kljavin, Ivar
Napier, Mary
 Tumas, Daniel
Wood, William
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 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 35.5%; Score 150; DB 9; Length 440; 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0; Indels
 100 FILING DATE: December 17, 1997

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101 APPLICATION NUMBER: 60/074,086

102 FILING DATE: February 9, 1998

103 APPLICATION NUMBER: 60/074,988

104 APPLICATION NUMBER: 60/075,945

105 FILING DATE: December 16, 1998

106 APPLICATION NUMBER: 60/113,286

107 APPLICATION NUMBER: 60/113,286

108 APPLICATION NUMBER: 60/113,286

108 APPLICATION NUMBER: 60/114,988

108 APPLICATION NUMBER: 60/146,222

108 FILING DATE: December 16, 1998

108 APPLICATION NUMBER: 90/146,122

108 FILING DATE: December 16, 1998

108 APPLICATION NUMBER: 90/146,121

108 FILING DATE: December 16, 1998

108 APPLICATION NUMBER: 90/218,211

108 FILING DATE: December 16, 1998

108 APPLICATION NUMBER: 90/254,311

108 FILING DATE: March 3, 1999

108 APPLICATION NUMBER: PCT/US99/21090

108 FILING DATE: September 15, 1999

108 APPLICATION NUMBER: PCT/US99/28301

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108 APPLICATION NUMBER: PCT/US99/28301

108 FILING DATE: No. US20020142419ALember 30, 1999

108 APPLICATION NUMBER: PCT/US99/28301

108 APPLICATION NUMBER: PCT/US99/28301

108 FILING DATE: December 16, 1999

108 APPLICATION NUMBER: PCT/US99/28301

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108 APPLICATION NUMBER: PCT/US99/28301

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PRIOR FILING DATE: February 5, 1998
PRIOR FILING DATE: February 9, 1998
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PRIOR FILING DATE: February 9, 1998
PRIOR FILING DATE: February 25, 1998
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 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-432-61
 SEQ ID NO 61
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE SEPREMENT PLANTONIN UNMERR: US/09/943,762
CURRENT APPLICATION NUMBER: US/09/943,762
CURRENT FILING DATE: 2001-09-26
FRIOR PILING DATE: 2001-05-25
FRIOR PELING DATE: December 11, 1997
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DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PIC1
 PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US9/28409
PRIOR FILING DATE: No. US20020142595Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US9/28313
PRIOR FILING DATE: No. US20020142595Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
 THIS KEFERENCE: P2546PICJ
CURRENT PEDELICATION NUMBER: US/09/944,654
CURRENT FILING DATE: 2001-09-26
PRIOR PELLING DATE: 2001-09-26
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 FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
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APPLICATION WINBER: 09/216,021
FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
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 Godowski, Paul
Grimaldi, Christopher
 June 22,
 Hillan, Kenneth
 Tumas, Daniel
Wood, William
 Roy,Margaret
 APPLICANT:
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IOR APPLICATION NUMBER: PCT/US98/19330

IOR FILING DATE: September 16, 1998

IOR APPLICATION NUMBER: PCT/US98/25108

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IOR FILING DATE: December 22, 1998

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IOR FILING DATE: March 3, 1999

IOR APPLICATION NUMBER: PCT/US99/12252

IOR FILING DATE: Warch 3, 1999

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IOR PELLING DATE: PCC-MDATION NUMBER: PCT/US99/30095

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IOR APPLICATION NUMBER: PCT/US99/3005

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IOR APPLICATION NUMBER: PCT/US99/010565

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PRIOR PELING DATE: PEDTUARY 28, 2001
 Sequence 61, Application US/09944654
Patent No. US20020142959A1
GENERAL INPORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaten, Dan
APPLICANT: Eaten, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
 Matches 150; Conservative
 NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
 ORGANISM: Homo Sapien
 Query Match
Best Local Similarity
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US-09-944-654-61
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PRIOR PILING DATE: December 16, 1998
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PRIOR PILING DATE: NO. US20020150976Alember 30, 1999
PRIOR PILING DATE: NO. US20020150976Alember 30, 1999
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 PRIOR APPLICATION NUMBER: PC1/USO/044149
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: March 2, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 28, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR PILING DATE: Pebruary 28, 2001
PRIOR PILING DATE: Pebruary 28, 2001
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PRIOR PILING DATE: Pebruary 28, 2001
 PRIOR FILING DATE: December1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
 PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: December 11, 1997
RELOR FLING DATE: December 11, 1997
RELOR FLING DATE: December 11, 1997
RELOR FILING DATE: December 11, 1997
RELOR APPLICATION NUMBER: 60/069,425
RELOR APPLICATION NUMBER: 60/069,696
RELOR APPLICATION NUMBER: 60/069,696
RELOR FILING DATE: December 16, 1997
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 FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/066,017
FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
 FILING DATE: January 5, 1998
APPLICATION WINBER: 60/074,086
APPLICATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
 FILING DATE: December 16, 199
APPLICATION NUMBER: 60/069,87
ALLING DATE: December 17, 199
APPLICATION NUMBER: 60/069,87
 FILING DATE: February 9, 1998 APPLICATION NUMBER: 60/075,94
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRPQLLNPSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPPRNLMIDIOK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 APPLICANT: Napier, Mary
APPLICANT: Tunas, Daniel
APPLICANT: Tunas, Daniel
APPLICANT: Tunas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/943, 851A
CURRENT FILING DATE: 2001-08-30
PRIOR PILING DATE: 2001-05-39
PRIOR PILING DATE: 2001-05-39
PRIOR PILING DATE: 2001-05-30
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 35.5%; Score 150; DB 9; Length 440; 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0; Indels
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR PLILING DATE: PEDTABAY 11, 2000
PRIOR PLILOATION NUMBER: PCT/US00/04414
PRIOR PLILOATION NUMBER: PCT/US00/06411
PRIOR PLILOATION NUMBER: PCT/US00/08419
PRIOR FILING DATE: March 2, 2000
PRIOR PLILOATION NUMBER: PCT/US00/08439
PRIOR PLILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR PLILING DATE: May 22, 2000
PRIOR PLILOATION NUMBER: PCT/US00/20710
PRIOR PLILING DATE: July 28, 2000
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 Sequence 61, Application US/09943851A
Patent No. US20020150976A1
GENERAL INFORMATION:
 Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 Best Local Similarity 100.
Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Kljavin, Ivar
 TYPE: PRT
ORGANISM: Homo Sapien
 RESULT 23
US-09-943-851A-61
 US-09-944-654-61
 92
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92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
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PRIOR APPLICATION NUMBER. 60/014, 092
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PRIOR APPLICATION NUMBER. 60/012, 945
PRIOR FILING DATE. PEDRILARY 9, 1998
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PRIOR FILING DATE. PEDRILARY 52, 1998
PRIOR FILING DATE. DECEMBER 16, 1998
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PRIOR PELING DATE. PEDRILARY 21, 2000

 Query Match 35.5%; Score 150; DB 9; Le Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 ; ORGANISM: Homo Sapien
US-09-944-413-61
 Best Local
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 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 11, 1997
PRIOR PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR PRIOR APPLICATION NUMBER: 60/069,278
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 0; Indels
 35.5%; Score 150; DB 9; L6
100.0%; Pred. No. 1.1e-125;
ive 0; Mismatches 0;
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 Sequence 61, Application US/09944413
Patent No. US20020156004A1
GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
 Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Goddard, Audrey
 Roy, Margaret
 Tumas, Daniel
Wood, William
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-943-851A-61
 Eaton, Dan
 RESULT 24
US-09-944-413-61
LENGTH: 440
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 92
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 152
 APPLICANT:
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76 DSRFQLLNPSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRPQLLNFSGSELKVSLINVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
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 35.5%; Score 150; DB 9; Length 440; 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0; Indels
 PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/1252
PRIOR APPLICATION NUMBER: PCT/US99/1252
PRIOR FILING DATE: June 22, 1999
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/2813
PRIOR APPLICATION NUMBER: PCT/US99/2813
PRIOR PILING DATE: No. US20020165143Alember 30, 1999
PRIOR FILING DATE: No. US20020165143Alember 30, 1999
PRIOR PILING DATE: December 1, 1999
PRIOR PLING DATE: December 16, 1999
PRIOR PLING DATE: December 16, 1999
PRIOR FILING DATE: PEDVILARY 11, 2000
PRIOR FILING DATE: PEDVILARY 11, 2000
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PRIOR PRILING DATE: PEDVILARY 22, 2000
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 152 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 PRIOR PLING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/USOU/04141
PRIOR PLING DATE: February 22, 2000
PRIOR PLING DATE: PEBRUARY 22, 2000
PRIOR PLING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/USOU/08439
PRIOR PLING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/USOU/14042
PRIOR PLING DATE: May 22, 2000
PRIOR PELING DATE: JULY 28, 2000
PRIOR PELING DATE: December 1, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR PELING DATE: Pebruary 28, 2001
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PRIOR PLING DATE: PEBRUARY 28, 2001
PRIOR PLING DATE: PEBRUARY 28, 2001
PRIOR PRIOR PRIOR SEQ ID NOS: 120
PRIOR
ION NUMBER: 09/254,311
 Sequence 61, Application US/09944896
Patent No. US20020168715A1
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Napier, Mary
 GENERAL INFORMATION:
 JS-09-944-896-61
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 APPLICANT:
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 APPLICANT: WOOD, WILLIAM
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
 FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
FILING DATE: 11919 28, 1999
APPLICATION NUMBER: PCT/US98/19330
 FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
 CURRENT APPLICATION NUMBER: Us, Us, Us, US, US, UGRRENT FILING DATE: 2001-05-26

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: December 3, 1997

PRIOR PILING DATE: December 11, 1997

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PRIOR PILING DATE: PEDILARY 9, 1998

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PRIOR PILING DATE: December 16, 1997

PRIOR PILING DATE: SEPTUARY 9, 1999

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 Sequence 61, Application US/09944403
Patent No. US20020165143A1
GENERAL INFORMATION:
 Grimaldi,Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Godowski, Paul
 Kljavin, Ivar
 Roy, Margaret
Tumas, Daniel
 Napier, Mary
 US-09-944-403-61
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Gaps ö ö

Length 440; Indels

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/944,944
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR PLING DATE: 2001-05-25
PRIOR PLING DATE: 2002-05-25
PRIOR PLING DATE: December 3, 1997
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 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPITGEGONLFTKDVTVIEGEVATISCOVNKSDDSVIQLINPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 35.5%; Score 150; DB 9; Le
ilarity 100.0%; Pred. No. 1.1e-125;
Conservative 0; Mismatches 0;
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 PRIOR APPLICATION NUMBER: PCT/USOO/14042
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 28, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR PLING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/USOO/32678
PRIOR APPLICATION NUMBER: PCT/USOI/06520
PRIOR PILING DATE: PECHUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
 PILING DATE: December 11, 1997
APPLICATION NUMBER: 60/669,425
FILING DATE: December 12, 1997
APPLICATION NUMBER: 60/669,696
PILING DATE: December 16, 1997
 Sequence 61, Application US/09944944
Patent No. US20020173463A1
GENERAL INFORMATION:
FILING DATE: March 30, 2000
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Goddard, Audrey
 Gerritsen, Mary
 Roy, Margaret
Tumas, Daniel
Wood, William
 Kljavin, Ivar
 Napier, Mary
 ; ORGANISM: Homo Sapien
US-09-944-896-61
 Eaton, Dan
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 US-09-944-944-61
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TITLE OF INVESTIONS SCREENED AND TANSABREANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVESTION: SCREENED AND TANSABREANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVESTION: SCREENED AND TANSABREANE POLYPEPTIDES AND NUCLEIC

CURRENT PELLIGION NUMBER: 105/09/344,896

PRIOR PELLICATION NUMBER: 105/09/344,896

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PRIOR PELLICATION NUMBER: 105/09/344

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PRIOR PELLICATION NUMBER: 105/09/34

PRIOR PELLICATION NUMBER: 105/09/34

PRIOR PELLICATION NUMBER: 105/09/34

PRIOR PELLICATION NUMBER: 105/09/34
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTIVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/944,929
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 Length 440;
 Indels
 Query Match 35.5%; Score 150; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Sequence 61, Application US/09944907; Publication No. US20020198147A1; GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baten, Dan
APPLICANT: Eaton, Dan
 Sequence 61, Application US/09944929
Publication No. US20020197612A1
GENERAL INFORMATION:
 Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
 Ferrara, Napoleone
 Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Kljavin, Ivar
 Wood, William
 Roy, Margaret
Tumas, Daniel
 Napier, Mary
 ; ORGANISM: Homo Sapien
US-09-944-929-61
 RESULT 28
US-09-944-929-61
 US-09-944-907-61
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 35.5%; Score 150; DB 9; Length 440;
 Indels
 10R FILING DATE: December 1, 1998

10R FILING DATE: December 1, 1998

10R FILING DATE: December 1, 1998

10R APPLICATION NUMBER: 09/216,021

10R FILING DATE: December 2, 1998

10R APPLICATION NUMBER: 09/218,517

10R FILING DATE: March 3, 1999

10R PILING DATE: March 3, 1999

10R PILING DATE: June 22, 1999

10R PILING DATE: June 22, 1999

10R APPLICATION NUMBER: PCT/US99/21090

10R FILING DATE: September 15, 1999

10R PILING DATE: NO. US200021734634meher 30, 1999

10R APPLICATION NUMBER: PCT/US99/28311

10R PILING DATE: December1, 1999

10R PILING DATE: December1, 1999

10R PILING DATE: December1, 1999

10R APPLICATION NUMBER: PCT/US99/3009

10R APPLICATION NUMBER: PCT/US99/3009

10R APPLICATION NUMBER: PCT/US09/3005

10R APPLICATION NUMBER: PCT/US09/03565

10R APPLICATION NUMBER: PCT/US00/03414
 100.0%; Pred. No. 1.1e-125; ive 0; Mismatches 0;
PRICOR FILING DATE: December 16, 1997
PRICOR FILING DATE: December 16, 1997
PRICOR FILING DATE: December 16, 1997
PRICOR FILING DATE: December 17, 1997
PRICOR FILING DATE: December 17, 1997
PRICOR FILING DATE: December 17, 1997
PRICOR FILING DATE: December 18, 1997
PRICOR FILING DATE: December 18, 1997
PRICOR FILING DATE: December 18, 1997
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PRICOR FILING DATE: December 19, 1998
PRICOR FILING DATE: Pebruary 9, 1998
PRICOR FILING DATE: Pebruary 9, 1998
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PRICOR FILING DATE: Pebruary 25, 1998
PRICOR FILING DATE: Pebruary 25, 1998
PRICOR FILING DATE: Pebruary 25, 1998
PRICOR FILING DATE: Pebruary 25, 1998
PRICOR FILING DATE: Pebruary 26, 1998
PRICOR FILING DATE: December 16, 1998
PRICOR FILING DATE: December 16, 1998
PRICOR PLICATION NUMBER: PCT/US99/12310
PRICOR PLILING DATE: December 16, 1998
PRICOR PLILING DATE: December 17, 1998
PRICOR PLILING DATE: December 17, 1998
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PRICOR PLILING DATE: DATE: PCT/US99/12313
PRICOR PLILING DATE: DATE: PCT/US99/12313
PRICOR PLILING DATE: September 16, 1999
PRICOR PLILING DATE: September 16, 1999
PRICOR PLILING DATE: September 16, 1999
PRICOR PLILING DATE: September 16, 1999
PRICOR PLILING DATE: September 16, 1999
PRICOR PLILING DATE: PCT/US99/12313
PRICOR PLILING DATE: PCT/US99/12313
PRICOR PLILING DATE: PCT/US99/12313
PRICOR PLILING DATE: PCT/US99/12313
PRICOR PLILING DATE: PCT/US99/12313
PRICOR PLILING DATE: PCT/US99/12313
PRICOR PLILING DATE: PCT/US99/12313
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PRICOR PLILING DATE: PCT/US90/1399
PRICOR PLILING DATE: PCT/US90/1250/1399
PRICOR PLILING DATE: PCT/US90/1250/1399
PRICOR PLILING DATE: PCT/US90/1250/1399
PRICOR PLILING DATE: PCT/US90/1250/1399
PRICOR PLILING DATE: PCT/US90/1250/1399
PRICOR PLILING DA
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
 US-09-944-944-61
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RESULT 31
US-09-944-852-61
'Sequence 61, Application US/09944852
'Publication No. US20030083479A1
'GENERAL INFORMATION:
 Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 Query Match
Best Local Similarity 100.0
Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Kljavin, Ivar
 Roy, Margaret
Tumas, Daniel
 Napier, Mary
 ; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-884-61
 ORGANISM: Homo Sapien
 Eaton, Dan
 Best Local Similarity
Matches 150; Conserv
 US-09-944-852-61
 APPLICANT:
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SEQ ID NO 61
 APPLICANT:
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 TYPE: PRT
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 APPLICANT: Godowski, Paul J
APPLICANT: Grimaldi, Christopher
APPLICANT: Grimaldi, Christopher
APPLICANT: Girnaldi, Christopher
APPLICANT: Hilan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Wood, Miliam
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPREMENCE: PS548PICI
CURRENT APPLICATION NUMBER: US/09/944,907
CURRENT APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 09/866,028
FRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRRQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P25.4910 NUMBER: US/09/944,884
CURRENT APPLICATION NUMBER: US/09/944,884
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 Query Match 35.5%; Score 150; DB 9; Length 440; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Sequence 61, Application US/09944884
Publication No. US20030077698A1
GENERAL INFORMATION:
 Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
 Ferrara,Napoleone
Filvaroff,Ellen
Gerritsen,Mary
 Ferrara, Napoleone
 Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Roy, Margaret
Tumas, Daniel
 Kljavin, Ivar
 Wood, William
 Napier, Mary
 TYPE: PRT
ORGANISM: Homo Sapien
 Eaton, Dan
 JS-09-944-907-61
 US-09-944-884-61
 LENGTH: 440
 152
 APPLICANT:
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 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITULVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Wood, William
TITLE OF INVENTION: BCRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P25-4891C1
CURRENT PELLICATION NUMBER: US/09/944,852
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
SEQ ID NO 61
LENGTH: 440
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK
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 Length 440;
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 35.5%; Score 150; DB 10; Lilarity 100.0%; Pred. No. 1.1e-125; Conservative 0; Mismatches 0;
35.5%; Score 150; DB 10; L 100.0%; Pred. No. 1.1e-125; iive 0; Mismatches 0;
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SARALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 0; Gaps
 Length 440;
 Indels
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: June 22, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20030096742A1ember 30, 1999
PRIOR FILING DATE: No. US20030096742A1ember 30, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR FILING DATE: December 1, 1999
PRIOR PLING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
 35.5%; Score 150; DB 10; 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0;
 152 DTAVEGEBIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 PRIOR FILING DATE: February 11, 2000
PRIOR PILING DATE: February 11, 2000
PRIOR PILING DATE: February 22, 2000
PRIOR PILING DATE: February 22, 2000
PRIOR FILING DATE: March 2, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR FILING DATE: Perluary 28, 2001
PRIOR FILING DATE: Pebruary 28, 2001
PRIOR FILING DATE: Pebruary 28, 2001
PRIOR FILING DATE: Pebruary 28, 2001
PRIOR FILING DATE: Pebruary 28, 2001
PRIOR FILING DATE: Pebruary 28, 2001
 Sequence 61, Application US/09945584 Publication No. US20030211570A1
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
 Gurney, Austin
Hillan, Kenneth
 Goddard, Audrey
 Kljavin, Ivar
 ; ORGANISM: Homo Sapien
US-09-943-780-61
 Napier, Mary
 GENERAL INFORMATION
 US-09-945-584-61
 LENGTH: 440
TYPE: PRT
 APPLICANT:
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 Sequence 61, Application US/09943780 Publication No. US20030096742A1 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 US-09-943-780-61
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2549PLC1
CURRENT APPLICATION NUMBER: US/09/943,664
CURRENT FILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-05-25
PRIOR PLING DATE: 2000-05-25
PRIOR PLING DATE: December 13, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
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PRIOR PRILING DATE: December 11, 1997
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PRIOR PRILING DATE: December 11, 1997
PRIOR PRILING DATE: December 11, 1997
PRIOR PRILING DATE: December 11, 1997
PRIOR PRILING DATE: December 11, 1997
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPFNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Length 440;
 35.5%; Score 150; DB 10; Length 4 100.0%; Pred. No. 1.1e-125; ive 0; Mismatches 0; Indels
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 PRIOR APPLICATION NUMBER: PCT/USO0/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/14042
PRIOR APPLICATION NUMBER: PCT/USO0/20710
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: Pebruary 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
 Sequence 61, Application US/09943664 Publication No. US20040091972A1 GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Goddard, Audrey
 Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William
 Kljavin, Ivar
 TYPE: PRT; ORGANISM: Homo Sapien
US-09-945-584-61
 Eaton, Dan
 US-09-943-664-61
 APPLICANT:
APPLICANT:
APPLICANT:
 152
 APPLICANT:
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 FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
 APPLICATION NUMBER: PCT/US00/05841
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PRIOR FILING DATE: Becember 16, 1937

PRIOR FILING DATE: December 16, 1937

PRIOR PLILING DATE: December 16, 1937

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PRIOR PLILING DATE: December 19, 1937

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PRIOR PLILING DATE: December 19, 1938

PRIOR APPLICATION NUMBER: 60/074, 006

PRIOR PLILING DATE: December 16, 1938

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PRIOR PLILING DATE: December 16, 1939

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PRIOR PRILING DATE: December 17, 1939

PRIOR PRILING DATE: December 17, 1939

PRIOR PRILING DATE: November 30, 1939

PRIOR PRILING DATE: November 30, 1939

PRIOR PRILING DATE: December 17, 1939

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PRIOR PRILING DATE: December 17, 1939

PRIOR PRILING DATE:
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35.5%; Score 150; DB 11; Length 440; 100.0%; Pred. No. 1.1e-125;

Query Match Best Local Similarity

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APPLICANT: Zanang, Zemin

APPLICANT: Zanang, Zemin

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REPERENCE: P4430R1C:
CURRENT APPLICATION NUMBER: US/10/052,586

CURRENT PILING DATE: 2002-01-15

PRIOR PILING DATE: 1997-09-18

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PRIOR PILING DATE: 1997-09-18

PRIOR PILING DATE: 1997-09-18

PRIOR PILING DATE: 1997-09-18

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-10-24

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PRIOR PILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-10-21

PRIOR PILING DATE: 1997-10-28

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 92 DSRFQLINFSSSELKVSLINVSISDEGRYFCQLYIDPPQESYTITVLVPPRNLMIDIQK 151
 9
 32 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYPRDFRPLK
 16 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 Indels
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
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Mismatches
 R FILING DATE: 1997-10-28

R APPLICATION NUMBER: 60/063564

R FILING DATE: 1997-10-28

R PILING DATE: 1997-10-29

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R APPLICATION NUMBER: 60/063870
 Sequence 34, Application US/10052586 Publication No. US20020127584A1 GENERAL INFORMATION:
 PILING DATE: 1997-10-31
APPLICATION NUMBER: 60/064103
FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
 APPLICATION NUMBER: 60/066120
FILING DATE: 1997-11-21
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 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Godowski, Paul J. Gurney, Austin L.
Conservative
 Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
Matches 150;
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| ER: 60<br>88-05-1<br>88-05-1<br>88-05-2<br>88-05-2<br>88-05-2<br>88-05-2<br>88-06-0<br>88-06-0 | 88 - 0 - 0 - 0 - 0 - 0 - 0 - 0 - 0 - 0 -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                      | E C C C C C C C C C C C C C C C C C C C                                                                 |
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35.5%; Score 150; DB 13; Length 440;

Query Match

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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK 91
 32 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: AZIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME PLLE REPERDECE: P3430RLC50 CURRENT APPLICATION NUMBER: US/10/175,737

CURRENT APPLICATION NUMBER: 2002-06-19
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
TYPE: PRT
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100.0%; Pred. No. 1.1e-125;
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 Score 150; DB 14; I
Pred. No. 1.1e-125;
 136 DTAVEGEBIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 0; Mismatches
 Sequence 34, Application US/10175737 Publication No. US20030013153A1 GENERAL INFORMATION:
 35.5%;
 Watanabe, Colin K.
 Godowski, Paul J
 Gurney, Austin L
 Best Local Similarity 100.
Matches 150; Conservative
 Wood, William I.
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 Desnoyers, Luc
Goddard, Audrey
 Pan, James
Smith, Victoria
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 LENGTH: 440
TYPE: PRT
CRGANISM: Homo Sapien
US-10-176-758-34
 ; ORGANISM: Homo Sapien
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 Query Match
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPTGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 32 SAAALIPTGDĞQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME PLIE REPERDICE: P943-0811C42 CURRENT APPLICATION NUMBER: US/10/174,590 CURRENT FILING DATE: 2002-06-18
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 Query Match 35.5%; Score 150; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels (
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NUMBER OF SEQ ID NOS: 612
Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Sequence 34, Application US/10174590; Publication No. US20030008352A1; GENERAL INFORMATION: APPLICANT: Baker Kevin P. APPLICANT: Chen, Jian
 Sequence 34, Application US/10176758 Publication No. US20030008353A1 GENERAL INFORMATION:
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddark, Paul J
APPLICANT: Godowski, Paul J
 Godowski, Paul J
Gurney, Austin L
 Desnoyers, Luc
Goddard, Audrey
 Desnoyers, Luc
 Zhang, Zemin
 TYPE: PRT
ORGANISM: Homo Sapien
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PRIOR PELING DATE: 1998-05-15
 PELLING DATE: 1998-04-08

R APPLICATION NUMBER: 60/081195

R APPLICATION NUMBER: 60/081195

R FILING DATE: 1998-04-15

R FILING DATE: 1998-04-15

R FILING DATE: 1998-04-12

R APPLICATION NUMBER: 60/082569

R FILING DATE: 1998-04-21

R APPLICATION NUMBER: 60/082569

R FILING DATE: 1998-04-21

R APPLICATION NUMBER: 60/082704

R FILING DATE: 1998-04-22

R FILING DATE: 1998-04-22

R FILING DATE: 1998-04-22

R FILING DATE: 1998-04-22

R FILING DATE: 1998-04-22
 R APPLICATION NUMBER: 60/077649
RR APPLICATION NUMBER: 60/077649
RR FILING DATE: 1998-03-11
RR APPLICATION NUMBER: 60/078886
RR FILING DATE: 1998-03-20
RR FILING DATE: 1998-03-20
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 R FILING DATE: 1998-03-27
R RAPPLICATION NUMBER: 60/079786
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/080107
R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080194
R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080327
 FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081070
 FILING DATE: 1998-03-10
APPLICATION NUMBER: 60/077632
 FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
 | TITLE OF INVENTION: SCIENCE AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENCE: P34309, SCHALT
| TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENCE: P343001401
| TILLE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: 106/10/5286 |
| PRIOR PAPLICATION NUMBER: 106/05286 |
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| PRIOR PAPLICATION NUMBER: 06/05286 |
| PRIOR PAPLICATION NUMBER: 06/05286 |
| PRIOR PAPLICATION NUMBER: 06/05280 |
| PRIOR PAPLICATION NUMBER: 06/05326 |
| PRIOR PAPLICATION NUMBER: 06/05320 |
| PRIOR PAPLICATION NUMBER: 06/05320 |
| PRIOR PAPLICATION NUMBER: 06/05340 |
| PRIOR PAPLICATION NUMBER: 06/05341 |
| PRIOR PAPLICATION NUMBER: 06/05341 |
| PRIOR PAPLICATION NUMBER: 06/05341 |
| PRIOR PAPLICATION NUMBER: 06/05341 |
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| PRIOR PAPLICATION NUMBER: 06/05341 |
| PRIOR PAPLICATION NUMBER: 06/06331 |
| PRIOR PAPLICATION NUMBER: 06/06331 |
| PRIOR PAPLICATION NUMBER: 06/06331 |
| PRIOR PAPLICATION NUMBER: 06/06331 |
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| PRIOR PAPLICATION NUMBER: 06/06331 |
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| PRIOR PAPLICATION NUMBER: 06/06331 |
| PRIOR PAPLICATION NUMBER: 06/06466 |
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| PRIOR PAPLICATION NUMBER: 06/06466 |
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| PRIOR PAPLICATION NUMBER: 06/06410 |
| PRIOR PAPLICATION NUMBER: 06/06410 |
| PRIOR PAPLICATION NUMBER: 06/06410 |
| PRIOR PAPLICATION NUMBER: 06/06410 |
| PRIOR PAPLICATION NUMBER: 06/06410 |
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| PRIOR PAPLICATION NUMBER: 06/06410 |
| PRIOR PAPLICATION NUMBER: 06/0
DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 ; Sequence 34, Application US/10174581; Publication No. US2030017540A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
 Watanabe, Colin K.
Wood, William I.
 Godowski, Paul J. Gurney, Austin L.
 Pan, James
Smith, Victoria
 Goddard, Audrey
 Desnoyers, Luc
 Zhang, Zemin
 RESULT 39
US-10-174-581-34
 136
 92
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIOK 151
 75
 32 SAAALIPTGGGONLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERDECE: P343 SHORTICGB CURRENT APPLICATION NUMBER: US/10/176,483
CURRENT FILING DATE: 2002-06-20
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35.5%; Score 150; DB 14; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0; Indels
 Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
TYPE: PRT
 136 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Sequence 34, Application US/10176483 Publication No. US20030017541A1 GENERAL INFORMATION:
 Sequence 34, Application US/10176749
Publication No. US20030017542A1
 Watanabe, Colin K. Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Gurney, Austin L.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J
 Pan, James
Smith, Victoria
 Smith, Victoria
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 APPLICANT: Baker, Kevin P.
 ; ORGANISM: Homo Sapien
US-10-176-483-34
 Chen, Jian
 GENERAL INFORMATION:
 -10-176-749-34
 152
96
 136
 152
 APPLICANT:
APPLICANT:
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 Gaps
 Length 440;
 Indels
 35.5%; Score 150; DB 14; L 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0;
 PRIOR APPLICATION NUMBER: 60/087208
PRIOR APPLICATION NUMBER: 60/087208
PRIOR PILING DATE: 1998-05-28
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/08905
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PRIOR PILING DATE: 1998-06-11
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PRIOR PILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08905
PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08905
PRIOR PILING DATE: 1998-06-11
PRIOR PI
FILING DATE: 1998-05-22
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
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OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC OF INVENTION: ACIDS ENCODING THE SAME

Watanabe, Colin K. Wood, William I.

Zhang, Zemin

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RESULT 43
US-10-176-915-34
; Sequence 34, Application US/10176915
; Publication No. US20030017544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
, ADPLICANT: Chen, Jian
 APPLICANT: Pan, Jämes
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ORGANISM: Homo Sapien
 US-10-173-706-34
 LENGTH: 440
 US-10-176-915-34
 APPLICANT:
APPLICANT:
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 8
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 DSRFQLINFSSSELKVSLINVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPIGGGQULFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGGGNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Zhang,Zenin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1031 CURRENT APPLICATION NUMBER: US/10/176,914 CURRENT FILING DATE: 2002-06-20 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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 Query Match 35.5%; Score 150; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 Length 440;
 0; Indels
FILE REFERENCE: P3430R1C76

CURRENT APPLICATION NUMBER: US/10/176,749

CURRENT FILING DATE: 2002-06-20

PARTOR APPLICATION FEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612

SEQ ID NO 34

LENGTH: 440

TYPE: PRT

ORGANISH: Homo Sapien
US-10-176-749-34
 35.5%; Score 150; DB 14; L
100.0%; Pred. No. 1.1e-125;
tive 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 US-10-176-914-34; Sequence 34, Application US/10176914; Sequence 34, Application US/1017543A1; Fublication No. US20030017543A1; GENERAL INFORMATION:
 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Conservative
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
ORGANISM: Homo Sapien
 Query Match
Best Local Similarity
Matches 150; Conserv
 US-10-176-914-34
 APPLICANT:
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 SEQ ID NO 34
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APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: ADANG-ED SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RLC7
CURRENT APPLICATION NUMBER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
FILE APPLICATION NUMBER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
SEQ ID NO 34
SEQ ID NO 34
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRROLLNRSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SARALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1010 CURRENT APPLICATION NUMBER: US/10/176,915 CURRENT FILING DATE: 2002-06-21 PTIC TAPPLICATION FORCE: See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
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 Length 440;
 Score 150; DB 14; Lengtn *:
; Pred. No. 1.1e-125;
. - - he 0; Indels
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Query Match
35.5%; Score 150; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 150; Conservative 0; Mismatches
 Sequence 34, Application US/10173706
Publication No. US20030022293A1
GENERAL INFORMATION:
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76 DSRPQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: APPLICANT: ADANG, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: 193430R1660
CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE REPRIENCE: P9430RIC70
CURRENT APPLICATION NUMBER: US/10/176,482
CURRENT FILING DATE: 2002-06-20
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125; ive 0; Mismatches 0; Indels
 Query Match
35.5%; Score 150; DB 14; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0; Indels
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 136 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Sequence 34, Application US/10176482
Publication No. US20030022296A1
GENERAL INFORMATION:
 Godowski, Paul J.
Gurney, Austin L.
 Godowski, Paul J.
 Gurney, Austin L.
 Best Local Similarity 100.
Matches 150; Conservative
 Desnoyers, Luc
Goddard, Audrey
 Pan, James
Smith, Victoria
 APPLICANT: Baker, Kevin P.
 ORGANISM: Homo Sapien
 TYPE: PRT
ORGANISM: Homo Sapien
 Pan,James
 Chen, Jian
 US-10-176-482-34
 US-10-175-752-34
 SEQ ID NO 34
LENGTH: 440
 Query Match
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRELK 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3430R1C45

CURRENT APPLICATION NUMBER: US/10/175,738

CURRENT FILING DATE: 2002-06-19

Prior application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612
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 Query Match
35.5%; Score 150; DB 14; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0; Indels
 Length 440;
 Query Match 35.5%; Score 150; DB 14; Length 4 Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEBIEVNCTAMASKPATTIRWFKGN 181
 RESULT 46
US-10-175-752-34
| Sequence 34, Application US/10175752
| Publication No US20030022295A1
| GENERAL INFORMATION:
| APPLICANT: Baker, Kevin P.
| APPLICANT: Chen, Jian
 Sequence 34, Application US/10175738; Publication No. US20030022294A1; GENERAL INFORMATION:
 Watanabe, Colin K. Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Pan, James
Smith, Victoria
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
; ORGANISM: Homo Sapien
US-10-173-706-34
 TYPE: PRT
ORGANISM: Homo Sapien
 RESULT 45
US-10-175-738-34
 US-10-175-738-34
 SEQ ID NO 34
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92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPITGOGGNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPIGGGULFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C66
CURRENT APPLICATION NUMBER: US/10/176,913
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
TYPE: PRT
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERBNCE: P3430R1C153
CURRENT APPLICATION NUMBER: US/10/180,552
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
TYPE: PRT
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 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125; ive 0; Mismatches 0; Indels
 Query Match 35.5%; Score 150; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 ; Sequence 34, Application US/10180552; Publication No. US20030022300A1; GENERAL INFORMATION:
 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Godowski, Paul J. Gurney, Austin L.
 Query Match
Best Local Similarity 100.
Matches 150, Conservative
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 ORGANISM: Homo Sapien
 ORGANISM: Homo Sapien
 RESULT 50
US-10-180-552-34
 US-10-176-913-34
 US-10-180-552-34
 APPLICANT:
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 APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Goddard, Austin L.
APPLICANT: Smith, Videcria
APPLICANT: Smith, Videcria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Alang, Zemin
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C86
CURRENT APPLICATION NUMBER: US/10/176,757
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NOS: 612
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGONLFTKDVTVIEGEVATISCOVNKSDDSVIOLLNPNROTIYFRDFRPLK 91
Gaps
 ö
 Length 440;
 0; Indels
 Query Match 35.5%; Score 150; DB 14; I
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 RESULT 49
US-10-176-913-34
; Sequence 34, Application US/10176913
; Publication No. US20030022298A1
; RENERAL INFORMATION:
; APPLICANT: Baker Kevin P.
appLICANT: Chen, Jian
 ; Sequence 34, Application US/10176757; Publication No. US20030022297A1; GENERAL INFORMATION:
 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
CORGANISM: Homo Sapien
US-10-176-757-34
 92
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 APPLICANT:
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Sequence 34, Application US/10174572 Publication No. US20030027263A1 GENERAL INFORMATION:
 ; Sequence 34, Application US/10174579; Publication No. US20030027264A1
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 Zhang, Zemin
 TYPE: PRT
CORGANISM: Homo Sapien
US-10-173-700-34
 ORGANISM: Homo Sapien
 RESULT 54
US-10-174-579-34
 JS-10-174-572-34
 SEQ ID NO 34
LENGTH: 440
 SEQ ID NO 34
LENGTH: 440
 136
 152
 TYPE: PRT
 92
 152
 APPLICANT:
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C14
CURRENT APPLICATION NUMBER: US/10/173,700
CURRENT APPLICATION NUMBER: US/10/173,700
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
 Gaps
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 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125; Live 0; Mismatches 0; Indels
 FILE REFERENCE: P3430R1C147
CURRENT APPLICATION NUMBER: US/10/180,557
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 ; Sequence 34, Application US/10173700
; Publication No. US20030027262A1
; GENERAL INFORMATION:
 Sequence 34, Application US/10180557
Publication No. US20030022301A1
GENERAL INFORMATION:
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Watanabe, Colin K. Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Best Local Similarity 100.
Matches 150, Conservative
 Pan, James
Smith, Victoria
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
 Zhang, Zemin
 ORGANISM: Homo Sapien
 Pan,James
 RESULT 52
US-10-173-700-34
 US-10-180-557-34
 TYPE: PRT
 9/
 92
 136
 APPLICANT:
APPLICANT:
 Query Match
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 91
 32 SAAALIPITGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C40
CURRENT APPLICATION NUMBER: US/10/174,572
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
 Gaps
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 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0; Indels (
 Length 440;
 Indels
Query Match 35.5%; Score 150; DB 14; L
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0;
 136 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
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0; Indels
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
0; Mismatches
 Sequence 34, Application US/10174588 Publication No. US20030027266A1 GENERAL INFORMATION:
APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Sequence 34, Application US/10175739 Publication No. US20030027267A1 GENERAL INFORMATION:
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
 APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godwski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Pan, James
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
Matches 150; Conservative
 US-10-174-588-34
 US-10-175-739-34
 US-10-174-588-34
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RLC36
CURRENT APPLICATION NUMBER: US/10/174,582
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P34.097RIC31
CURRENT APPLICATION NUMBER: US/10/174,579
CURRENT FILING DATE: 2002-06-18
FILE REPERSON FILING DATE: 2002-06-18
NUMBER OF SEQ ID NOS: 612
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 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125;
 Length 440;
 Query Match 35.5%; Score 150; DB 14; Deliger Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 ; Sequence 34, Application US/10174582; Publication No. US20030027265A1; GENERAL INFORMATION:
 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William I.
 Desnoyers, Luc
 Baker, Kevin P.
Chen, Jian
 TYPE: PRT
ORGANISM: Homo Sapien
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174~582-34
 Best Local Similarity
 US-10-174-579-34
 US-10-174-582-34
 SEQ ID NO 34
 136
 152
 Query Match
 APPLICANT:
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 APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Zhang, Zemin
ITTLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITTLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITTLE OF INVENTION: AD1028 ENCODING THE SAME
FILE REFERENCE: P3430R1C28
CURRENT APPLICATION NUMBER: US/10/174,588
CURRENT FILING DATE: 2002-06-18
PTIOT APPLICATION TEMOVED See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
TYPE: PRT
ORGANISM: AM ORGANISM:
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRRQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRRQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPK 91
 32 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
0; Gaps
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 Length 440;
 35.5%; Score 150; DB 14; Length 4 100.0%; Pred. No. 1.1e-125; Live 0; Mismatches 0; Indels
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Sequence 34, Application US/10175743
Publication No. US20030027269A1
 FILING DATE: 1997-10-24
APPLICATION UNDRER: 60/063121
ALING DATE: 1997-10-24
APPLICATION NUMBER: 60/063486
 FILING DATE: 1997-10-21
APPLICATION NUMBER: 60/063540
FILING DATE: 1997-10-28
 APPLICATION NUMBER: 60/066466
FILING DATE: 1997-11-24
 FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
 FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063734
 APPLICATION NUMBER: 60/063870
 FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/064103
 FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066120
 APPLICATION NUMBER: 60/069425
 FILING DATE: 1997-12-17
APPLICATION NUMBER: 60/068017
 APPLICATION NUMBER: 60/063541
 APPLICATION NUMBER: 60/063544
 APPLICATION NUMBER: 60/063564
 APPLICATION NUMBER: 60/065311
 APPLICATION NUMBER: 60/066772
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 FILING DATE: 1997-10-28
 FILING DATE: 1997-10-28
 FILING DATE: 1997-10-29
 FILING DATE: 1997-11-24
 FILING DATE: 1997-11-2:
 Godowski, Paul J.
Gurney, Austin L.
 FILING DATE: 1997-10-2
 FILING DATE: 1997-12-
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 JS-10-175-743-34
 136
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRPQLLNPSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SABALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430RLC46 CURRENT APPLICATION NUMBER: US/10/175,739 CURRENT FILING DATE: 2002-06-19 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 SEQ ID NO 34
 APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430811C61
CURRENT APPLICATION NUMBER: 105/10/175,740
CURRENT FILING DATE: 2002-06-18
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 Query Match
35.5%; Score 150; DB 14; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0; Indels
 Length 440;
 Indels
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
 Score 150; DB 14; L
Pred. No. 1.1e-125;
0; Mismatches 0;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Sequence 34, Application US/10175740
Publication No. US20030027268A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey,
APPLICANT: Goddard, Audrey,
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
 35.5%; bc.
100.0%; Pred
0; V
 Watanabe, Colin K.
Wood, William I.
 Pan, James
Smith, Victoria
 Conservative
Smith, Victoria
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-739-34
 Zhang, Zemin
 ; ORGANISM: Homo Sapien
US-10-175-740-34
 Similarity
 RESULT 58
US-10-175-740-34
 150;
 Query Match
Best Local S:
Matches 150
 APPLICANT:
 92
 16
 TYPE: PRT
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT
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 LENGTH:
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92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3430R1C52
CURRENT APPLICATION NUMBER: US/10/175,743
CURRENT FILING DATE: 2002-06-16
PRIOR APPLICATION NUMBER: 10/052586
 PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR PLING DATE: 1997-00-18
PRIOR FILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-24
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PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
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| FALCAR PALLICATION NUMBER: 60/091094
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| FALCAR PALLICATION NUMBER: 60/091094
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135

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CURRENT APPLICATION NUMBER: US/10/176,492 CURRENT FILING DATE: 2002-06-21
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 ; ORGANISM: Homo Sapien
US-10-176-492-34
 ORGANISM: Homo Sapien
 Pan, James
 US-10-176-747-34
 APPLICANT:
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APPLICANT:
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTIIVLVPPPRIMIMIDIQK 151
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C119
CURRENT APPLICATION NUMBER: US/10/176,488
CURRENT APPLICATION NUMBER: US/210/176,488
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITTLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C107
 Gaps
 ö
 35.5%; Score 150; DB 14; Length 440;
 Pred. No. 1.1e-125;
Mismatches 0; Indels
 100.0%; Prec. ...
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 ; Sequence 34, Application US/10176492; Publication No. US20030027272A1; GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
 US-10-176-488-34
; Sequence 34, Application US/10176488
; Publication No. US20030027271A1
; GENERAL INFORMATION:
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Watanabe, Colin K.
Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 Smith, Victoria
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
ORGANISM: Homo Sapien
 Pan, James
 US-10-176-488-34
 RESULT 61
US-10-176-492-34
 SEQ ID NO 34
 32
 92
 136
 152
 APPLICANT:
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92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRPQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACTDS ENCODING THE SAME FILE REFERENCE: P3430781C92 CURRENT APPLICATION NUMBER: 105/10/176,747 CURRENT PILING DATE: 2002-06-20
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 0; Gaps
 Query Match 35.5%; Score 150; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 Length 440;
 Indels
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
TYPE: PRT
 Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 SEQ ID NO 34 LENGTH: 440
 Query Match 35.5%; Score 150; DB 14; I Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Sequence 34, Application US/10176747 Publication No. US20030027273A1 GENERAL INFORMATION:
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92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 76 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Smith, Victoria
APPLICANT: Watenabe, Colin K.
APPLICANT: Watenabe, Colin K.
APPLICANT: Watenabe, Colin K.
APPLICANT: Watenabe, Colin K.
APPLICANT: Watenabe, Colin K.
APPLICANT: Zhang, Zemian I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430RIC93
CURRENT APPLICATION NUMBER: US/10/176, 987
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Length 440;
 Query Match 35.5%; Score 150; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 Query Match 35.5%; Score 150; DB 14; Length 4 Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 RESULT 65
US-10-176-987-34
IS-10-176-987-34, Application US/10176987
Publication No. US20030027278A1
GENERAL INFORMATION:
 Sequence 34, Application US/10176992; Publication No. US20030027279A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-987-34
 US-10-176-992-34
US-10-176-985-34
 APPLICANT:
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430NCE: P3430NCE: P3430NCE: V350
CURRENT APPLICATION NUMBER: US/10/176,750
CURRENT FILING DATE: 2002-06-21
 32 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ö
 Length 440;
 0; Indels
 FILE REFERENCE: P3430R1C99
CURRENT APPLICATION NUMBER: US/10/176,985
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 35.5%; Score 150; DB 14; L 100.0%; Pred. No. 1.1e-125; Live 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 ; Sequence 34, Application US/10176750; Publication No. US20030027274A1; GENERAL INFORMATION:
 ; Sequence 34, Application US/10176985; Publication No. US20030027277A1; GENERAL INFORMATION:
 APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-750-34
 TYPE: PRT
ORGANISM: Homo Sapien
 Рап, Јашев
 US-10-176-985-34
 APPLICANT:
APPLICANT:
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 SEQ ID NO 34
 92
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76 DSRFQLLNPSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRPQLIANFSSSELKVSLTAVVSISDEGRYPCQLYTDPPQESYTTITVLVPPRALMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRPQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 32 SARALIPTGDGQNLFTXDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERDICE: P3430R1C228
CURRENT APPLICATION NUMBER: US/10/184,658
CURRENT FILING DATE: 2002-20
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 ;
0
 Length 440;
 Indels
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
 Query Match 35.5%; Score 150; DB 14; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0;
 136 DTAVEGERIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Sequence 34, Application US/10184658 Publication No. US20030027281A1 GENERAL INFORMATION:
 Sequence 34, Application US/10176991
Publication No. US20030027324A1
 Watanabe, Colin K.
Wood, William I.
 Watanabe, Colin K. Wood, William I.
 Godowski, Paul J.
Gurney, Austin L.
 Smith, Victoria
 Goddard, Audrey
 Goddard, Audrey
Godowski, Paul
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P.
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 ; ORGANISM: Homo Sapien
US-10-184-658-34
 GENERAL INFORMATION
 US-10-184-658-34
 92
 136
 152
 APPLICANT:
 TYPE: PRT
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430RIG100 CURRENT APPLICATION NUMBER: US/10/176,992 CURRENT FILING DATE: 2002-06-21 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C89
CURRENT APPLICATION NUMBER: US/10/176,993
CURRENT FILING DATE: 2002-06-20
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0; Indels (
 Length 440;
 0; Indels
 35.5%; Score 150; DB 14; L 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0;
 Prior Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 612
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Sequence 34, Application US/10176993
Publication No. US20030027280A1
GENERAL INFORMATION:
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Godowski, Paul J. Gurney, Austin L.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Matches 150; Conservative
 Conservative
Goddard, Audrey
 Desnoyers, Luc
 Zhang, Zemin
 TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-992-34
 Query Match
Best Local Similarity
Matches 150; Conservat
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-993-34
 Query Match
Best Local Similarity
 SEQ ID NO 34
 SEQ ID NO 34
 92
 APPLICANT:
APPLICANT:
APPLICANT:
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLBIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430RD: CURRENT APPLICATION NUMBER: US/10/173,697
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
 32 SAAALIPIGDGQNLFIKDVIVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C18
CURRENT APPLICATION NUMBER: US/10/173,705
CURRENT FILING DATE: 2002-06-17
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
 0;
 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125; ive 0; Mismatches 0; Indels
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 152 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Sequence 34, Application US/10173697
Publication No. US20030032102A1
GENERAL INFORMATION:
 Sequence 34, Application US/10173705
Publication No. US2030032103A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
 Godowski, Paul J.
Gurney, Austin L.
Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Godowski, Paul J. Gurney, Austin L.
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 Desnoyers, Luc
Goddard, Audrey
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 TYPE: PRT
ORGANISM: Homo Sapien
 Chen, Jian
 Pan, James
 US-10-173-705-34
 US-10-173-697-34
 US-10-173-697-34
 APPLICANT:
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRRQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERBENCE: P343 ORIGIC122 CURRENT APPLICATION NUMBER: US/10/176,991 CURRENT FILING DATE: 2002-06-21 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 SEQ ID NO 34 LENGTH: 440
 16 SAAALIPTGDGONLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P343-931C3
CURRENT APPLICATION NUMBER: US/10/173,695
CURRENT FILING DATE: 2002-06-17
 16 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 0; Gaps
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 Length 440;
 Length 440;
 0; Indels
 0; Indels
 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 SEQ ID NO 34
 35.5%; Score 150; DB 14; I 100.0%; Pred. No. 1.1e-125;
 35.5%; Score 150; DB 14; I 100.0%; Pred. No. 1.1e-125; Live 0; Mismatches 0;
 100.0%; Pred.
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 ; Sequence 34, Application US/10173695; Publication No. US20030032101A1; GENERAL INFORMATION:
 Watanabe, Colin K. Wood, William I.
 Gurney, Austin L.
Pan, James
Smith, Victoria
 Godowski, Paul J
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 Best Local Similarity 100.
Matches 150; Conservative
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 TYPE: PRT
ORGANISM: Homo Sapien
 ORGANISM: Homo Sapien
 RESULT 70
US-10-173-695-34
 US-10-176-991-34
 US-10-173-695-34
 92
 136
 TYPE: PRT
 APPLICANT:
 Query Match
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
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 32 SAAALIPTGGGGNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPRQTIYFRDFRPLK 91
 APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TILLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SACIDS ENCODING THE SAME FILE REPERENCE: P3430R1C23
CURRENT APPLICATION NUMBER: US/10/174,576
CURRENT PILING DATE: 2002-06-18
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; Publication No. US20030032104A1
 Sequence 34, Application US/10174585; Publication No. US20030032105A1; GENERAL INFORMATION:
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Watanabe, Colin K. Wood, William I.
 Query Match 35.5
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Smith, Victoria
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Godowski, Paul J.
Gurney, Austin L.
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CURRENT FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 120

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TYPE: PRT

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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
n PDI_ICANT: BOTELEIN_David
 Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
 Ferrara, Napoleone
Filvaroff, Ellen
 Query Match
Best Local Similarity 100.
Matches 423; Conservative
 Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
 APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
 ORGANISM: Mus musculus
 421 EYF 423
 421 EYF 423
 US-09-778-510-22
 APPLICANT:
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 361
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 ; TYPE: PRT
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 Sequence 46336, A
Sequence 2, Appli
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Sequence 2, Appli
Sequence 2, Appli
Sequence 15507, A
 Sequence 22, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 4, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 11, Appli
 Sequence 21225, A
Sequence 6366, Ap
Sequence 27877, A
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Sequence 32290, A
Sequence 63, Appl
Sequence 48707, A
Sequence 13553, A
Sequence 15844, A
Sequence 21930, A
Sequence 21930, A
Sequence 2117, Appl
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 20867
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 Sequence
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 APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILLE REFERENCE: 2844-08.
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR PILING DATE: 1999-08-05
PRIOR PILING DATE: 1998-08-07
PRIOR PILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 423
US-09-248-796A-22901

US-09-248-796A-14958

US-09-248-796A-14994

US-09-248-796A-16779

US-09-248-796A-16779

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US-09-248-796A-18305

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US-09-248-796A-21830

US-09-248-796A-21832

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US-09-213-9990C-6366

US-09-270-767-5807

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US-09-270-767-5807

US-09-270-767-5807
 -09-248-796A-15844
-09-248-796A-21930
 RESULT 1
US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. 6512095
; GENERALINFORMATION
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92
 136
 152
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 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME TILE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/09/944,457

CURRENT APPLICATION NUMBER: US/08/66,028

PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 11, 1997

PRIOR PRILING DATE: December 11, 1997

PRIOR PRILING DATE: December 11, 1997

PRIOR PRILING DATE: December 11, 1997

PRIOR PRILING DATE: December 11, 1997

PRIOR PRILING DATE: December 12, 1997

PRIOR PRILING DATE: December 12, 1997

PRIOR PRILING DATE: December 16, 1997

PRIOR PRILING DATE: December 16, 1997

PRIOR PRILING DATE: December 16, 1997

PRIOR PRILING DATE: December 16, 1997

PRIOR PRILING DATE: December 16, 1997

PRIOR PRILING DATE: December 16, 1997

PRIOR PRILING DATE: December 17, 1997

PRIOR PRILING DATE: December 17, 1997

PRIOR APPLICATION NUMBER: 60/069, 694

PRIOR PRILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069, 873

PRIOR APPLICATION NUMBER: 60/069, 873

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PRIOR APPLICATION NUMBER: 60/069, 873

PRIOR APPLICATION NUMBER: 60/069, 873

PRIOR APPLICATION NUMBER: 60/069, 873

PRIOR APPLICATION NUMBER: 60/069, 873

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PRIOR APPLICATION NUMBER: 60/069, 873

PRIOR APPLICATION NUMBER: 60/069, 873

PRIOR APPLICATION NUMBER: 60/069, 873

PRIOR APPLICATION NUMBER: 60/069, 873

PRIOR APPLICATION NUMBER: 60/069, 873

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PRIOR APPLICATION NUMBER: 60/069, 873

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PRIOR APPLICATION NUMBER: 60/069, 873

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 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 SAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 Length 440;
 0; Indels
 35.5%; Sco...
100.0%; Pred. No. %...
0; Mismatches
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
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US-09-944-457-61
; Sequence 61, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION
 FILING DATE: February 9, 1998
 FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,0
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Hillan, Kenneth
 Gurney, Austin
 Roy, Margaret
Tumas, Daniel
Wood, William
 Kljavin, Ivar
 Napier, Mary
US-09-866-028-61
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIOK 135
 DSRFQLLNFSSSELKVSLINVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 SAAALIPTGGGQULFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 Query Match 35.5%; Score 150; DB 4; Length 440; Best Local Similarity 100.0%; Pred. No. 4.3e-132; Matches 150; Conservative 0; Mismatches 0; Indels
 RIOR FILLING DATE: December 1, 1998
RIOR PAPLICATION NUMBER: PCT/USSS/2-2-2-2
RIOR FILING DATE: December 16, 1998
RIOR PILING DATE: December 16, 1998
RIOR PILING DATE: December 16, 1998
RRIOR PELICATION NUMBER: 09/218,517
RRIOR APPLICATION NUMBER: 09/218,517
RRIOR PILING DATE: March 3, 1999
RRIOR PILING DATE: March 3, 1999
RRIOR PILING DATE: March 3, 1999
RRIOR PILING DATE: March 3, 1999
RRIOR PILING DATE: September 15, 1999
RRIOR PILING DATE: No. 6734286ember 30, 1999
RRIOR PILING DATE: No. 6734286ember 30, 1999
RRIOR PILING DATE: No. 6734286ember 30, 1999
RRIOR FILING DATE: No. 6734286ember 30, 1999
RRIOR FILING DATE: December1, 1999
RRIOR FILING DATE: December1, 1999
RRIOR FILING DATE: December 16, 1999
RRIOR FILING DATE: Pebruary 11, 2000
RRIOR PILING DATE: Pebruary 11, 2000
RRIOR PILING DATE: February 22, 2000
RRIOR PILING DATE: February 22, 2000
RRIOR FILING DATE: March 2, 2000
RRIOR FILING DATE: March 3, 2000
RRIOR PILING DATE: March 3, 2000
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RRIOR PILING DATE: March 3, 2000
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RRIOR FILING DATE: PEDTUARY 28, 2001
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 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 PELING DATE: February 9, 1998

RAPPLICATION NUMBER: 60/075,945

RAPLICATION NUMBER: 60/112,850

RELING DATE: February 25, 1998

RELING DATE: December 16, 1998

RELING DATE: December 22, 1998

RELING DATE: December 22, 1998

RELING DATE: December 22, 1998

RELING DATE: September 16, 1998

RELING DATE: September 16, 1998

RELING DATE: September 16, 1998

RELING DATE: September 16, 1998
 TYPE: PRT
CORGANISM: Homo Sapien
US-09-944-457-61
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GENERAL INFORMATION:
APPLICANT PETERSEN, CAROLYN
APPLICANT LECH, JAMES
APPLICANT LECH, JAMES
APPLICANT LECH, JAMES
APPLICANT LECH, JAMES
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: NUMBER: US/08/700,651B
TITLE OF INVENTION: NUMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: 08/415,751
ARALIER APPLICATION NUMBER: 08/415,751
EARLIER PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 9
SEQ ID NO 9
LENGTH: 130
 Sequence 5, Application US/09060767B

Patent No. 6720152

GENERAL INFORMATION:

APPLICANT: Well, Gary

APPLICANT: Chandrashekar, Ramaswamy

TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for TITLE OF INVENTION: UNBER: US/09/060,767B

CURRENT APPLICANTION NUMBER: US/09/060,767B

CURRENT PILING DATE: 1998-04-15

PRIOR FILING DATE: 1997-04-15

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.0

SEQ ID NO 5-40-15

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 Query Match 3.3%; Score 14; DB 3; Length 130; Best Local Similarity 100.0%; Pred. No. 3.3e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 Length 41;
 0; Indels
 Score 15; DB 4; Le
Pred. No. 1.3e-06;
 OTHER INFORMATION: mutant/variant of SEQ ID NO:5
 Query Match 3.5%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 1.3 Matches 15; Conservative 0; Mismatches
 ; Sequence 14, Application US/08928361B; Patent No. 6071518
 US-08-700-651-9
; Sequence 9, Application US/08700651B
; Patent No. 6015882
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 321 PPTTTTTTTTTT 335
 1 PPTTTTTTTTT 15
 322 PTTTTTTTTTT 335
 TYPE: PRT
ORGANISM: Leishmania
 RESULT 8
US-08-928-361B-14
 US-09-060-767B-5
 US-09-060-767B-5
 US-08-700-651-9
 FEATURE:
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 Sequence 1, Application US/09930803

Patent No. 6596493

GENERAL INFORMATION:
APPLICANT: TREEVES, ROGER
APPLICANT: TREEVES, ROGER
APPLICANT: YOSHINORI, MUTAMAKI
TITLE OF INVENTION: DIGGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS FILE REFERENCE: JUJ1770-1
CURRENT APPLICATION NUMBER: US/09/930,803
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 1
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 94 DSRRQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
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 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINDNRQTIYFRDFRPLK 93
 16 SAAALIPTGDGONLFTKDVTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 Query Match 35.5%; Score 150; DB 4; Length 442; Best Local Similarity 100.0%; Pred. No. 4.3e-132; Matches 150; Conservative 0; Mismatches 0; Indels
 35.5%; Score 150; DB 4; Length 442;
 0; Indels
 APPLICANT:
ITILE OF INVENTION:
PRICE OF INVENTION:
PRICE REFERENCE:
CURRENT PELLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIN Ver. 2.0
 Best Local Similarity 100.0%; Pred. No. 4.3e-132; Matches 150; Conservative 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 154 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
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 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Sequence 20, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
 ; ORGANISM: Homo sapiens US-09-930-803-1
 TYPE: PRT
ORGANISM: Homo sapien
US-09-778-510-20
 SOFTWARE:
SEQ ID NO 20
LENGTH: 442
 US-09-778-510-20
 LENGTH: 442
 RESULT 5
US-09-930-803-1
 136
 136
 Query Match
 TYPE: PRT
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; PRIOR FILING DATE: 1995-04-03; NUMBER OF SEQ ID NOS: 115; SCQ ID NO 14; LENGTH: 130; TYRDE: PATENTE: 7; OYDALS: RYDEOSPORTHING DATENTE: 7; OYDALS: CYPLOSPORTHING DATENTE: 7; OYDALS: CYPLOSPORTHING DATENTE: 7; OYDALS: CYPLOSPORTHING DATENTE: 7; OYDALS: 7
 TYPE: PRT
ORGANISM: Cryptosporidium parvum
 322 PTTTTTTTTTT 335
 322 PTTTTTTTTTT 335
 48 Pritritritrit 61
 Query Match
Best Local Similarity 100.(
Matches 14; Conservative
 COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
 STREET: 385 Sher
CITY: Palo Alto
STATE: CA
 US-08-928-361B-17
 US-08-700-651-12
 US-08-700-651-12
 RESULT 11
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 1, Carolyn PEPTIDES, GLYCOPROTEINS, PEPTIDES, POLYPEPTIDES, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
 KESULT 9

US-09-588-995A-14

i Sequence 14, Application US/09588995A

j Sequence 14, Application US/09588995A

j Sequence 14, Application US/09588995A

j GENERAL INFORMATION:

j APPLICANT: PETERSEN, CAROLYN

j APPLICANT: BARNES, DEBRA A.

j APPLICANT: BARNES, DEBRA A.

j APPLICANT: GIT, JIRI

TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: OF ORDINARY

TITLE OF INVENTION: INFECTIONS

FILE REPERENCE: 480.19-5

CURRENT APPLICATION NUMBER: 08/926,361

PRIOR FILING DATE: 1997-09-12

PRIOR PILING DATE: 1997-09-12

PRIOR PILING DATE: 1996-08-14

PRIOR FILING DATE: 1996-08-14

PRIOR FILING DATE: 1996-08-14
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 Score 14; DB 3; Length 130;
Pred. No. 3.3e-05;
 Indels
 COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAETENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECHOMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS
TITLE OF INVENTION: FOR TREATMENT AND DETECT
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
 Mismatches
 3.3%; Sc
Query Match
Best Local Similarity 100.0%; P:
Matches 14; Conservative 0;
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
 322 PTTTTTTTTTT 335
 LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS:
 Prirrirriri 61
 TOPOLOGY: linear
MOLECULE TYPE: protein
 GENERAL INFORMATION:
 US-08-928-361B-14
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SEPROTES PRESENT 190

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87 PTTTTTTTTT 100
 323 TTTTTTTTTT 336
 113 TTTTTTTTTT 126
 TYPE: PRT;
CRGANISM: Candida albicans
US-09-248-796A-21069
 COUNTRY: USA
ZIP: 94306-1840
 US-08-928-361B-8
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 GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BLSON, RICHARD C.
APPLICANT: GUT, JIRI
APPLICANT: GUT, JIRI
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: OF CRYPTOSPORIDIUM
TITLE OF INVENTION: OF CRYPTOSPORIDIUM
TITLE OF INVENTION: OF CRYPTOSPORIDIUM
FILING DAPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 1997-03-27
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PATENTIN VET. 2.1
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 Query Match 3.3%; Score 14; DB 4; Length 175; Best Local Similarity 100.0%; Pred. No. 4.4e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 3.3%; Score 14; DB 3; Length 175; 100.0%; Pred. No. 4.4e-05;
 0; Indels
 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: VETNY, HARA
REGISTRATION NUMBER: 30,518
REFERENCE/POCKET UNDERER: 30,518
REFERENCE/POCKET UNDERER: 480.76-1(HV)
TELECOMMUNICATION:
TELEPHONE: 650-324-1677
 100.0%; Prec. ...
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 17, Application US/09588995A Patent No. 6514697 GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-17
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
 322 PTTTTTTTTTT 335
 322 PITITITITIT 335
 LENGTH: 175 amino acids TYPE: amino acid
 Matches 14; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
 Best Local Similarity
 US-08-928-361B-17
 RESULT 12
US-09-588-995A-17
 SEQ ID NO 17
LENGTH: 175
 Query Match
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Sequence 21069, Application US/09248796A

Sequence 21069, Application US/09248796A

Sequence 21069, Application US/09248796A

Sequence 21069, Application US/09248796A

Sequence 21069, Application US/09248796A

GENERAL INFORMATION: UNCLETC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANI: TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQUENCE OF THE OF T
 Patent No. 6071518
GENERAL INFORMATION:
PATENT PETERSON.
TITLE OF INVENTION: PETIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS:
TITLE OF INVENTION: SPECIES INFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
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 Gaps
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0
 Length 197;
 Indels
 COMPUTER FADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: EN PC COMPATIBLE
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
 Query Match 3.3%; Score 14; DB 4; Ler
Best Local Similarity 100.0%; Pred. No. 4.9e-05;
Matches 14; Conservative 0; Mismatches 0;
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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us-10-622-237-4.oligo.rai

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Sequence 8, Application US/09588995A
Patent No. 6514697
 322 PTTTTTTTTTT 335
 322 PTTTTTTTTTT 335
 70 Priritiritir 83
 US-09-588-995A-8
 FEATURE:
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 Sequence 27, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: POR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
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 ö
 Query Match 3.3%; Score 14; DB 3; Length 216; Best Local Similarity 100.0%; Pred. No. 5.3e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 3.3%; Score 14; DB 3; Length 216;
100.0%; Pred. No. 5.3e-05;
 COMPUTEY: USA

ZIP: 94306-1840

COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb Foc Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: VEITY, Hann
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 480.76-1(HV)
TELECOMMUNICATION:
 100.0%; Pred.
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
 322 PTTTTTTTTT 335
 322 PTTTTTTTTTT 335
 LENGTH: 216 amino acids
TYPE: amino acid
STRANDEDNESS:
 70 Pritririririr 83
 LENGTH: 216 amino acids
 14; Conservative
 TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
 TOPOLOGY: linear
MOLECULE TYPE: protein
 Query Match
Best Local Similarity
 USA
 RESULT 15
US-08-928-361B-27
 US-08-928-361B-27
 US-08-928-361B-8
 STATE: CA
 Matches
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 8
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RESULT 16 US-09-588-995A-8

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RESULT 17

US-08-700-651-15

Sequence 15, Application US/08700651B

Sequence 15, Application US/08700651B

Sequence 15, Application US/08700651B

Sequence 15, Application US/08700651B

APPLICANT: PETERSEN, CAROLYN

APPLICANT: GEGH, JAMES

APPLICANT: GEGH, JAMES

APPLICANT: GEGH, JAMES

TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum

TITLE OF INVENTION: PROR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum

TITLE OF INVENTION: UNFECTIONS

TITLE OF INVENTION: 1970-08-14

CURRENT FILING DATE: 1997-08-14

EARLIER APPLICATION NUMBER: 08/415,751

EARLIER FILING DATE: 1995-04-03

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 15

LENGTH: 249
APPLICANT: ETERASAN, CANCULINA
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, RICHARD C.
APPLICANT: BARNES, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM FILLS OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION NUMBER: US/09/588,995A
CURRENT FILING DATE: 1990-06-06
PRIOR FILING DATE: 1990-09-12
PRIOR FILING DATE: 1990-09-12
PRIOR FILING DATE: 1995-04-14
PRIOR FILING DATE: 1995-04-03
PRIOR FILING DATE: 1995-04-03
NUMBER: OF SEQ ID NOS: 115
SEQ ID NO 8
SEQ ID NO 8
SEQ ID NO 8
SEQ ID NO 8
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SEQ ID NO 8
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 Query Match 3.3%; Score 14; DB 4; Length 216; Best Local Similarity 100.0%; Pred. No. 5.3e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 Query Match 3.3%; Score 14; DB 3; Length 249; Best Local Similarity 100.0%; Pred. No. 6.1e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 , OTHER INFORMATION: mutant/variant of SEQ ID NO:5 US-08-700-651-15
 ORGANISM: Cryptosporidium parvum
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 165 Pritriririti 178
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APPLICANT: Slade, Martin B
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
 Gaps
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 Query Match 3.3%; Score 14; DB 1; Length 887; Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 14; Conservative 0; Mismatches 0; Indels
 3.3%; Score 14; DB 4; Length 249;
100.0%; Pred. No. 6.1e-05;
tive 0; Mismatches 0; Indels
 COMPUTRY: U.C. ZIP: 19103

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: O2-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: 35,134
REFERENCE/DOCKET NUMBER: 35,134
REFERENCE/DOCKET NUMBER: 35,134
REFERENCE/DOCKET NUMBER: ACT/AU9007
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 215-568-3100
TELEFAX: 215-568-3139
TELEFAX: 215-568-3139
 PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR FILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 249
PRIOR APPLICATION NUMBER: 08/928,361
 Sequence 3, Application US/07867106
Patent No. 5389526
GENERAL INFORMATION:
 TYPE: PRT Cryptosporidium parvum US-09-588-995A-20
 322 PITITITITIT 335
 165 PÍTTTTTTTTTT 178
 322 PTTTTTTTTT 335
 LENGTH: 887 amino acids
TYPE: AMINO ACID
 14; Conservative
 TOPOLOGY: linear; MOLECULE TYPE: protein US-07-867-106-3
 Best_Local Similarity
Matches 14; Conserv
 US-07-867-106-3
 Query Match
 RESULT 20
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 RESULT 18
US-08-928-361B-20
i Sequence 20, Application US/08928361B
i Sequence 20, Application US/08928361B
i Patent No. 6071518
i GENERAL INFORMATION:
 APPLICANT: Petersen, Carolyn
 TITLE OF INVENTION: THEIR FUNCTIONAL MUTAATS, VARIANTS, ANALOGS AND FRAGMENTS
 TITLE OF INVENTION: SPECIES INFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
 TITLE OF INVENTION: SPECIES INFECTIONS
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSE: PETERS, VERNY, JONES & BIKSA
 STREET: 385 Sherman Avenue, Suite 6
 CITY: Palo Alto
 ; Sequence 20, Application US/09588995A
; Sequence 20, Application US/09588995A
; Patent No. 6514697
; GENREAL INFORMATION:
; APPLICANT: BARNES, DEBRA A.
; APPLICANT: BARNES, DEBRA A.
; APPLICANT: BARNES, DEBRA A.
; APPLICANT: BARNES, DEBRA A.
; TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
; TITLE OF INVENTION: INFECTIONS
; TITLE OF INVENTION: INFECTIONS
; TITLE OF INVENTION: UNFECTIONS
; TITLE OF INVENTION: US/09/588,995A
; CURRENT APPLICATION NUMBER: US/09/588,995A
; CURRENT PILING DATE: 2000-06-06
; PRIOR FILING DATE: 1997-03-27
; PRIOR FILING DATE: 1997-03-27
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 Query Match 3.3%; Score 14; DB 3; Length 249; Best Local Similarity 100.0%; Pred. No. 6.1e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OCHENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKAT NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-324-1677
 322 PTTTTTTTTT 335
 LENGTH: 249 amino acids TYPE: amino acid
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 TOPOLOGY: linear
MOLECULE TYPE: protein
 STRANDEDNESS
 US-08-928-361B-20
 RESULT 19
US-09-588-995A-20
 165
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Sequence 5, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: PETERSEN, CATOLYN
TITLE OF INVENTION: PEPTIDES, MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS;
TITLE OF INVENTION: PERTIDES, MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS;
TITLE OF INVENTION: PREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM;
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
 APPLICANT: BARNES DBERA A.
APPLICANT: BARNES DBERA C.
APPLICANT: BARNES DBERA C.
APPLICANT: WELSON, RICHARD C.
APPLICANT: WELSON, RICHARD C.
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
FILE: REFERENCE: 480.19-5
CURRENT FILING DATE: 2000-06-06
CURRENT FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1996-08-14
PRIOR PRILING DATE: 1996-08-14
PRIOR PRILING DATE: 1996-08-14
PRIOR PRILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
COLUMBER PARENTE PARENTIN VET: 2.1
 Gaps
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 Query Match 3.3%; Score 14; DB 4; Length 1721; Best Local Similarity 100.0%; Pred. No. 0.00036; Matches 14; Conservative 0; Mismatches 0; Indels
 3.3%; Score 14; DB 3; Length 1721; 100.0%; Pred. No. 0.00036; tive 0; Mismatches 0; Indels
 RESULT 23
US-09-588-995A-6
Sequence 6, Application US/09588995A
Patent No. 6514697
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 LENGTH: 1721 amino acids
TYPE: amino acid
STRANDEDNESS:
 322 PTTTTTTTTT 335
 307 Pritriririri 320
 322 PTTTTTTTTTT 335
 307 PITITITITITI 320
 650-324-1677
 Matches 14; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
 Best Local Similarity
 TELEPHONE:
 SEQ ID NO 6
1.RNGTH: 1721
 RESULT 24
US-08-928-361B-5
 US-08-928-361B-6
 US-09-588-995A-6
 Query Match
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), Carolyn
PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
 us-vuc-tou-bal-s
sequence S. Application US/08700651B
Patent No. 6015802
GENERAL INFORMATION:
APPLICANT: BEECH, JAMES
APPLICANT: BEECH, JAMES
APPLICANT: GUT, JIRI
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: 180-19-4 (HV)
CURRENT FILING DATE: 1997-08-14
CURRENT FILING DATE: 1997-08-14
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 1721
 DNAS AND RNAS
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 Gaps
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 Score 14; DB 3; Length 1721;
Pred. No. 0.00036;
 0; Indels
 STATE: CA
COUNTRY: USA
ZIP: 94306-1840
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FTIING DATE: 12-SEP-1997
 Sequence 6, Application US/08928361B; Sequence 6, Application US/08928361B; Patent No. 6071518; SENERAL INFORMATION:
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS; TITLE OF INVENTION: SPECIES INFECTIONS; NUMBER OF SEQUENCES: 30.
CORRESPONDENCES: 30.
CORRESPONDENCE ADDRESS:
ADDRESSER: PETERS, VERYY, JONES & BIKSA; STREET: 385 Sherman Avenue, Suite 6
 3.3%; Scor.
100.0%; Pred. No. v...
0; Mismatches
 NAME: Verny, Hana
REGISTATION UNBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
 FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
 , ORGANISM: Cryptosporidium parvum US-08-700-651-5
 307 PTTTTTTTTT 320
250 PITITITITIT 263
 322 PTTTTTTTTTT 335
 14; Conservative
 Query Match
Best Local Similarity
 Palo Alto
 RESULT 22
US-08-928-361B-6
 US-08-700-651-5
 TYPE: PRT
 Matches
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RESULT 26
US-09-205-258-953
'S Gequeo 953, Application US/09205258
'Patent No. 6525174
 TTTTT 335
 378 Prirrirririr 391
 Best Local Similarity 100.0
Matches 14; Conservative
 322 PTTTTTT
 Query Match
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 a
 ## Sequence 5, Application US/09580995A

Sequence 5, Application US/09580995A

Retent No. 6514697

GENERAL INFORMATION:

APPLICANT: PETERSEN;

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES: 180-19-5

CURRENT FILING DATE: 1997-09-12

PRIOR FILING DATE: 1997-09-12

PRIOR FILING DATE: 1995-08-14

PRIOR FILING DATE: 1995-08-14

PRIOR FILING DATE: 1995-08-14

PRIOR FILING DATE: 1995-08-14

PRIOR FILING DATE: 1995-08-14

PRIOR FILING DATE: 1995-08-14

PRIOR FILING DATE: 1995-08-14

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PRIOR FILING DATE: 1995-08-14

PRIOR FILING DATE: 1995-08-14

PRIOR FILING DATE: 1995-08-14

PRIOR FILING DATE: 1995-08-14

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PRIOR FILING DATE: 1995-08-14

PRIOR FILING DATE: 1995-08-14

PRIOR FILING DATE: 1995-08-14

PRIOR FILING DATE: 1995-08-14

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 Query Match 3.3%; Score 14; DB 3; Length 1837; Best Local Similarity 100.0%; Pred. No. 0.00038; Matches 14; Conservative 0; Mismatches 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 480.76-1(HV)
TELECOMMULCATION:
385 Sherman Avenue, Suite 6
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-5
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
 TITITITI
 378 PTTTTTTTTT 391
 / MOLECULE TYPE: protein US-08-928-361B-5
 amino acid
 linear
 Palo Alto
 USA
 322 PTTT
 RESULT 25
US-09-588-995A-5
 COUNTRY:
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Gaps
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0
3.3%; Score 14; DB 4; Length 1837;
100.0%; Pred. No. 0.00038;
tive 0; Mismatches 0; Indels
 APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
 FILE REPERENCE: PAZOU PLI
CURRENT PELLING DATE: 1938-12-04

EARLIER APPLICATION NUMBER: US/09/205,258

CURRENT FILING DATE: 1938-06-04

EARLIER PILING DATE: 1939-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

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EARLIER PILING DATE: 1997-06-06

EARLIER PILING DATE: 1997-06-06

EARLIER PILING DATE: 1997-06-
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GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-08-13
PRIOR PILING DATE: 1998-08-13
PRIOR PILING DATE: 1998-08-13
SEQ ID NOS: 28208
SEQ ID NO 23083
LENGTH: 63
 GENERAL INFORMATION:
APPLICANT: Weil, Gary
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for
TITLE OF INVENTION: H. capsulatum
FILE REFERENCE: B/OF 1986
CURRENT APPLICATION NUMBER: US/09/060,767B
CURRENT FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/043,332
PRIOR PILING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 9
SEQ ID NO 9
 Gaps
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 Length 57;
 3.1%; Score 13; DB 4; Length 57; 100.0%; Pred. No. 0.00014;
 0: Indels
 DB 3; Le
0.00014;
 Pred. No. 0.0
 Mismatches
 Sequence 23083, Application US/09248796A Patent No. 6747137
 Sequence 9, Application US/09060767B Patent No. 6720152
 100.0%; Pre
 , ORGANISM: Histoplasma Capsulatum
US-09-060-767B-9
 Query Match
3.1%; Sci
Best Local Similarity 100.0%; P.
Matches 13; Conservative 0;
 323 TTTTTTTTT 335
 320 PPPTTTTTTT 332
 TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
 TYPE: PRT ORGANISM: Candida albicans
 Query Match 3.1
Best Local Similarity 100.
Matches 13; Conservative
 single
 TYPE: amino acid
STRANDEDNESS: si
 linear
 US-09-248-796A-23083
 MOLECULE TYPE:
 HYPOTHETICAL:
 TELEPHONE:
 ANTI-SENSE:
US-08-900-230-59
 TOPOLOGY:
 US-09-060-767B-9
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 ; Sequence 59, Application US/08900230
; Patent No. 6329197
; GENERAL INFORMATION:
 APPLICANT: Bard, Jonathan A.
 TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 59
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLp
; STREET: 1185 Avenue of The Americas
; STATE: New York
; STATE: New York
; COUNTRY: U.S.A.
 Score 13; DB 4; Length 44;
Pred. No. 0.00011;
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,230
FILING DATE: 3-JUL-1997
CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
ANALY AGENT INFORMATION:
ANALY AGENT INFORMATION:
 NAME: White, John P. REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM FELECOMMUNICATION INFORMATION:
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER APPLICATION NUMBER: 60/048,833
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,997
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER PPLICATION NUMBER: 60/048,973
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
LENGTH: 44
 401 DADTAIINAEGGQ 413
 21 DADTAIINAEGGO 33
 Query Match 3.1
Best Local Similarity 100.
Matches 13; Conservative
 TYPE: PRT
CORGANISM: Homo sapiens
US-09-205-258-953
 RESULT 27
US-08-900-230-59
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US-08-928-361B-19
Sequence 19, Application US/08928361B
Patent No. 6071518
Patent No. 6071518
GENERAL INFORMATION:
APPLICAT'S PECTENSIAN PREPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PREPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
 ö
 NGS-08-995A-19
Sequence 19, Application US/09588995A
Sequence 19, Application US/09588995A
PRECAL NG 6514697
GENERAL INFORMATION:
APPLICANT: BARNES, DEBRA A.
APPLICANT: GUT, JIR.
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: INFOCTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
 Gaps
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 3.1%; Score 13; DB 3; Length 91;
100.0%; Pred. No. 0.00021;
tive 0; Mismatches 0; Indels
 FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATE: US 60/026,062
ATORNEY/AGBNT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
 323 TTTTTTTTTT 335
 323 TTTTTTTTTT 335
 18 TTTTTTTTTT 30
 18 rrrrrrrrrrrr 30
 Best Local Similarity 100.
Matches 13; Conservative
 MOLECULE TYPE: protein
 amino acid
 linear
 USA
 STRANDEDNESS
 S
 TOPOLOGY:
 COUNTRY:
 LENGTH:
 Query Match
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 RESULT 30
US-09-248-796A-25289
is Sequence 25289, Application US/09248796A
is Patent No. 6747137
is GENERAL INFORMATION:
is APPLICANTON:
it TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
it TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
it TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
it CURRENT FILING DATE: 1999-02-12
is PRIOR PLILING DATE: 1998-02-13
is PRIOR PLILING DATE: 1998-08-13
is NUMBER: US 60/074,725
is PRIOR PLILING DATE: 1998-08-13
is NUMBER OF SEQ ID NOS: 28208
is SEQ ID NO 25289
it ENGTH: 75
 GLYCOPROTEINS, DNAS AND RNAS
 ö
 ö
 ö
 APPLICANT: PETERSEN, CAROLYN
APPLICANT: BECH, JAMES
APPLICANT: BECH, JAMES
APPLICANT: BECH, JAMES
APPLICANT: BECH, JAMES
APPLICANT: BELSON, RICHARD, C.
APPLICANT: GUT, JIR
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND
TITLE OF INVENTION: NOR PROPHYLAXIS AND TREATMENT OF CRYPCOSPORIGIUM PARVUM
TITLE OF INVENTION: INPECTIONS
FILE REFERENCE: 480-19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER PLILNG DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PALENTIN VET: 2.0
 Gaps
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 Query Match 3.1%; Score 13; DB 3; Length 91; Best Local Similarity 100.0%; Pred. No. 0.00021; Matches 13; Conservative 0; Mismatches 0; Indels
 Query Match 3.1%; Score 13; DB 4; Length 75; Best Local Similarity 100.0%; Pred. No. 0.00017; Matches 13; Conservative 0; Mismatches 0; Indels
 Length 63;
 0; Indels
 Score 13; DB 4; L
Pred. No. 0.00015;
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-14
 3.1%; Sco...
100.0%; Pred. No. co...
0; Mismatches
 ; Sequence 14, Application US/08700651B; Patent No. 6015882; GENERAL INFORMATION:
 ORGANISM: Cryptosporidium parvum
 322 PTTTTTTTTT 334
 323 TTTTTTTTTT 335
 36 prrrrrrrrrrr 48
 1111111111
 Query Match 3.1
Best Local Similarity 100.
Matches 13; Conservative
US-09-248-796A-23083
 RESULT 31
US-08-700-651-14
 SEQ ID NO 14
LENGTH: 91
 FEATURE:
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APPLICANT: PETERS. Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PRETIDES, POLYPEPTIDES, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
TOTALE OF INVENTION: SPECIES INFECTIONS
TOTALE OF INVENTION: SPECIES INFECTIONS
TOTALE: ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STRATE: CA
STATE: CA
CITY: PALO ALCO
STATE: CA
 Gaps
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 Length 124;
 Indels
 COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
 Pred. No. 0.00024;
. Mismatches 0;
 Query Match
3.1%; Score 13; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 0;
 SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 11

LENGTH: 124

TYPE: PRT

ORGANISM: Cryptosporidium parvum
FEATURE:
COTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-11
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EEECH, JAMES
APPLICANT: EEECH, JAMES
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTITILE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION INVENER: US/08/700,651B
CURRENT APPLICATION NUMBER: US/08/100,651B
CURRENT FILING DATE: 1997-08-14
ERALIER PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
 Best Local Similarity 100.0%; Pred. No. 0.(
Matches 13; Conservative 0; Mismatches
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
 US-08-928-361B-16; Sequence 16, Application US/08928361B; Patent No. 6071518; GENERAL INFORMATION:
 Sequence 11, Application US/08700651B
Patent No. 6015882
 323 TTTTTTTTTT 335
 323 TITITITITI 335
 33 Tritiriririri 45
 JS-08-700-651-11
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 Sequence 36192, Application US/09270767
; Sequence 36192, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PATENTIN Ver. 2.0
 GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: T326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51409
LENGTH: 106
 Gaps
 Gaps
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 Score 13; DB 4; Length 106;
Pred. No. 0.00024;
 3.1%; Score 13; DB 4; Length 106;
 3.1%; Score 13; DB 4; Length 91;
100.0%; Pred. No. 0.00021;
ive 0; Mismatches 0; Indels
 Query Match 3.1%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/588,995A CURRENT FILING DATE: 2000-04-04
 CURRENT FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 08/827,171
PRIOR PILING DATE: 1997-03-27
PRIOR PILING DATE: 1997-03-27
PRIOR PILING DATE: 1997-09-12
PRIOR PILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR APPLICATION NUMBER: 08/715,751
PRIOR PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SEQ ID NO 19
LENGTH: 91
 ; Sequence 51409, Application US/09270767
; Patent No. 6703491
 ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-36192
 ; ORGANISM: Drosophila melanogaster
US-09-270-767-51409
 ORGANISM: Cryptosporidium parvum
 323 TTTTTTTTTT 335
 323 TTTTTTTTTT 335
 13; Conservative
 Query Match
Best Local Similarity
 RESULT 34
US-09-270-767-36192
 RESULT 35
US-09-270-767-51409
 SEQ ID NO 36192
LENGTH: 106
 US-09-588-995A-19
 Query Match
 Matches
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APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PERTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
 GLYCOPROTEINS, DNAS AND RNAS
 ALTELE OF INVENTION: VACINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND TITLE OF INVENTION: POR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4(4)0.651B
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
BARLIER APPLICATION NUMBER: 08/415,751
BARLIER PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARR: PARENTIN Ver. 2.0
SEQ ID NO 7
LENGTH: 128
 Query Match 3.1%; Score 13; DB 3; Length 128; Best Local Similarity 100.0%; Pred. No. 0.00028; Matches 13; Conservative 0; Mismatches 0; Indels
 CUNTY: USA
COUNTY: USA
ZIP: 94306-1840

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
FELEPHONE: 650-324-1677
TELEPHONE: 650-324-1677
TELEPHONE: 650-324-1678
TELEPROMUNICATIOS:
TELEPHONE: 650-324-1678
TELEPHONE: 650-324-1678
TELEPHONE: 650-324-1678
TELEPHONE: 650-324-1678
TELEPHONE: FREEFINGE: 650-324-1678
TELEPHONE: 650-324-1678
TELEPHONE: 650-324-1678
 FEATURE:
CHER INFORMATION: mutant/variant of SEQ ID NO:5
 Sequence 12, Application US/08928361B Patent No. 6071518 GENERAL INFORMATION:
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 APPLICANT: NELSON, RICHARD, C.
 LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS:
 323 TTTTTTTTTT 335
 TOPOLOGY: linear MOLECULE TYPE: protein
 US-08-928-361B-12
 RESULT 40
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 RESULT 38

US-09-588-995A-16

Sequence 16, Application US/09588995A

Sequence 16, Application US/09588995A

GENERAL INFORMATION:
APPLICANT: PETERSEN.
APPLICANT: BETERSEN.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES A.
APPLICANT: BARNES A.
APPLICANT: BARNES: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A

CURRENT APPLICATION NUMBER: US/09/589,361
PRIOR FILING DATE: 1997-03-12
PRIOR PELING DATE: 1997-09-12
PRIOR PELING DATE: 1996-08-14
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PRIOR PELING DATE: 1996-08-14
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PRIOR PELING DATE: 1996-08-14
PRIOR PELING DATE: 1996-08-14
PRIOR PELING DATE: 1996-08-14
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 Gaps
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 Query Match
3.1%; Score 13; DB 3; Length 124;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 0; Indels
 3.1%; Score 13; DB 4; Length 124;
100.0%; Pred. No. 0.00028;
iive 0; Mismatches 0; Indels
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verry, Hana
REGISTRATION WUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEPHORA : 650-324-1677
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
 RESULT 39
US-08-700-651-7
Sequence 7, Application US/08700651B;
Patent No. 6015882;
GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Cryptosporidium parvum
 LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-928-361B-16
 323 TTTTTTTTTT 335
 323 TTTTTTTTTT 335
 ; APPLICANT: PETERSEN, CAROLYN ; APPLICANT: LEECH, JAMES
 33 ririririririr 45
 33 rrrrrrrrrrr 45
 Best Local Similarity 100.
Matches 13; Conservative
 US-09-588-995A-16
 Query Match
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Patent No. 6071518

GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: FRET FUNCTIONAL MOTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: PERCIES INFECTIONS
 ö
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 Query Match 3.1%; Score 13; DB 3; Length 130; Best Local Similarity 100.0%; Pred. No. 0.00029; Matches 13; Conservative 0; Mismatches 0; Indels
 Length 130;
 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
 3.1%; Score 13; DB 3; L. 100.0%; Pred. No. 0.00029; ive 0; Mismatches 0;
 FEATURE:

CHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-8
 TITLE OF INVENTION: PEPTIDES, TITLE OF INVENTION: PEPTIDES, TITLE OF INVENTION: THEIR FUNCTIONAL MUTANT TITLE OF INVENTION: FOR TREATMENT AND DETECTIONS NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS: ADDRESSE: PETERS, VERNY, JONES & BIKSA STREET: 385 Sherman Avenue, Suite 6 CITY: Palo Alto
 CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verry, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMUNICATION INFORMATION:
 ; Sequence 13, Application US/09588995A; Patent No. 6514697
 ORGANISM: Cryptosporidium parvum
 INFORMATION FOR SEQ ID NO: 13:
 LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS:
 323 TTTTTTTTTT 335
 323 TITITITITE 335
 Ouery Match
Best Local Similarity 100.0
Matches 13; Conservative
 39 ririririririr 51
 SEQUENCE CHARACTERISTICS
 650-324-1678
 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-928-361B-13
 USA
 TELEPHONE:
 JS-08-928-361B-13
 US-09-588-995A-13
 COUNTRY:
 RESULT 44
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 # APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: WICHARD, C.
APPLICANT: WILLIANT:
 Sequence 12, Application US/09588995A

Patent No. 6514697

GENERAL INPORMATION:

APPLICANT: PETERSEN, CAROLYN

APPLICANT: BARNES, DEBRA A.

APPLICANT: GUT, JIRI

TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND

TITLE OF INVENTION: INPECTIONS

TITLE OF INVENTION: INPECTIONS

TITLE OF INVENTION: INPECTIONS

TITLE OF INVENTION: 1NPECTIONS

TITLE OF INVENTION: 1NPECTIONS

TITLE OF INVENTION: 1NPECTIONS

TITLE OF INVENTION: 1NPECTIONS

FILE REPRESENCE: 480.19-5

CURRENT FILING DATE: 1997-09-12

PRIOR APPLICATION NUMBER: 08/928,361

PRIOR APPLICATION NUMBER: 08/928,361

PRIOR FILING DATE: 1997-09-12

PRIOR APPLICATION NUMBER: 08/100,651

PRIOR FILING DATE: 1996-08-14

PRIOR FILING DATE: 1996-08-14

PRIOR FILING DATE: 1995-04-03

NUMBER OF SEQ ID NOS: 115

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 3.1%; Score 13; DB 3; Length 128; 100.0%; Pred. No. 0.00028; rive 0; Mismatches 0; Indels
 Length 128;
 0; Indels
 Query Match 3.1%; Score 13; DB 4; Lu Best Local Similarity 100.0%; Pred. No. 0.00028; Matches 13; Conservative 0; Mismatches 0;
 US-08-700-651-8
; Sequence 8, Application US/08700651B
Patent No. 6015882
; GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-12
 323 TITITITITI 335
 323 TITITITITI 335
 Query Match 3.1%
Best Local Similarity 100.0
Matches 13; Conservative
 37 TTTTTTTTTT 49
 37 Tritititit 49
 RESULT 41
US-09-588-995A-12
US-08-928-361B-12
 SEQ ID NO 12
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Sequence 15, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
CORRESPONDENCE ADDRESS: 30
CORRESPONDENCE ADDRESS: ADDRESSE: PETERS, VERY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
 US-09-588-995A-15

| Sequence 15, Application US/09588995A |
| Sequence 15, Application US/09588995A |
| Sequence 15, Application US/09588995A |
| GENERAL INFORMATION: |
| APPLICANT: BARNES, DEBRA A. |
| APPLICANT: BARNES, DEBRA A. |
| APPLICANT: GUT, JIRI METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND |
| TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM |
| TITLE OF INVENTION: INPECTIONS |
| FILE REPRESENTE: 800.19-5 |
| CURRENT FILING DATE: 2000-06-06 |
| PRIOR PILING DATE: 1997-03-27 |
| PRIOR APPLICATION NUMBER: 08/928,361 |
| PRIOR FILING DATE: 1997-09-12 |
 Gaps
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 Length 138;
 0; Indels
 ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: PROPER FO-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
 DB 3; Le
0.00031;
 3.1%; Scort
100.0%; Pred. No. vo.
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
 : 138 amino acids
amino acid
 323 TTTTTTTTT 335
 Query Match 3.13
Best Local Similarity 100.
Matches 13; Conservative
 47 Trirrrrrrrrr 59
 TOPOLOGY: linear MOLECULE TYPE: protein
 USA
 STRANDEDNESS:
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 US-08-928-361B-15
 US-08-928-361B-15
 COUNTRY:
 LENGTH:
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 Sequence 10, Application US/08700651B
; Sequence 10, Application US/08700651B
; Patent No. 601582
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
; TITLE OF INVENTION: POR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORTION
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-4 (HV)
; CURRENT APPLICATION NUMBER: US/08/700,651B
; CURRENT APPLICATION NUMBER: 08/415,751
; BARLIER FLING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PATENT OF 12.00
; SEQ ID NO 10
; LENGTH: 138
 APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: OBLOWN: RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INSCLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INSCLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INSCLATORS
TITLE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT PILING DATE: 1997-03-27
FRIOR APPLICATION NUMBER: 08/703.27
FRIOR FILING DATE: 1997-09-12
FRIOR PILING DATE: 1996-08-14
FRIOR PILING DATE: 1996-08-14
FRIOR PILING DATE: 1996-08-14
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 3.1%; Score 13; DB 3; Length 138;
100.0%; Pred. No. 0.00031;
iive 0; Mismatches 0; Indels
 Query Match
3.1%; Score 13; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 13; Conservative 0; Mismatches 0; Indels
 OTHER INFORMATION: mutant/variant of SEQ ID NO:5
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-13
 ORGANISM: Cryptosporidium parvum
 323 TTTTTTTTTT 335
 TTTTTTTTTT 335
 39 riririririris 51
 rrrrrrrrrrrr 59
 13; Conservative
 Query Match
Best Local Similarity
Matches 13; Conserv
GENERAL INFORMATION:
 RESULT 45
US-08-700-651-10
 US-08-700-651-10
 SEQ ID NO 13
LENGTH: 130
 323
 47
 RESULT 46
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Sequence 21631, Application US/09248796A

Sequence 21631, Application US/09248796A

Sequence 21631, Application US/09248796A

SEQUENCE 21631, Application US/09248796A

GENERAL INFORMATION:
GENERAL INFORMATION:
FAPPLICATION NUMBER: US/09/248,796A

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WHERE: US/09/248,796A

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 21631

LENGTH: 159
 JUNEARLY LINGARTION

JUNEARL LINGART BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: GUT, JIRI

TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND

TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM

TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM

TITLE OF INVENTION: 180.19-5

CURRENT APPLICATION NUMBER: US/09/588,995A

CURRENT FILING DATE: 1997-03-27

PRIOR APPLICATION NUMBER: 08/700,651

PRIOR APPLICATION NUMBER: 08/700,651

PRIOR APPLICATION NUMBER: 08/415,751

PRIOR APPLICATION NUMBER: 08/415,751

PRIOR APPLICATION NUMBER: 08/415,751

PRIOR APPLICATION NUMBER: 08/415,751

PRIOR APPLICATION NUMBER: 08/415,751

PRIOR APPLICATION NUMBER: 08/415,751

PRIOR APPLICATION NUMBER: 08/415,751

PRIOR APPLICATION NUMBER: 08/415,751

PRIOR FILING DATE: 1995-04-03

NUMBER OF SEQ ID NOS: 115

SEQ ID NO 18

LENGTH: 150
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 3.1%; Score 13; DB 4; Length 150; 100.0%; Pred. No. 0.00033;
 Query Match 3.1%; Score 13; DB 4; Length 159; Best Local Similarity 100.0%; Pred. No. 0.00035; Matches 13; Conservative 0; Mismatches 0; Indels
 0; Mismatches
 JS-09-588-995A-18
Sequence 18, Application US/09588995A
Patent No. 6514697
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-18
 323 TTTTTTTTT 335
 324 TTTTTTTTTI 336
 62 rrrrrrrrrrrr 74
 ORGANISM: Candida albicans
 52 řřřřřřřřřřřří 64
 Best Local Similarity 100.
Matches 13; Conservative
 US-09-248-796A-21631
 US-09-248-796A-21631
 Query Match
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 US-08-928-361B-18
Sequence 18, Application US/08928361B
Sequence 18, Application US/08928361B
Sequence 18, Application US/08928361B
Sequence 18, Application US/08928361B
Sequence 18, Application US/08928361B
SECTION OF TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
STATE OF INVENTION: SPECIES INFECTIONS
SCARRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
 °
 Gaps
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 Query Match 3.1%; Score 13; DB 3; Length 150; Best Local Similarity 100.0%; Pred. No. 0.00033; Matches 13; Conservative 0; Mismatches 0; Indels
 3.1%; Score 13; DB 4; Length 138; 100.0%; Pred. No. 0.00031; tive 0; Mismatches 0; Indels
 COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTONERY/AGENT INFORMATION:
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR FLING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SEQ ID NO 15
LENGTH: 138
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
 LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS:
 323 TITITITITI 335
 323 TTTTTTTTTT 335
 47 TTTTTTTTTTT 59
 13; Conservative
 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-928-361B-18
 Local Similarity
 CITY: Palo Alto
 US-09-588-995A-15
 Query Match
Best Local S
Matches 13
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Sequence 17391, Application US/09248796A

Sequence 17391, Application US/09248796A

Patent No. 6747137

GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR PELLOR PEPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17391
LENGTH: 216
 LOCATION: (212)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknov
 ; Sequence 24111, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 APPLICANT: Weil, Gary
APPLICANT: Chandrashekar, Ramaswamy
TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for
TITLE OF INVENTION: H. capsulatum
FILE REFERENCE: BJCH 9986
CURRENT APPLICATION NUMBER: US/09/060,767B
CURRENT APPLICATION NUMBER: 60/043,332
PRIOR FILING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 211
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 3.1%; Score 13; DB 4; Length 211;
100.0%; Pred. No. 0.00045;
iive 0; Mismatches 0; Indels
 3.1%; Score 13; DB 4; Length 216; 100.0%; Pred. No. 0.00046; Pred. No. 0. 10046; ive 0; Mismatches 0; Indels
 Sequence 3, Application US/09060767B Patent No. 6720152
 TYPE: PRT
ORGANISM: Histoplasma capsulatum
 320 PPPTTTTTTT 332
 323 TTTTTTTTTT 335
 37 PPPTTTTTTTT 49
 ORGANISM: Candida albicans FEATURE:
 Best Local Similarity 100.
Matches 13; Conservative
 13; Conservative
 Best Local Similarity
Matches 13; Conserv
 GENERAL INFORMATION:
 US-09-248-796A-17391
 NAME/KEY: UNSURE
 RESULT 55
US-09-248-796A-24111
 US-09-248-796A-17391
 US-09-060-767B-3
 Query Match
 Query Match
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 RESULT 52
US-09-248-796A-16058
1 Sequence 16058, Application US/09248796A
2 Patent No. 6747137
3 GENERAL INFORMATION:
3 APPLICANT: Keith Weinstock et al
4 TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
5 TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
6 CURRENT FILING DATE: 1999-02-12
7 CURRENT FILING DATE: 1999-02-13
8 PRIOR PLILING DATE: 1998-03-13
9 PRIOR PLILING DATE: 1998-08-13
1 PRIOR FILING DATE: 1998-08-13
1 NUMBER OF SEQ ID NOS: 28208
1 SEQ ID NO 16058
1 LENGTH: 207
 Sequence 13, Application US/08700651B

Patent No. 6015882
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: DETERSEN, CAROLYN
APPLICANT: DETERSEN, CAROLYN
TITLE OF INVENTION: VACTINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS;
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: WAGGINS, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS;
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: WAGGINS, ANTIBODIES, PROTEINS, DNAS AND RNAS;
TITLE OF INVENTION: WAGGINS, ANTIBODIES, PROTEINS
TITLE OF INVENTION: WAGGINS, ANTIBODIES, PROTEINS
TITLE OF INVENTION: WAGGINS, ANTIBODIES, PROTEINS
TITLE OF INVENTION: WAGGINS, ANTIBODIES, PROTEINS
TITLE OF INVENTION WAGGINS, ANTIBODIES, PROTEINS
TITLE OF INVENTION WAGGINS, 1987-08-14
SCHEMENT FILING DATE: 1997-08-14
WAGGINS OF SEQ ID NOS: 15
SOFTWARE PATENTER PLEING DATE: 2.0
 LOCATION: (204)
JTHER INFORMATION: Identity of amino acid sequences at the above locations are unknd
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 3.1%; Score 13; DB 3; Length 162;
100.0%; Pred. No. 0.00035;
tive 0; Mismatches 0; Indels
 3.1%; Score 13; DB 4; Length 207; 100.0%; Pred. No. 0.00044; ive 0; Mismatches 0; Indels
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5 US-08-700-651-13
 TYPE: PRT
ORGANISM: Cryptosporidium parvum
 TTTTTTTTTTT 335
 TTTTTTTTTTT 335
 TTTTTTTTTTT 73
 Best Local Similarity 100.
Matches 13; Conservative
 Conservative
 Best Local Similarity
Matches 13; Conserva
 US-09-248-796A-16058
RESULT 51
US-08-700-651-13
 SEQ ID NO 13
LENGTH: 162
 323
 LOCATION:
 323
 Query Match
 Query Match
 FEATURE:
 RESULT 53
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. LOCATION: (287), (288), (289)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-25055
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 Gaps
 Gaps
 Gaps
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 Length 292;
 Indels
 Indels
Pred. No. 0.0006;
 Score 13; DB 4; Le
Pred. No. 0.00081;
 3.1%; Score 13; DB 4; Lo
100.0%; Pred. No. 0.00061;
tive 0; Mismatches 0;
 Baum, Peter
TION: Molecules Designated B7L1
 TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
 Query Match
Best Local Similarity 100.0%; Pred. No. ...
Marches 13; Conservative 0; Mismatches
 Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 Sequence 4, Application US/09778510; Patent No. 6512095; GENERAL INFORMATION: APPLICANT: Baum, Peter
 323 TITITITITIT 335
 401 DADTAIINAEGGQ 413
 375 DADTAIINAEGGO 387
 323 TITITITITI 335
 TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: UNSURE
 Query Match
Best Local Similarity 100.
Matches 13; Conservative
 TYPE: PRT
ORGANISM: Mus musculus
US-09-778-510-4
 RESULT 59
US-09-778-510-4
 SEQ ID NO 4
LENGTH: 398
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 US-09-216-393B-344
Sequence 344, Application US/09216393B
Patent No. 6514694
GENERAL INFORMATION:
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER FILE REPERENCE: TX.1-C2
CURRENT APPLICATION NUMBER: US/09/216,393B
CURRENT FILING DATE: 1998-12-18
PRIOR FILING DATE: 1997-12-19
 DESCRIPTION OF STATES AND USES THER SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE STATES AND USES THER SEQUENCE
 Gaps
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 Score 13; DB 4; Length 247;
Pred. No. 0.00052;
 DB 4; Length 288;
 Length 288;
 0; Indels
 Score 13; DB 4; 1
Pred. No. 0.0006;
 FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR PILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SQ ID NO 24111
 3.1%; Score 13; DB
ilarity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
 Query Match 3.1%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 3.1%; Score 13;
 NUMBER OF SEQ ID NOS: 366
SOFTWARE: Patentin version 3.1
SEQ ID NO 344
LENGTH: 288
 323 TTTTTTTTTT 335
 164 Tritritritrit 176
 TYPE: PRT ORGANISM: Toxoplasma gondii
 323 TTTTTTTTTT 335
 ; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393B-341
 TYPE: PRT; ORGANISM: Candida albicans
US-09-248-796A-24111
 58 TTTTTTTTTT 70
 Local Similarity
nes 13; Conservat
 US-09-216-393B-344
 Query Match
Best Local S:
Matches 13,
 Query Match
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3.1%; Score 13; DB 4; Length 398;
100.0%; Pred. No. 0.00081;
tive 0; Mismatches 0; Indels
 PRIOR FILING DATE: 1999-09-08
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-03
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PRIOR PELING DATE: 1999-09-15
PRIOR PELICATION NUMBER: PCT/US99/21547
PRIOR PELING DATE: 1999-10-05
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PRIOR PELING DATE: 1999-11-30
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PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DAT
PRIOR APPLICATION NUMBER: US 60/146,222
 Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 Sequence 84, Application US/09905125A
Patent No. 6664376
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
 Ferrara, Napoleone
Filvaroff, Ellen
 Pan, James
Paoni, Nicholas F.
 FILING DATE: 1999-07-28
 Gerritsen, Mary E
 Gerber, Hanspeter
 Kljavin, Ivar J.
Mather, Jennie P.
 401 DADTAIINAEGGQ 413
 375 DADTAIINAEGGQ 387
 Query Match
Best Local Similarity 100.
Matches 13; Conservative
 Desnoyers, Luc
Eaton, Dan L.
 Fong, Sherman
Gao, Wei-Qiang
 TYPE: PRT
ORGANISM: Homo sapiens
 US-09-905-125A-84
 US-09-907-794A-84
 APPLICANT:
APPLICANT:
 APPLICANT:
 APPLICANT
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 IIILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
 Length 398;
 Indels
 TITLE OF INVENTION: Molecules Designated B7L1; FILE REFERENCE: 2044-02; CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07; PRIOR PILING DATE: 1999-08-05; PRIOR PILING DATE: 1999-08-05; PRIOR PILING DATE: 6/095,663; PRIOR FILING DATE: 6/095,663; PRIOR FILING DATE: 1998-08-07; NUMBER OF SEQ ID NOS: 22; SOFTWARE: PATENTIN VET: 2.0; SOFTWARE: PATENTIN VET: 2.0; SEQ ID NO 6; LENGTH: 398
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3.1%; Score 13; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 13; Conservative 0; Mismatches 0;
 FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
 FILING DATE: 2000-02-22
APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
 ; Sequence 84, Application US/09907794A ; Patent No. 6635468
 Godowski, Paul J.
Grimaldi, Christopher J.
 Sequence 6, Application US/09778510; Patent No. 6512095; GENERAL INFORMATION:
 Stewart, Timothy A. Tumas, Daniel Williams, P. Mickey Wood, William, I.
 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
 Filvaroff, Ellen
 Gao, Wei-Qiang
Gerber, Hanspeter
 Nicholas F.
 Gerritsen, Mary E.
 Paoni, Nicholas F
Roy, Margaret Ann
 401 DADTAIINAEGGQ 413
 375 DADTAIINAEGGQ 387
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bustein, David
APPLICANT: Benoyers, Luc
APPLICANT: Baton, Dan L.
 Sherman
 Goddard, A.
 TYPE: PRT
ORGANISM: Homo sapien
US-09-778-510-6
 Fong,
 US-09-907-794A-84
 RESULT 60
US-09-778-510-6
 APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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Gaps

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Transmembrane Polypeptides and Nucleic
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 Length 398;
 Indels
 DB 4; Le
 CURRENT PEPLICATION NUMBER: US/09/902,775A CURRENT FILING DATE: 2001-07-10
PRIOR FULING DATE: 2001-07-10
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1099-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
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PRIOR PILING DATE: 1999-09-08
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PRIOR PLING DATE: 1999-09-15
PRIOR PELICATION NUMBER: PCT/US99/21647
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PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
 ITLE OF INVENTION: Secreted and Transmembra ITLE OF INVENTION: Acids Encoding the Same
 FRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-30

PRIOR PELICATION NUMBER: PCT/US99/28313

PRIOR APPLICATION NUMBER: PCT/US99/28564,

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR PILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-04

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/3099

PRIOR PILING DATE: 1999-12-20

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

LENGTH: 398
 Godowski, Paul J.
Grimaldi, Christopher J.
 ; Sequence 84, Application US/09906700; Patent No. 6723535; GENERAL INFORMATION:
 100.08;
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Hillan, Kenneth, J
 aoni, Nicholas F
 Mather, Jennie P.
Pan, James
 401 DADTAIINAEGGQ 413
 375 DADTAIINAEGGO 387
 Query Match 3.1
Best Local Similarity 100.
Matches 13; Conservative
 Cljavin, Ivar
 FILE REFERENCE: 10466-14
 TYPE: PRT
ORGANISM: Homo sapiens
 JS-09-902-775A-84
 RESULT 64
US-09-906-700-84
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APPLICANT: Wood, William, I.

TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
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TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE APPLICATION NUMBER: DS 00/145,698
TRIOR PILLING DATE: 1999-00-06
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 3.1%; Score 13; DB 4; Length 398; 100.0%; Pred. No. 0.00081; tive 0; Mismatches 0; Indels
 Parent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: APPLICANT
 Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
 Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
 401 DADTAIINAEGGQ 413
 375 DADTAIINAEGGQ 387
 Query Match 3.1
Best Local Similarity 100.
Matches 13; Conservative
 NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
 TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-125A-84
 RESULT 63
US-09-902-775A-84
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Indels

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Mismatches

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Matches 13; Conservative
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 PLICANT: Williams, P. Mickey
PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TILE OF INVENTION: Acids Encoding the Same
 CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR PLILING DATE: 2000-02-22
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
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PRIOR APPLICATION NUMBER: US 60/145,698
 PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,022
PRIOR PILING DATE: 1999-07-28
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PRIOR PELING DATE: 1999-12-02
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 Godowski, Paul J.
Grimaldi, Christopher J.
 Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Gurney, Austin L.
Hillan, Kenneth, J.
 errara, Napoleone
 Gerber, Hanspeter
Gerritsen, Mary E
 Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
 Wei-Qiang
 Sherman
 NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
 TYPE: PRT
ORGANISM: Homo sapiens
US-09-906-700-84
 Goddard, A.
 Fong,
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: GNE.1618P2C12
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT PILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR AFELING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08-08
PRIOR PELING DATE: 1999-09-13
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PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
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PRIOR APPLICATION NUMBER: PCT/US99/28214
 FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
 RIOR APPLICATION NUMBER: PCT/US99/30095
 APPLICATION NUMBER: PCT/US99/30999
 PRIOR APPLICATION NUMBER: PCT/US99/28564
 5-09-903-603A-84
Sequence 84, Application US/09903603A
Patent No. 6767995
 Godowski, Paul J.
Grimaldi, Christopher J.
 Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerritsen, Mary E.
 Gao, Wei-Qiang
Gerber, Hanspeter
 Gurney, Austin L.
 FILING DATE: 1999-11-29
401 DADTAIINAEGGO 413
 375 DADTAIINAEGGO 387
 Eaton
 PRIOR
 Query Match 3.1%; Score 13; DB 4; Length 398; Best Local Similarity 100.0%; Pred. No. 0.00081;
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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 Query Match 3.1%; Score 13; DB 4; Length 398; Best Local Similarity 100.0%; Pred. No. 0.00081; Matches 13; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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PRIOR APPLICATION NUMBER: US 60/145,698
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 PRIOR FILING DATE: 1999-11-30
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
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PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
TYPE: PRI
 ION NUMBER: PCT/US99/28313
 Grimaldi, Christopher J. Gurney, Austin L.
 JS-09-909-064-84; Sequence 84; Application US/09909064; Patent No. 6818449
 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerritsen, Mary E.
Goddard, A.
 Gerber, Hanspeter
 Godowski, Paul J.
 401 DADTAIINAEGGQ 413
 375 DADTAIINAEGGQ 387
 Fong, Sherman
Gao, Wei-Qiang
 ORGANISM: Homo sapiens US-09-904-920A-84
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 APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
 Gaps
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0
 3.1%; Score 13; DB 4; Length 398; 100.0%; Pred. No. 0.00081; ive 0; Mismatches 0; Indels
 FILEE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904,920A

CURRENT FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

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PRIOR PLING DATE: 1999-07-28

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PRIOR PILING DATE: 1999-07-8

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PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
 FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
 APPLICATION NUMBER: PCT/US99/28214
 Sequence 84, Application US/09904920A Patent No. 6806352
 Godowski, Paul J.
Grimaldi, Christopher J.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Gurney, Austin L.
Hillan, Kenneth, J.
 Ferrara, Napoleone
Filvaroff, Ellen
 Nicholas F.
 Gerritsen, Mary E
 Gao, Wei-Qiang
Gerber, Hanspeter
 Kljavin, Ivar J.
Mather, Jennie P.
 375 DADTAIINAEGGQ 387
 401 DADTAIINAEGGO 413
 Query Match
Best Local Similarity 100.'
Matches 13; Conservative
 Desnoyers, Luc
 Pong, Sherman
 TYPE: PRT
ORGANISM: Homo sapiens
US-09-903-603A-84
 Goddard, A.
 Pan, James
Paoni, Nich
 US-09-904-920A-84
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Gaps

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
 Gaps
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 3.1%; Score 13; DB 4; Length 398; 00.00%; Pred. No. 0.00081; ve 0; Mismatches 0; Indels
 TITLE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/905,381A

CURRENT APPLICATION NUMBER: US/09/905,381A

CURRENT APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 2000-02-22

PRIOR PLILING DATE: 1999-07-26

PRIOR PLILING DATE: 1999-07-26

PRIOR PLILING DATE: 1999-07-26

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PRIOR PLILING DATE: 1999-09-08

PRIOR PLILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR PLILING DATE: 1999-09-13

PRIOR PLILING DATE: 1999-09-15

PRIOR PLILING DATE: 1999-09-15

PRIOR PLILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21690

PRIOR PLILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/2189

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PRIOR APPLICATION NUMBER: PCT/US99/2189

PRIOR APPLICATION NUMBER: PCT/US99/2891

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PRIOR APPLICATION NUMBER: PCT/US99/2865

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PRIOR APPLICATION NUMBER: PCT/US99/3091

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PRIOR APPLICATION NUMBER: PCT/US99/3099

PRIOR APPLICATION NUMBER: PCT/US99/3099

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PRIOR APPLICATION NUMBER: PCT/US99/3099
 PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/USOO/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
 RESULT 69
US-09-906-618-84
; Sequence 84, Application US/09906618
; Parent No. 6828146
 Query Match
3.1%; Sc
Best Local Similarity 100.0%; P:
Matches 13; Conservative 0;
 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
 Ferrara, Napoleone
Filvaroff, Ellen
 Godowski, Paul J.
 401 DADTAIINAEGGQ 413
 375 DADTAIINAEGGQ 387
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Baton, Dan L.
 TYPE: PRT
ORGANISM: Homo sapiens
 GENERAL INFORMATION:
 US-09-905-381A-84
 APPLICANT:
APPLICANT:
 APPLICANT:
 APPLICANT:
 APPLICANT
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 Gaps
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0
 3.1%; Score 13; DB 4; Length 398; 100.0%; Pred. No. 0.00081; tive 0; Mismatches 0; Indels
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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US-09-905-381A-84
IS-09-905-381A-84
; Sequence 84, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher J.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
 Gurney, Austin L.
Hillan, Kenneth, J.
 Gerritsen, Mary E
 Nicholas F
 Kljavin, Ivar J.
Mather, Jennie P.
 375 DADTAIINAEGGQ 387
 401 DADTAIINAEGGO 413
 Query Match
Best Local Similarity 100.
Matches 13; Conservative
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-064-84
 Goddard, A.
 Pan, James
 Paoni,
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
 APPLICANT
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Length 421;
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Crossk, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 2.1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
 SOFTWARE PATENTIN STATEM:
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
ATTORNEY/AGENT INFORMATION:
NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/POCKET NUMBER: 15270-002810US
TELECOMMUNICATION NUMBER: 15270-002810US
 ADDRESSEE: Townsend and Townsend and Crew LLP STREEF: Two Embarcadero Ctr., 8th Floor STREEF: San Francisco STATE: California
 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Ctr., 8th Floor STREET: San Francisco STATE: California
 3.1%; Score 13; DB 2; L
100.0%; Pred. No. 0.00085;
 100.0%; Pred. ...
 GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVANTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
 COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 1, Application US/08660531
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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415-326-2422
 285 LNKTDNGTYRCEA 297
 272 LNKTDNGTYRCEA 284
 13; Conservative
 TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
 MOLECULE TYPE: protein US-08-659-984A-1
 TYPE: amino acid
STRANDEDNESS: si
 linear
 Query Match
Best Local Similarity
Matches 13; Conserv
 ZIP: 94111-3834
 Patent No. 6221645
 TELEPHONE:
 COUNTRY:
 ò
 셤
 APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
 Gaps
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 Length 398;
 0; Indels
 Score 13; DB 4; Li
Pred. No. 0.00081;
 TILLE OF LIVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/09/06,618
CURRENT FILING DATE: 2001-07-16
PRIOR PELICATION NUMBER: PCT/USOO/04414
PRIOR PELICATION NUMBER: PCT/USOO/04414
PRIOR PELICATION NUMBER: PCT/USOO/04414
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
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PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-13
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PRIOR PELING DATE: 1999-11-29
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PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
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 Mismatches
 Sequence I, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
 Query Match 3.1%; Sco
Best Local Similarity 100.0%; P:
Matches 13; Conservative 0;
 Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 375 DADTAIINAEGGQ 387
 401 DADTAIINAEGGQ 413
 ; ORGANISM: Homo sapiens
US-09-906-618-84
 US-08-659-984A-1
 RESULT 70
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Gaps

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SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

COMPUTER: IBM PC OPERATING SYSTEM:

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Length 444;
 0; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY AGENT INFORMATION:
NAME: Heslin, James M.
 GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Keim, Pamela S.
TITLE OF INVENTION: Beca-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LIP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
 E: Townsend and Townsend and Crew LLP Two Embarcadero Ctr., 8th Floor
 Ouery Match 3.1%; Score 13; DB 2; L
Best Local Similarity 100.0%; Pred. No. 0.00089;
Matches 13; Conservative 0; Mismatches 0;
 REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
 ZIP: 34111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 5, Application US/08660531
Patent No. 6221645
 NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
 INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
 444 amino acids
 285 LNKTDNGTYRCEA 297
 STREET: TWO Embarcaue
CITY: San Francisco
STATE: California
COUNTRY: USA
 TYPE: amino acid
STRANDEDNESS: single
 TOPOLOGY: linear MOLECULE TYPE: protein
 CORRESPONDENCE ADDRESS:
 US-08-660-531-5
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 Gaps
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 3.1%; Score 13; DB 3; Length 421; 100.0%; Pred. No. 0.00085; tive 0; Mismatches 0; Indels
 3.1%; Score 13; DB 4; Length 432; 100.0%; Pred. No. 0.00087;
 RESULT 73
US-08-659-984A-5
Sequence 5. Application US/08659984A
Setent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukant, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase;
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
 0; Indels
 US-09-778-510-2

Sequence 2, Application US/09778510

Patent No. 6512095

GENERAL INFORMATION:
FILE REFERENCE:
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT PELLICATION NUMBER: US/09/778,510

CURRENT FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: PCT/US99/17906

PRIOR FILING DATE: 1999-08-05

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

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HEADTH: 432
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 15270-002210US
 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/660,531
 NAME: Hedlin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 1527(
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-326-240
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acids
TYPE: amino acids
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 285 LNKTDNGTYRCEA 297
 272 LNKTDNGTYRCEA 284
 401 DADTAIINAEGGQ 413
 409 DADTAIINAEGGQ 421
 Query Match 3.1
Best Local Similarity 100.
Matches 13; Conservative
 TOPOLOGY: linear MOLECULE TYPE: protein
 TYPE: PRT
ORGANISM: Homo sapien
 JS-09-778-510-2
 US-08-660-531-1
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RESULT 75

US-09-248-796A-22504

J Sequence 22504, Application US/09248796A

Sequence 22504, Application US/09248796A

Setent No. 6747137

GENERAL INFORMATION:

APPLICANT: Reith Wedistock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US 60/094,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-02-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 22504
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 15270-002210US
 Search completed: June 28, 2005, 10:22:32 Job time: 31.341 sec8
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Healin, James N.

REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 15270

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2422

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 444 amino acids

TYPE: amino acid

STRANDEDNESS: single

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: pinear

US-08-660-531-5
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 323 TITITITITE 335
 285 LNKTDNGTYRCEA 297
 372 rriririririri 384
 ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22504
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